

NT2RP3000232	2.7	2.7	8.01	7.1	5.52	5.92		
NT2RP3000233	1.55	1.55	6.01	6.9	5.91	4.06		
NT2RP3000234	3.23	3.23	9.09	12.89	10.4	11.41	*	+
NT2RP3000235	1.57	1.57	3.3	2.35	2.92	1.38		
NT2RP3000239	4.61	4.61	11.11	9.51	9.71	14.92		
NT2RP3000247	3.25	3.25	5.82	2.92	4.04	1.96		
NT2RP3000251	6.11	6.11	6.52	5.22	5.82	3.25		
NT2RP3000252	3.73	3.73	7.99	7.61	8.53	8.4		
NT2RP3000255	2.18	2.18	2.96	3.26	3.13	1.97		
NT2RP3000262	6.72	6.72	9.43	11.67	7.95	9.13		
NT2RP3000266	6.47	6.47	15.5	13.38	10.83	12.64		
NT2RP3000267	2.71	2.71	4.04	2.9	2.64	3.03		
NT2RP3000271	4.38	4.38	5.57	5.11	4.84	3.72		
NT2RP3000278	7.84	7.84	56.85	48.55	82.07	42.57		
NT2RP3000281	4.94	4.94	10.72	8.19	8.22	7.27		
NT2RP3000292	5.63	5.63	14.1	9.17	6.77	6.93		
NT2RP3000299	2.31	2.31	4.92	3.73	4.89	4.98		
NT2RP3000304	2.15	2.15	3.48	2.85	3.36	1.64		
NT2RP3000310	7.24	7.24	24.22	18.94	23.07	19.88		
NT2RP3000312	2.99	2.99	8.16	3.31	5.25	3.87		
NT2RP3000320	7.06	7.06	6.17	5.25	4.74	4.74	**	-
NT2RP3000322	11.05	11.05	18.76	32.59	45.13	46.95	**	+
NT2RP3000324	6.91	6.91	46.42	36.64	43.53	39.68		
NT2RP3000326	1.95	1.95	6.17	4.02	5.75	3.53		
NT2RP3000329	2.5	2.5	5.96	4.97	8.84	5.9		
NT2RP3000330	4.1	4.1	6.18	4.62	5.53	6.12		
NT2RP3000333	3.23	3.23	7.45	4.36	5.28	4.52		
NT2RP3000341	8.8	8.8	12.85	14.81	18.59	14.41	*	+
NT2RP3000344	2.73	2.73	3.75	2.69	3.54	2.29		

NT2RP3000345	3.09	3.09	3.57	1.65	1.97	2.66	*	-
NT2RP3000348	444.59	444.59	802.63	824.62	1016.01	909.68		
NT2RP3000350	4.25	4.25	10.34	4.57	9.28	6.4		
NT2RP3000359	9.53	9.53	24.44	8.54	11.36	16.62		
NT2RP3000361	7.5	7.5	11.12	7.89	7.81	8.95		
NT2RP3000366	7.38	7.38	14.27	9.52	11.84	16.13		
NT2RP3000378	2.67	2.67	5.75	3.92	4.78	2.47		
NT2RP3000384	5.42	5.42	10.88	9.52	13.1	9.28		
NT2RP3000389	12.54	12.54	21.49	23.95	35.02	27.32	*	+
NT2RP3000393	3.74	3.74	6.16	5.03	4.53	4.77		
NT2RP3000395	110.27	110.27	212	108.33	38.18	148.45		
NT2RP3000397	2.83	2.83	5.28	2.51	5.26	3.31		
NT2RP3000398	3.39	3.39	10.12	11.46	11.18	12.26		
NT2RP3000403	3.22	3.22	9.39	10.1	8.2	8.44		
NT2RP3000418	3.4	3.4	10.22	7.12	11.08	13.42		
NT2RP3000424	2.86	2.86	9.43	6.25	9.52	6.86		
NT2RP3000427	4.65	4.65	9.05	11.55	13.43	12.35	*	+
NT2RP3000431	2.05	2.05	4.93	3.43	3.26	3.93		
NT2RP3000433	2.63	2.63	8.65	5.65	7.09	6.65		
NT2RP3000436	11.39	11.39	20.93	18.76	9.35	18.86		
NT2RP3000439	1.4	1.4	3.61	2.54	3.56	2		
NT2RP3000441	3.88	3.88	7.4	7.56	7.92	6.39		
NT2RP3000444	3.31	3.31	7.29	2.36	3.25	2.2		
NT2RP3000448	4.45	4.45	10.15	4.05	6.54	3.93		
NT2RP3000449	2.84	2.84	4.59	3.1	3.94	2.93		
NT2RP3000451	1.76	1.76	5.12	3.7	5	2.96		
NT2RP3000456	1.69	1.69	5.48	4.23	6.67	4.21		
NT2RP3000460	18.87	18.87	36.67	24.52	25.24	26.25		
NT2RP3000471	3.14	3.14	6.49	2.74	4.98	5.84		

NT2RP3000477	19.96	19.96	23.67	28.98	17.78	32.78		
NT2RP3000478	5.86	5.86	8.95	5.21	8.98	2.6		
NT2RP3000481	5.48	5.48	5.76	2.76	3.61	1.52	**	-
NT2RP3000484	3.51	3.51	4.26	2.32	2.55	1.76	*	-
NT2RP3000487	1.77	1.77	7.4	5.07	4.03	4.97		
NT2RP3000512	3.29	3.29	17.7	15.17	15.9	14.52		
NT2RP3000523	13.05	13.05	30.74	31.75	27.83	34.4		
NT2RP3000526	3.07	3.07	7.38	5.18	6.31	4.64		
NT2RP3000527	2.83	2.83	6.5	3.76	7.25	5.03		
NT2RP3000531	2.9	2.9	7.71	5.11	5.51	4.69		
NT2RP3000532	5.74	5.74	5.6	5.75	8.39	4.26		
NT2RP3000542	6.23	6.23	8.1	7.21	7.3	6.39		
NT2RP3000554	8.81	8.81	15.22	13.78	10.56	14.95		
NT2RP3000561	1.21	1.21	3.51	3.11	2.76	2.25		
NT2RP3000562	1.84	1.84	3.5	3.7	3.87	3.23		
NT2RP3000578	1.56	1.56	2.54	2.54	3.37	2.36		
NT2RP3000582	1.26	1.26	4.66	2.24	2.52	0.41		
NT2RP3000584	2.82	2.82	6.52	3.2	2.5	2.02		
NT2RP3000586	4.08	4.08	4.59	3.28	3.9	2.87		
NT2RP3000590	5.69	5.69	4.61	3.78	4.35	2.57		
NT2RP3000592	1.8	1.8	2.99	2.97	2.75	3.15		
NT2RP3000596	2.27	2.27	4.89	4.5	3.33	3.03		
NT2RP3000599	1.67	1.67	3.07	3.88	4.98	3.82	*	+
NT2RP3000603	6.09	6.09	39.25	40.43	44.88	35.89		
NT2RP3000605	2.84	2.84	6.66	4.56	4.23	2.56		
NT2RP3000607	5.35	5.35	7.59	5.74	8.46	7.55		
NT2RP3000616	3.26	3.26	5.45	2.56	2.38	1.21		
NT2RP3000621	5.18	5.18	8.48	10.28	10.29	6.01		
NT2RP3000622	2.36	2.36	8.76	5.85	6.21	4.72		

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NT2RP3000624	1.53	1.53	3.19	3.97	3.06	2.78		
NT2RP3000628	2.44	2.44	8.04	10.27	7.85	5.58		
NT2RP3000631	4.71	4.71	14.95	22.82	16.45	14.2		
NT2RP3000632	2.35	2.35	5.5	7.78	8.91	5.91	*	+
NT2RP3000638	6.95	6.95	17.93	11.8	11.6	9.97		
NT2RP3000644	25.72	25.72	48.41	57.98	72.01	52.49	*	+
NT2RP3000645	5.85	5.85	10.48	9.84	12.55	8.43		
NT2RP3000652	3.39	3.39	5.34	6.22	5.9	7.74	*	+
NT2RP3000658	2.26	2.26	5.01	6.16	4.24	4.86		
NT2RP3000660	2.34	2.34	6.25	6.98	6.91	5.14		
NT2RP3000661	1.98	1.98	4.49	4.06	3.87	3.1		
NT2RP3000665	4.79	4.79	12.26	11.83	11.92	7		
NT2RP3000676	4.46	4.46	7.55	6.65	7.81	5.42		
NT2RP3000677	2.87	2.87	4.13	2.44	3.07	1.54		
NT2RP3000681	19.85	19.85	30.12	32.94	41.51	34.34	*	+
NT2RP3000683	2.68	2.68	9.67	6.69	7.09	6.69		
NT2RP3000685	1.7	1.7	2.5	3.63	2.36	3.44		
NT2RP3000690	2.77	2.77	3.29	3.82	3.75	2.72		
NT2RP3000698	10	10	22.49	25.66	17.08	27.43		
NT2RP3000708	3.45	3.45	5.5	8.17	9.22	8.56	**	+
NT2RP3000719	2.83	2.83	2.83	1.16	1.7	1.91	**	-
NT2RP3000721	5.63	5.63	24.61	23.43	39.76	21.55		
NT2RP3000728	3.33	3.33	2.57	1.4	1.64	1.05	**	-
NT2RP3000730	2.06	2.06	5.04	2.76	4.23	1.86		
NT2RP3000733	2.87	2.87	6.32	3.48	4.47	4.25		
NT2RP3000735	1.74	1.74	4.22	1.81	2.22	1.26		
NT2RP3000736	2.71	2.71	6.35	3.29	5.05	3.65		
NT2RP3000739	13.76	13.76	12.16	18.05	9.37	20.19		
NT2RP3000742	3.89	3.89	10.06	4.54	4.97	4.43		

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NT2RP3000753	2.29	2.29	3.9	2.17	2.65	6.3		
NT2RP3000759	9.07	9.07	15.99	11.11	17.14	23.05		
NT2RP3000789	1.58	1.58	5.76	4.89	4.23	3.69		
NT2RP3000815	1.91	1.91	5.92	4.49	5.57	3.08		
NT2RP3000818	4.35	4.35	11.29	6.64	10.49	8.27		
NT2RP3000820	9.01	9.01	18.49	18.58	20.1	16.9		
NT2RP3000821	2.13	2.13	4.83	3.28	5.19	2.02		
NT2RP3000825	1.87	1.87	4.94	1.92	1.47	2.27		
NT2RP3000826	4.04	4.04	13.59	10.86	13.8	12.94		
NT2RP3000836	5.33	5.33	11.61	11.55	14.11	13.3		
NT2RP3000838	319.2	319.2	741.74	710.2	743.55	1049.86		
NT2RP3000839	2.35	2.35	6.67	4.53	6.38	4.36		
NT2RP3000841	2.17	2.17	4.32	3.79	5.55	4.72		
NT2RP3000845	3.96	3.96	8.89	5.76	6.71	7.85		
NT2RP3000847	3.7	3.7	7.94	4.48	5.94	5.28		
NT2RP3000848	2.84	2.84	8.34	5.36	6.81	6.3		
NT2RP3000850	5.67	5.67	7.04	6.58	11.29	7.47		
NT2RP3000852	3.27	3.27	3.17	4.02	5.23	5.8	*	+
NT2RP3000859	2.76	2.76	7.12	4.46	7.11	8.43		
NT2RP3000861	2.58	2.58	10.51	6.13	10.36	6.43		
NT2RP3000862	15.29	15.29	24.16	16.36	9.81	23.13		
NT2RP3000865	1.58	1.58	4.26	2.54	4.21	1.83		
NT2RP3000866	2.08	2.08	5.03	2.37	3.59	5.22		
NT2RP3000868	2.2	2.2	7.09	3.04	3.84	2.28		
NT2RP3000869	3.54	3.54	11.36	9.61	15.76	7.9		
NT2RP3000871	1.75	1.75	3.79	1.81	3.24	1.94		
NT2RP3000875	0.99	0.99	4.25	2.57	2.71	3.64		
NT2RP3000895	2.54	2.54	5.56	2.84	3.55	4.93		
NT2RP3000900	6.01	6.01	11.86	11.3	7.7	14.58		

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NT2RP3000901	3.67	3.67	7.03	4.11	6.39	5.3		
NT2RP3000903	3.76	3.76	7.87	3.12	5.92	3.93		
NT2RP3000904	3.83	3.83	8.67	3.05	4.87	3.16		
NT2RP3000907	5.66	5.66	10.03	8.94	10.67	10.14		
NT2RP3000913	6.04	6.04	15.01	17.87	25.57	17.37	*	+
NT2RP3000917	7.64	7.64	16.58	7.66	6.56	13.51		
NT2RP3000919	1.99	1.99	5.15	3.5	4.3	2.68		
NT2RP3000921	2.26	2.26	7.67	4.88	4.07	6.51		
NT2RP3000942	2.66	2.66	3.89	2.68	4.12	2.63		
NT2RP3000968	70.24	70.24	87.55	105.89	110.05	115.38	**	+
NT2RP3000974	5.36	5.36	9.06	3.21	4.48	2.64		
NT2RP3000980	5.77	5.77	5.77	2.09	4.14	2.26	*	-
NT2RP3000984	3.17	3.17	7.65	6.33	6.68	4.58		
NT2RP3000994	2.09	2.09	4.88	2.4	3.14	3.37		
NT2RP3001001	1.46	1.46	3.45	3.75	4.14	1.31		
NT2RP3001004	3.37	3.37	6.52	3.51	5.63	5.01		
NT2RP3001007	4.46	4.46	9.87	10.02	10.62	6.81		
NT2RP3001012	2.78	2.78	5.4	4.99	6.83	3.65		
NT2RP3001042	4.74	4.74	5.52	2.99	5.18	1.38		
NT2RP3001044	6.26	6.26	7.12	7.16	6.76	4.92		
NT2RP3001048	2.52	2.52	3.01	3.5	3.93	2.42		
NT2RP3001050	1.79	1.79	4.99	4.68	5.94	4.7		
NT2RP3001055	6.55	6.55	15.6	16.48	12.44	20.49		
NT2RP3001057	2.79	2.79	10.84	5.57	6.05	5.67		
NT2RP3001061	3.18	3.18	6.57	5.03	7.85	5.42		
NT2RP3001069	6.03	6.03	14.95	18.49	17.53	15.08		
NT2RP3001074	4.2	4.2	7.22	8.72	10	6.64		
NT2RP3001078	5.11	5.11	7.29	7.51	8.72	5.18		
NT2RP3001081	4	4	5.72	4.65	5.19	3.52		

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NT2RP3001084	2.7	2.7	7.92	6.85	6.71	6.23		
NT2RP3001095	1.57	1.57	3.88	3.69	3.68	3.42		
NT2RP3001096	2.52	2.52	7.33	16.78	8.08	18.7	*	+
NT2RP3001097	3.65	3.65	4.28	6.42	8.11	8.5	**	+
NT2RP3001107	3.69	3.69	4.79	3.77	4.03	2.37		
NT2RP3001109	3.2	3.2	5.5	6.01	9.56	7.26	*	+
NT2RP3001111	4.58	4.58	4.19	3.41	3.51	2.29	*	-
NT2RP3001112	12.61	12.61	18.48	25.73	29.85	24.61	**	+
NT2RP3001113	1.21	1.21	2.59	2.47	3.24	2.19		
NT2RP3001115	1.51	1.51	3.32	2.57	3.77	2.19		
NT2RP3001116	1.01	1.01	2.66	2.55	4.4	2.91		
NT2RP3001119	3.69	3.69	6.75	9.07	6.67	5.44		
NT2RP3001120	5.02	5.02	8.24	8.85	7.87	6.71		
NT2RP3001126	6.16	6.16	12.34	17.84	19.66	17.49	**	+
NT2RP3001127	6.93	6.93	6.76	4.79	7.63	6.36		
NT2RP3001133	3.95	3.95	4.95	3.95	4.16	3.62		
NT2RP3001140	1.46	1.46	2.43	3.21	2.38	6.71		
NT2RP3001147	3.16	3.16	6.96	16.08	14.49	13.84	**	+
NT2RP3001150	1.99	1.99	4.32	4.06	5.68	3.76		
NT2RP3001152	1.7	1.7	3.29	3.15	3.62	2.51		
NT2RP3001155	2.95	2.95	4.35	3.68	4.35	3.58		
NT2RP3001156	4.38	4.38	6.57	2.91	5.72	5.67		
NT2RP3001159	5.38	5.38	10.5	7.87	10.86	7.25		
NT2RP3001170	7.38	7.38	5.96	6.12	8.01	4.56		
NT2RP3001176	3.49	3.49	10.75	6.27	8.23	9.49		
NT2RP3001195	2.35	2.35	4.81	6.79	5.79	6.22	*	+
NT2RP3001209	3.47	3.47	5.98	5.96	4.64	5.22		
NT2RP3001214	1.63	1.63	4.91	3.44	3.87	3.81		
NT2RP3001216	3.58	3.58	6.38	6.25	4.33	3.6		

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NT2RP3001221	3.33	3.33	4.27	3.07	3.06	1.79		
NT2RP3001226	5.96	5.96	29.04	21.93	31.45	17.76		
NT2RP3001230	3.17	3.17	2.41	3.09	3.14	1.56		
NT2RP3001232	1.8	1.8	4.72	2.36	3.7	2.85		
NT2RP3001236	1.68	1.68	4.3	1.7	3.26	1.47		
NT2RP3001239	1.58	1.58	5.21	2.81	4.31	2.01		
NT2RP3001240	12.83	12.83	22.18	23.01	24.3	14.46		
NT2RP3001245	3.53	3.53	9.88	4.08	6.36	3.39		
NT2RP3001253	2.79	2.79	4.87	3.34	4.53	5.21		
NT2RP3001259	6.62	6.62	11.97	12.33	15.62	11.83		
NT2RP3001260	3.74	3.74	5.15	3.45	5.44	3.97		
NT2RP3001264	2.2	2.2	10.29	5.99	6.92	6.38		
NT2RP3001268	2.25	2.25	7.18	4.93	4.72	4.35		
NT2RP3001271	7.06	7.06	16.29	13.07	12.27	14.24		
NT2RP3001272	3.73	3.73	12.45	9.43	11.09	10.15		
NT2RP3001274	6.08	6.08	8.09	6.72	6.35	5.11		
NT2RP3001275	9.78	9.78	11.58	21.56	26.84	22.59	**	+
NT2RP3001280	3.39	3.39	5.5	3.58	5.24	4.18		
NT2RP3001281	3.15	3.15	3.89	3.08	4.48	5.14		
NT2RP3001288	49.31	49.31	103.24	124.07	142.92	164.41	*	+
NT2RP3001297	6.39	6.39	42.01	37.04	42.75	41.14		
NT2RP3001300	5.23	5.23	15.92	16.78	17.41	17.76		
NT2RP3001301	2.91	2.91	6.59	3.96	4.58	3.9		
NT2RP3001307	1.76	1.76	7.67	2.07	2.81	2.06		
NT2RP3001310	11.55	11.55	17.04	25.54	26.07	28.13	**	+
NT2RP3001318	2.11	2.11	3.4	2.49	3.37	2.37		
NT2RP3001322	3.58	3.58	5.23	2.62	3.84	5.48		
NT2RP3001325	2.7	2.7	8.39	5.82	6.82	5.58		
NT2RP3001338	2.67	2.67	6.19	4.1	4.21	3.5		

NT2RP3001339	2.53	2.53	5.64	3.08	4.89	2.91
NT2RP3001340	2.9	2.9	8.42	6.36	7.07	5.79
NT2RP3001341	2.26	2.26	6.97	5.1	5.62	4.73
NT2RP3001354	3.22	3.22	9.77	4.28	6.93	9.35
NT2RP3001355	1.9	1.9	5.41	2.65	3.82	2.74
NT2RP3001356	2	2	5.34	2.59	3.2	3.55
NT2RP3001359	1.09	1.09	4.05	1.63	2.5	1.75
NT2RP3001364	2.34	2.34	5.31	3.26	6.67	2.67
NT2RP3001373	1.12	1.12	3.22	2.1	3.74	1.71
NT2RP3001374	1.9	1.9	4.17	3.18	3.92	3.1
NT2RP3001383	3.84	3.84	8.96	3.92	6.65	3.85
NT2RP3001384	4.11	4.11	9.47	3.54	4.46	2.41
NT2RP3001388	3.98	3.98	8.79	9.48	10.99	9.4
NT2RP3001392	4.61	4.61	6.19	3.91	6.14	3.23
NT2RP3001396	1.7	1.7	6.39	4.04	4.66	4.53
NT2RP3001398	2.51	2.51	6.55	3.85	7.05	2.94
NT2RP3001399	4.91	4.91	20.67	15.86	16.12	12.44
NT2RP3001402	6.46	6.46	36.36	33.37	41.61	39.66
NT2RP3001407	6.96	6.96	19.16	13.69	17.65	12.35
NT2RP3001416	7.92	7.92	15.88	13.02	18.3	14.72
NT2RP3001420	5.33	5.33	6.4	3.27	3.64	1.8 *
NT2RP3001425	3.73	3.73	4.92	4.74	5.67	3.15
NT2RP3001426	2.39	2.39	6.08	5.45	4.45	5.11
NT2RP3001427	1.82	1.82	5.61	3.46	2.89	3.59
NT2RP3001428	2.42	2.42	6.29	5.69	4.81	3.77
NT2RP3001429	3.08	3.08	5.91	4.15	7.37	4.73
NT2RP3001432	2.14	2.14	6.61	3.72	4.44	3.58
NT2RP3001439	4.14	4.14	6.39	5.87	7.27	4.41
NT2RP3001441	6.45	6.45	12.63	11.13	14.61	11.2

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NT2RP3001446	4.99	4.99	4.99	4.64	5.22	4.39		
NT2RP3001447	2.72	2.72	5.21	6.64	5.14	6.33		
NT2RP3001449	3.95	3.95	11.85	16.9	14.57	13.16	*	+
NT2RP3001453	1.84	1.84	3.66	3.5	4.4	2.81		
NT2RP3001457	3.86	3.86	7.71	6.06	6.93	5.5		
NT2RP3001459	2.39	2.39	6.03	2.64	2.78	1.17		
NT2RP3001463	2.77	2.77	6.74	5.93	5.94	3.98		
NT2RP3001466	2.87	2.87	3.56	1.19	1.43	0.78	**	-
NT2RP3001472	5.74	5.74	4.02	3.7	4.85	4.32		
NT2RP3001475	3.54	3.54	7.61	6.91	6.65	7.39		
NT2RP3001479	2.54	2.54	6.66	4.37	5.69	5.16		
NT2RP3001490	3.18	3.18	9.26	4.4	6.02	5.21		
NT2RP3001492	4.36	4.36	7.84	7.59	7.08	5.72		
NT2RP3001495	4.14	4.14	3.85	2.75	2.92	1.76	*	-
NT2RP3001497	5.8	5.8	6.32	7.47	9.96	6.8		
NT2RP3001501	5.36	5.36	5.52	3.12	4.49	3.43	*	-
NT2RP3001527	4.89	4.89	6.71	4.9	5.14	3.52		
NT2RP3001529	1.51	1.51	3.5	4.12	3.95	4.18	*	+
NT2RP3001538	1.78	1.78	6.2	6.93	7.81	6.23		
NT2RP3001539	5.81	5.81	14.5	15.19	14.15	16.47		
NT2RP3001542	1.52	1.52	5.26	4.23	4.38	2.13		
NT2RP3001549	4.75	4.75	11.12	14.57	11.37	13.44		
NT2RP3001554	3.06	3.06	6.16	6.37	7.5	5.05		
NT2RP3001560	4.96	4.96	5.73	4.67	6.35	2.36		
NT2RP3001561	8.85	8.85	20.77	20.38	27.2	17.15		
NT2RP3001564	1.54	1.54	8.24	6.43	4.53	5.96		
NT2RP3001568	2.1	2.1	7.68	11.84	10.29	8.49	*	+
NT2RP3001575	3.94	3.94	7.24	6.39	6.97	6.16		
NT2RP3001580	1.78	1.78	4.49	4.35	3.8	3.11		

NT2RP3001587	4.38	4.38	8.74	10.75	10.04	7.77		
NT2RP3001589	3.17	3.17	8.21	5.6	7.79	4.36		
NT2RP3001592	4.52	4.52	21.6	19	32.62	14.54		
NT2RP3001607	3.42	3.42	1.86	1.59	2.8	1		
NT2RP3001608	1.05	1.05	3.59	2.41	1.73	2.31		
NT2RP3001613	3.08	3.08	2.77	3.89	2.91	3.99		
NT2RP3001619	4.31	4.31	8.15	7.69	6.45	7.62		
NT2RP3001621	1.18	1.18	2.69	2.39	2.28	2.02		
NT2RP3001629	2.58	2.58	3.28	2.68	2.41	1.7		
NT2RP3001630	3.39	3.39	4.56	1.67	2.02	1.17	**	-
NT2RP3001631	9.01	9.01	14.34	18.65	21.16	15.24	*	+
NT2RP3001634	4	4	5.29	4.51	6.89	5.11		
NT2RP3001642	3.71	3.71	7.45	5.77	4.41	5.09		
NT2RP3001646	1.56	1.56	3.7	0.89	2.79	0.95		
NT2RP3001650	2.06	2.06	5.81	4.86	7.03	2.08		
NT2RP3001667	4.66	4.66	11.91	6.93	9.95	5.13		
NT2RP3001671	2.28	2.28	7.98	7.7	4.69	5.99		
NT2RP3001672	1.33	1.33	4.55	1.66	1.47	1.72		
NT2RP3001676	2.18	2.18	5.02	2.35	3.14	2.24		
NT2RP3001678	2.86	2.86	9.24	5.12	5.14	6.03		
NT2RP3001679	6.12	6.12	9.19	6.74	4.73	6.91		
NT2RP3001682	1.82	1.82	5.09	4.45	6.18	3.35		
NT2RP3001685	3.02	3.02	6.74	3.52	6.53	3.01		
NT2RP3001688	3.01	3.01	9.42	5.46	8.21	6.43		
NT2RP3001690	3.21	3.21	4.87	2.91	3.54	2.99		
NT2RP3001693	5.69	5.69	10.93	16.59	18.34	16.12	**	+
NT2RP3001696	2.28	2.28	3.63	1.77	3.68	3.39		
NT2RP3001698	35.35	35.35	79.65	85.09	91.88	105.32		
NT2RP3001708	4.82	4.82	8.78	6.34	6.95	9.01		

NT2RP3001712	8.69	8.69	16.06	10.22	14.19	13		
NT2RP3001716	1.44	1.44	5.45	2.14	3.42	2.31		
NT2RP3001724	2.75	2.75	6	4.08	4.54	2.63		
NT2RP3001727	11.73	11.73	38.73	39.17	49.36	31.26		
NT2RP3001729	3.36	3.36	4.7	5.69	6.55	3.06		
NT2RP3001730	12.54	12.54	26.52	12.53	19.94	16.4		
NT2RP3001733	1.46	1.46	3.04	2.09	3.7	1.62		
NT2RP3001737	3.02	3.02	7.12	4.62	5.49	2.78		
NT2RP3001738	1.59	1.59	8.22	3.38	6.01	3.03		
NT2RP3001739	3.26	3.26	5.25	5.63	6.1	2.51		
NT2RP3001742	2.54	2.54	5.36	3.86	4.55	4.03		
NT2RP3001751	3.61	3.61	11.54	9.94	12.82	8.76		
NT2RP3001752	2.58	2.58	7.01	2.1	3.59	2.76		
NT2RP3001753	5.73	5.73	9.48	10.83	15.3	13.69	*	+
NT2RP3001754	4.63	4.63	9.08	5.86	3.73	5.33		
NT2RP3001756	4.66	4.66	7.36	9.37	5.75	8.03		
NT2RP3001764	2.1	2.1	3.76	2.54	4.25	2.49		
NT2RP3001771	2.63	2.63	3.2	1.52	4.14	1.22		
NT2RP3001777	2.59	2.59	5.99	3.25	5.19	3.26		
NT2RP3001782	3.52	3.52	14.68	6.47	6.63	6.47		
NT2RP3001792	2.27	2.27	4.35	2.91	4.09	1.35		
NT2RP3001799	1.76	1.76	5.18	5.71	6.36	5.68		
NT2RP3001819	1.36	1.36	4.54	1.7	1.52	2.06		
NT2RP3001829	21.63	21.63	43.14	35.64	17.14	24.87		
NT2RP3001836	7.31	7.31	10.67	15.24	7.26	11.37		
NT2RP3001839	18.86	18.86	31.77	31.97	19.23	17.53		
NT2RP3001844	4.15	4.15	11.37	8.33	9.59	8.54		
NT2RP3001848	9.61	9.61	52.04	44.52	74.75	43.87		
NT2RP3001854	6.41	6.41	11.29	12.86	16.75	13.26	*	+

NT2RP3001855	2.27	2.27	3.94	1.87	1	1.74		
NT2RP3001857	3.1	3.1	5.22	5.13	5.6	3.33		
NT2RP3001858	1.53	1.53	4.45	4.41	6.04	2.97		
NT2RP3001861	7.35	7.35	16.34	11.85	14.46	10.42		
NT2RP3001866	4.35	4.35	9.63	5.52	10.42	7.93		
NT2RP3001871	4.82	4.82	6.34	5.55	6.38	4.55		
NT2RP3001874	6.8	6.8	9.73	7.72	11.19	6.14		
NT2RP3001878	5.98	5.98	6.35	4.59	6.89	5.02		
NT2RP3001885	3.21	3.21	5.3	5.65	5.25	4.42		
NT2RP3001896	1.64	1.64	3.49	3.37	2.13	2.02		
NT2RP3001898	9.03	9.03	17.69	14.71	8.69	11.94		
NT2RP3001899	3.21	3.21	7.33	4.52	6.9	5.81		
NT2RP3001901	4.58	4.58	9.18	8.19	9.44	9.21		
NT2RP3001915	4.84	4.84	11.12	14.09	15.67	14.04	*	+
NT2RP3001926	2.8	2.8	4.88	2.47	2.45	1.65		
NT2RP3001929	3.74	3.74	4.06	2.56	3.38	0.86		
NT2RP3001931	4.63	4.63	5.26	3.9	5.62	2.98		
NT2RP3001938	2.27	2.27	5.53	4.93	3.93	4.75		
NT2RP3001943	3.27	3.27	5.36	5.77	6.5	5.56		
NT2RP3001944	1.77	1.77	3.72	4.08	5.91	4.34		
NT2RP3001945	4.25	4.25	12.2	11.86	11.78	6.11		
NT2RP3001947	2.94	2.94	5.89	4.06	5.41	3.4		
NT2RP3001949	4.21	4.21	8.9	10.49	11.08	8.08		
NT2RP3001952	23.54	23.54	43.64	48.59	88.56	41.86		
NT2RP3001954	5.06	5.06	3.68	4.34	4.79	1.85		
NT2RP3001956	4.97	4.97	9.44	7.76	8.22	6.29		
NT2RP3001967	3.78	3.78	7.74	6.7	5.37	5.66		
NT2RP3001969	1.71	1.71	2.91	4.05	4.39	3.62	*	+
NT2RP3001976	2.25	2.25	4.67	6.22	6.25	4.84	*	+

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NT2RP3001986	3.55	3.55	3.88	3.43	2.82	2.19		
NT2RP3001989	3.76	3.76	5.23	2.86	3.58	2.54		
NT2RP3002002	6.68	6.68	9.47	6.25	8.85	3.86		
NT2RP3002004	5.02	5.02	6.23	3.79	5.74	3.55		
NT2RP3002007	1.29	1.29	2.3	3.46	4.05	1.69		
NT2RP3002014	1.38	1.38	6.23	6.04	6.24	4.21		
NT2RP3002015	3.61	3.61	10.33	14.17	9.94	8.85		
NT2RP3002033	1.54	1.54	5.03	7.29	5.03	3.65		
NT2RP3002045	1.89	1.89	5.29	4.67	4.36	2.5		
NT2RP3002054	5.26	5.26	8.12	6.27	9.17	5.42		
NT2RP3002056	5.67	5.67	5.52	4.24	4.24	2.7	*	-
NT2RP3002057	4.35	4.35	3.5	2.87	2.41	0.81	*	-
NT2RP3002061	4.71	4.71	13.94	8.64	8.9	10.74		
NT2RP3002062	0.8	0.8	2.42	3.58	3.26	1.11		
NT2RP3002063	5.61	5.61	10.31	9.29	9.3	7.31		
NT2RP3002064	2.6	2.6	3.37	2.72	3.74	2.52		
NT2RP3002071	1.6	1.6	3.91	1.99	3.29	1.45		
NT2RP3002073	6.47	6.47	9.55	10.45	11.13	8.64		
NT2RP3002074	4.2	4.2	7.25	6.33	7.82	4.24		
NT2RP3002075	7.58	7.58	11.93	21.64	30.17	18.15	*	+
NT2RP3002077	3.81	3.81	5.95	2.48	3.05	2.78		
NT2RP3002081	4.25	4.25	7.55	13.22	12.62	11.13	**	+
NT2RP3002086	3.86	3.86	9.77	5.59	8.66	6.95		
NT2RP3002094	7.34	7.34	10.28	13.84	14.79	11.67	*	+
NT2RP3002096	1.98	1.98	4.53	1.28	3.12	1.73		
NT2RP3002097	3.77	3.77	6.16	6.1	8.34	6.88		
NT2RP3002098	1.61	1.61	4.3	1.04	1.8	1.46		
NT2RP3002102	2	2	4.86	3.11	3.4	3.16		
NT2RP3002106	2.74	2.74	4.98	2.83	4.9	2.51		

NT2RP3002108	3.69	3.69	7.8	3.11	3.39	3.15		
NT2RP3002109	12.49	12.49	32.04	31.61	27.15	25.12		
NT2RP3002110	36.38	36.38	54.93	55.24	58.94	46.55		
NT2RP3002113	11.15	11.15	13.99	10.66	15.22	11.44		
NT2RP3002120	2.22	2.22	4.42	2.31	4.13	2.7		
NT2RP3002121	5.93	5.93	14.39	13.38	14.39	15.06		
NT2RP3002126	34.03	34.03	108.96	121.18	130.55	142.49	*	+
NT2RP3002128	4.06	4.06	8.23	3.36	6.87	3.92		
NT2RP3002130	8.29	8.29	18.59	11.69	10.7	14.03		
NT2RP3002133	14.24	14.24	18.31	10.06	8.3	19.51		
NT2RP3002136	10.32	10.32	15.42	12.49	17.64	17.49		
NT2RP3002140	3.13	3.13	6.35	6.15	3.9	4.16		
NT2RP3002142	16.86	16.86	50.85	56.54	81.25	62.65	*	+
NT2RP3002146	4	4	7.22	5.14	9.31	6.56		
NT2RP3002147	3.8	3.8	10.45	6.06	7.4	6.2		
NT2RP3002151	5.62	5.62	10.64	6.27	4.43	7.33		
NT2RP3002155	1.62	1.62	3.27	2.01	4.98	0.8		
NT2RP3002156	3.15	3.15	4.82	2.55	4.08	2.42		
NT2RP3002160	1.57	1.57	3.43	1.36	3.43	1.56		
NT2RP3002163	20.86	20.86	55.1	35.13	44.03	32.6		
NT2RP3002165	4.17	4.17	3.67	6.21	8.31	4.86		
NT2RP3002166	4.04	4.04	10.53	7.76	8.79	5.58		
NT2RP3002173	2.24	2.24	5.75	2.95	3.34	3.53		
NT2RP3002174	8.41	8.41	15.8	13.21	7.82	14.77		
NT2RP3002181	1.1	1.1	3.46	1.87	3.51	1.61		
NT2RP3002185	2.69	2.69	4.51	2.94	4.35	2.61		
NT2RP3002193	5.51	5.51	13.38	16.39	15.35	11.36		
NT2RP3002204	5.66	5.66	12.49	17.04	24.14	18.95	*	+
NT2RP3002244	4.03	4.03	8.29	5.28	6.11	4.8		

NT2RP3002248	5.42	5.42	11.1	8.19	11.78	6.52
NT2RP3002253	2.61	2.61	9.3	9.66	11.26	6.18
NT2RP3002255	11.07	11.07	26.56	22.78	11.53	20.93
NT2RP3002264	3.06	3.06	5.54	5.88	7.37	4.07
NT2RP3002267	1.26	1.26	4.33	3.1	4.65	1.82
NT2RP3002273	7.51	7.51	12.98	10.15	13.8	12.11
NT2RP3002276	5.22	5.22	7.89	3.08	7.68	3.48
NT2RP3002281	6.37	6.37	6.83	7.45	8.46	3.44
NT2RP3002286	3	3	4.79	3.54	4.34	3.88
NT2RP3002297	10.62	10.62	29.36	22.26	20.57	23.93
NT2RP3002301	5.73	5.73	13.24	9.47	7.55	6.21
NT2RP3002303	3.01	3.01	6.39	5.29	6.65	4.58
NT2RP3002304	2.66	2.66	7.17	6.3	7.3	4.91
NT2RP3002309	2.3	2.3	7.18	9.26	13	4.39
NT2RP3002311	4.54	4.54	6.67	3.17	4.02	1.83
NT2RP3002315	15.27	15.27	20.91	25.82	33.13	21.82
NT2RP3002319	2.37	2.37	5.06	3.07	3.51	2.38
NT2RP3002324	8.97	8.97	61.42	49.85	51.23	55.4
NT2RP3002330	4.74	4.74	8.33	10.31	8.24	8.15
NT2RP3002333	5.13	5.13	14.32	13.14	13.65	8.12
NT2RP3002337	2.61	2.61	5.14	4.8	5.57	4.87
NT2RP3002342	5.16	5.16	11.56	5.52	7.51	6.43
NT2RP3002343	3.38	3.38	7.29	5.8	7.03	4.13
NT2RP3002351	4.32	4.32	4.55	4.38	3.9	2.55
NT2RP3002352	6.3	6.3	8.01	4.4	6.76	4.31
NT2RP3002353	3	3	4.85	4.87	6.18	5.9
NT2RP3002362	5	5	11.74	15.86	11.03	10.49
NT2RP3002363	2.41	2.41	3.67	5.53	6.17	2.32
NT2RP3002377	2.61	2.61	5.47	6.8	7.31	4.73

NT2RP3002377	4.47	4.47	7.73	11.4	5.31	7.09		
NT2RP3002394	5.58	5.58	7.35	7.82	10.17	4.46		
NT2RP3002397	3.77	3.77	4.81	2.7	3.12	1.68	*	-
NT2RP3002399	4.61	4.61	7.69	14.65	13.02	16.16	**	+
NT2RP3002402	2.84	2.84	6.99	8.94	8.7	6.99		
NT2RP3002404	2.88	2.88	5.6	3.12	3.73	1.83		
NT2RP3002410	4.85	4.85	15.65	17.05	14.13	10.65		
NT2RP3002411	2.98	2.98	5.68	3.7	5.29	2.85		
NT2RP3002414	5.62	5.62	9.35	10.28	6.81	7.92		
NT2RP3002430	5.11	5.11	14.63	18.24	19.29	14.51		
NT2RP3002448	5.4	5.4	4.6	4.35	5.25	3.62		
NT2RP3002454	7.3	7.3	15.31	12.9	12.71	9.32		
NT2RP3002455	4.62	4.62	12.11	14.31	9.11	13.25		
NT2RP3002456	3.21	3.21	7.75	7.09	6.57	5.9		
NT2RP3002462	2.79	2.79	4.16	4.94	6.17	4.79	*	+
NT2RP3002469	3.84	3.84	6.38	9.24	6.78	8.07	*	+
NT2RP3002470	6.7	6.7	14.71	17.86	16.99	13.48		
NT2RP3002484	4.01	4.01	6.86	6.81	8.01	4.59		
NT2RP3002491	3.62	3.62	4.1	2.05	2.51	1.46	**	-
NT2RP3002494	79.24	79.24	131.02	118.47	163.2	105.2		
NT2RP3002497	1.07	1.07	1.57	2.37	1.39	1.37		
NT2RP3002500	1.23	1.23	1.13	2.72	2.02	2.07	**	+
NT2RP3002501	5.25	5.25	8.49	8.45	8.11	9.69		
NT2RP3002512	2.85	2.85	3.97	3.3	2.74	3.57		
NT2RP3002529	3.94	3.94	7.5	6.59	5.14	5.85		
NT2RP3002533	7.95	7.95	10.26	9.79	10.51	8.18		
NT2RP3002539	4.39	4.39	4.32	5.66	6.61	2.85		
NT2RP3002540	5.24	5.24	5.5	3.48	4.76	3.65	*	-
NT2RP3002543	3.44	3.44	7.17	4.93	6.21	5.31		

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NT2RP3002545	7.34	7.34	7.46	5.17	5.52	6.8	*	-
NT2RP3002549	3.27	3.27	7.8	4.98	6.11	4.54		
NT2RP3002552	3.05	3.05	6.04	4.17	5.81	4.06		
NT2RP3002558	9.54	9.54	9.39	9.93	4.26	11.27		
NT2RP3002565	1.94	1.94	4.83	1.73	2.48	1.52		
NT2RP3002566	3.62	3.62	7.02	4.03	8.51	3.65		
NT2RP3002571	2.53	2.53	4.85	3.77	5.41	3.74		
NT2RP3002572	2.98	2.98	5.28	4.75	4.74	5.21		
NT2RP3002573	4.31	4.31	11.38	7.06	9.48	7.06		
NT2RP3002577	1.57	1.57	4.61	2.71	2.32	1.9		
NT2RP3002579	3.92	3.92	6.41	4.03	7.75	11.16		
NT2RP3002582	5.02	5.02	7.17	11.51	14.07	8.45	*	+
NT2RP3002587	1.9	1.9	3.13	2.68	3.04	1.97		
NT2RP3002590	3.16	3.16	5.65	9.06	10.39	8.06	**	+
NT2RP3002602	3.02	3.02	4.24	3.95	5.85	3.77		
NT2RP3002603	71.53	71.53	214.41	268.41	257.84	298.26	*	+
NT2RP3002621	1.95	1.95	3.42	2.13	5.13	1.85		
NT2RP3002622	2.63	2.63	7.38	3.7	7.36	4.67		
NT2RP3002624	2.29	2.29	7.4	4.04	4.9	3.64		
NT2RP3002628	6.36	6.36	16.17	19.57	22.15	16.21		
NT2RP3002629	8.96	8.96	13.58	15.4	18.26	15.57	*	+
NT2RP3002631	1.95	1.95	1.67	0.91	1.65	1.69		
NT2RP3002647	4.04	4.04	4.01	5.44	7.16	4.6		
NT2RP3002649	2.99	2.99	5.99	2.15	5.84	3.23		
NT2RP3002650	3.32	3.32	11.62	4.98	8.53	6.88		
NT2RP3002652	2.27	2.27	6.59	4.91	6.83	4.25		
NT2RP3002654	3.05	3.05	7.5	5.58	5.4	4.2		
NT2RP3002657	14.14	14.14	13.87	17.27	26.08	18.87		
NT2RP3002659	1.92	1.92	6.01	3.91	5.78	3.47		

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NT2RP3002660	3.09	3.09	4.84	3.77	7.72	3.52		
NT2RP3002663	2.39	2.39	3.33	2.54	3.13	2.84		
NT2RP3002664	2.74	2.74	7.28	3.65	2.56	2.13		
NT2RP3002667	2.92	2.92	6.59	6.63	5.46	5.35		
NT2RP3002671	2.37	2.37	5.02	3.91	5.52	4.11		
NT2RP3002682	6.34	6.34	20.62	14.37	17.64	21.7		
NT2RP3002684	4	4	6.34	3.32	6.16	3.18		
NT2RP3002687	3.25	3.25	6.22	2.7	3.87	6.41		
NT2RP3002688	3.22	3.22	4.98	2.63	3.91	2.61		
NT2RP3002698	2.2	2.2	3.99	3.07	4.28	2.38		
NT2RP3002701	2.93	2.93	6.73	3.45	3.07	3.6		
NT2RP3002705	2.17	2.17	8.01	4.36	8.76	4.72		
NT2RP3002708	3.69	3.69	9.88	5.64	7.34	4.9		
NT2RP3002711	6.67	6.67	7.85	7.77	7.56	6.69		
NT2RP3002712	55.99	55.99	75.28	146.74	168.42	130.64	**	+
NT2RP3002713	4.31	4.31	7.06	2.66	2.19	1.87	*	-
NT2RP3002721	5.77	5.77	10.06	11.06	16.94	8.96		
NT2RP3002722	7.11	7.11	10.08	7.8	6.45	6.62		
NT2RP3002723	42.31	42.31	75.85	60.39	46.74	58.76		
NT2RP3002737	8.35	8.35	18.1	10.97	11.6	9.37		
NT2RP3002738	1.9	1.9	6.13	3.09	5.23	3.54		
NT2RP3002742	14.11	14.11	23.22	30.39	28.27	27.66	*	+
NT2RP3002744	4.09	4.09	5.24	3.92	4.92	1.71		
NT2RP3002756	5.8	5.8	5.8	3.19	2.68	1.55	**	-
NT2RP3002757	12	12	17.79	19.76	24.24	19.75	*	+
NT2RP3002758	21.11	21.11	42.35	44.47	63.91	36.38		
NT2RP3002762	5.07	5.07	8.82	7.21	7.43	7.76		
NT2RP3002763	1.62	1.62	4.86	3.76	4.99	2.18		
NT2RP3002770	1.78	1.78	5.14	3.46	3.7	2.93		

NT2RP3002771	17.04	17.04	39.53	24.93	40.21	34.4		
NT2RP3002785	2.42	2.42	5.45	3.36	4.09	2.66		
NT2RP3002790	4.65	4.65	4.22	3.16	3.57	2.33	*	-
NT2RP3002799	4.73	4.73	6.33	3.42	2.7	1.43	*	-
NT2RP3002801	4.14	4.14	3.59	3.6	3.22	2.49		
NT2RP3002802	2.31	2.31	6.3	6.78	5.43	4.4		
NT2RP3002810	2.98	2.98	5.41	7.44	12.32	13.27	*	+
NT2RP3002818	1.5	1.5	2.44	2.18	4.16	2.47		
NT2RP3002821	12.8	12.8	33.14	26.1	35.81	23.02		
NT2RP3002823	3.85	3.85	8.98	4.65	5.92	3.87		
NT2RP3002825	5.47	5.47	13.04	13.47	19.19	7.12		
NT2RP3002829	5.37	5.37	6.25	4.75	4.89	3.8		
NT2RP3002831	4.01	4.01	6.13	9.07	8.77	5.19		
NT2RP3002836	7.33	7.33	19.42	11.56	16.91	20.66		
NT2RP3002845	4.17	4.17	6.63	7.87	8.6	8.45	*	+
NT2RP3002852	3.37	3.37	7.57	7.8	8.72	8.21		
NT2RP3002861	3.82	3.82	6.4	7.34	7.35	4.63		
NT2RP3002869	3.66	3.66	3.26	2.49	1.86	0.49	*	-
NT2RP3002874	11.25	11.25	21.44	25.33	31.95	25.54	*	+
NT2RP3002876	6.98	6.98	11.06	12.8	14.93	14.39	*	+
NT2RP3002877	4.7	4.7	5.96	3.3	5.24	2.53		
NT2RP3002887	0.47	0.47	3.42	2.81	3.53	3.91		
NT2RP3002900	6.46	6.46	19.64	21.86	21.54	22.3		
NT2RP3002902	4.01	4.01	10.25	11.72	8.52	8.06		
NT2RP3002909	2.61	2.61	6.19	6.67	5.38	3.93		
NT2RP3002911	3.05	3.05	3.68	3.09	3.73	2.24		
NT2RP3002948	4.09	4.09	4.81	2.73	4.44	2.07		
NT2RP3002953	3.85	3.85	3.6	2.27	2.52	0.84	*	-
NT2RP3002955	6.55	6.55	3.78	1.93	2.47	0.86	*	-

NT2RP3002958	5.85	5.85	11.4	16.5	10.57	16.64		
NT2RP3002969	4.28	4.28	8.27	12.91	7.49	7.33		
NT2RP3002972	3.55	3.55	4.82	4.41	6.18	2.29		
NT2RP3002978	1.48	1.48	2.99	2.61	3.7	1.49		
NT2RP3002983	2.89	2.89	4.69	4.46	6.12	4.37		
NT2RP3002985	4.23	4.23	17.87	13.64	20.26	11.12		
NT2RP3002988	3.97	3.97	4.6	4.12	5.64	4.13		
NT2RP3003000	3.11	3.11	3.46	2.46	3.2	1.51		
NT2RP3003008	3.26	3.26	5.87	3.95	4.55	2.96		
NT2RP3003012	3.43	3.43	6.06	3.9	4.96	2.79		
NT2RP3003015	1.35	1.35	4.9	1.5	2.5	0.54		
NT2RP3003018	2.15	2.15	6.09	3.45	7.24	2.59		
NT2RP3003028	3.53	3.53	7.23	3.5	5.05	4.01		
NT2RP3003029	111.75	111.75	149.73	175.13	159.77	181.4	*	+
NT2RP3003032	7.06	7.06	9.05	11.87	18.84	9.94		
NT2RP3003041	2.07	2.07	1.88	1.61	1.41	0.69		
NT2RP3003044	3.06	3.06	7.45	5.72	6.11	7.57		
NT2RP3003047	3.09	3.09	5.16	2.4	4.67	2.06		
NT2RP3003050	5.96	5.96	12.03	6.74	10.3	8.42		
NT2RP3003053	7.46	7.46	18	14.42	17.14	13.72		
NT2RP3003059	1.93	1.93	4.76	2.88	4.41	3.06		
NT2RP3003061	2.8	2.8	8.59	5.49	5.68	5.16		
NT2RP3003068	5.99	5.99	11.77	9.41	8.75	10.04		
NT2RP3003071	7.22	7.22	10.77	10.39	14.52	10.39		
NT2RP3003076	2.67	2.67	9.49	6.57	6.57	4.01		
NT2RP3003078	1.5	1.5	4.12	2.09	4.52	2.43		
NT2RP3003081	6.21	6.21	10.54	9.94	9.6	9.97		
NT2RP3003090	1.49	1.49	5.95	3.28	3.57	3.25		
NT2RP3003097	2.42	2.42	7.15	2.71	3.72	2.93		

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NT2RP3003098	2.75	2.75	4.22	2.73	3.43	1.73
NT2RP3003101	5.56	5.56	7.24	7.73	10.35	7.18
NT2RP3003109	16.11	16.11	27.38	27.36	41.03	21.91
NT2RP3003121	3.39	3.39	11.03	4.61	8	2.44
NT2RP3003133	2.09	2.09	5.78	4.93	8.58	3.96
NT2RP3003137	3.42	3.42	5.74	6.32	7.59	5.29
NT2RP3003138	2.36	2.36	5.27	5.26	5.7	3.74
NT2RP3003139	2.53	2.53	7.8	3.15	5.74	2.7
NT2RP3003145	5.08	5.08	32.56	25.8	29.74	19.72
NT2RP3003150	2.03	2.03	5.17	3.56	3.76	1.97
NT2RP3003157	2.52	2.52	8.34	6.4	10.1	4.94
NT2RP3003185	1.77	1.77	3.88	1.91	3.34	2.62
NT2RP3003193	2.62	2.62	5.75	6.03	4.59	2.65
NT2RP3003197	2.38	2.38	3.8	3.11	4.02	2.2
NT2RP3003203	11.82	11.82	14.35	16.85	10.17	15.27
NT2RP3003204	3.76	3.76	7.93	4.04	6.17	3.79
NT2RP3003210	14.48	14.48	75.3	58.97	84.6	68.66
NT2RP3003212	5.15	5.15	9.44	9.21	10.67	7.36
NT2RP3003213	4.16	4.16	5.68	5.15	7.02	5.44
NT2RP3003224	1.7	1.7	4.75	2.43	2.11	2.64
NT2RP3003226	3.25	3.25	5.68	6.57	5.94	3.63
NT2RP3003230	7.79	7.79	11.47	12.39	8.89	6.72
NT2RP3003235	7.61	7.61	10.79	7.77	7.73	6.89
NT2RP3003242	12.17	12.17	23.49	26.68	32.03	19.25
NT2RP3003251	5.61	5.61	9.47	3.73	4.95	4.08
NT2RP3003252	3.95	3.95	5.95	2.19	3.7	2.42
NT2RP3003258	4.92	4.92	7.89	19.94	24.95	15.47
NT2RP3003260	4.54	4.54	12.34	13.46	11.52	12.68
NT2RP3003264	1.64	1.64	5.99	3.18	4.32	1.86

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NT2RP3003273	2.18	2.18	4.93	4.57	3.58	1.72		
NT2RP3003278	1.33	1.33	4	1.31	5.12	0.63		
NT2RP3003280	9.85	9.85	23.11	18.18	19.52	18.19		
NT2RP3003282	5.29	5.29	6.25	3.62	3.97	3.48	**	-
NT2RP3003290	6.64	6.64	9.09	4.8	5.38	3.78	*	-
NT2RP3003301	4.01	4.01	5.73	4.31	4.59	3.23		
NT2RP3003302	1.45	1.45	2.31	2.91	2.64	1.91		
NT2RP3003311	2.45	2.45	6.76	15.72	13.09	11.55	**	+
NT2RP3003312	1.81	1.81	3.35	3.73	3.87	2.41		
NT2RP3003313	1.61	1.61	4.2	2.91	5.4	2.87		
NT2RP3003327	1.62	1.62	6.24	4.81	4.95	3.34		
NT2RP3003330	5.13	5.13	8.01	15.68	16.13	12.78	**	+
NT2RP3003344	3.36	3.36	4.14	2.92	3.74	2.6		
NT2RP3003346	3.81	3.81	4.83	4.38	4.05	1.24		
NT2RP3003349	4.04	4.04	6.93	9.96	9.41	9.65	**	+
NT2RP3003353	1.95	1.95	3.24	4.06	5.37	2.45		
NT2RP3003354	5.09	5.09	13.72	16.29	12.02	13.5		
NT2RP3003368	3.03	3.03	4.73	4.04	4.08	2.63		
NT2RP3003375	4.1	4.1	7.4	7.41	9.67	6.62		
NT2RP3003377	4.16	4.16	3.98	2.57	3.58	1.65		
NT2RP3003384	5.77	5.77	4.55	2.83	3.43	2.56	**	-
NT2RP3003385	4.55	4.55	3.12	1.9	2.36	1.47	*	-
NT2RP3003396	3.93	3.93	13.63	16.4	8.38	12.32		
NT2RP3003403	1.62	1.62	2.54	3.24	4.73	1.92		
NT2RP3003409	1.18	1.18	2.97	3.3	4.48	3.03		
NT2RP3003411	4.59	4.59	15.42	14.11	15.42	10.96		
NT2RP3003420	3.79	3.79	4.36	3.68	2.13	1.85		
NT2RP3003425	3.25	3.25	6.71	5.85	7.25	5.49		
NT2RP3003426	9.11	9.11	16.3	10.88	11.12	17.45		

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NT2RP3003427	5.95	5.95	10.09	9.15	13.58	8.03		
NT2RP3003433	2.55	2.55	6.26	8.42	9.57	4.87		
NT2RP3003437	22.12	22.12	49.85	51.81	44	38.77		
NT2RP3003448	1.88	1.88	4.24	3.5	3.83	2.63		
NT2RP3003455	5.23	5.23	12.16	11.8	9.96	8.44		
NT2RP3003462	4.96	4.96	10.07	10.76	8.25	7.08		
NT2RP3003464	3.79	3.79	5.03	3.01	4.76	1.2		
NT2RP3003469	4.1	4.1	7.77	6.62	7.56	5.07		
NT2RP3003473	22.06	22.06	36.6	54.82	69.25	56.46	**	+
NT2RP3003474	8.26	8.26	23.04	13.23	12.04	13.52		
NT2RP3003475	2.84	2.84	4.04	4.55	4.45	3.28		
NT2RP3003490	2.7	2.7	5.81	4.21	4.43	3.12		
NT2RP3003491	2.26	2.26	3	2.14	2.75	1.26		
NT2RP3003493	11.75	11.75	30.77	34.59	28.9	34.45		
NT2RP3003500	4.93	4.93	5.26	4.99	7.46	3.65		
NT2RP3003527	2.73	2.73	3.09	2.42	2.92	1.72		
NT2RP3003532	2.7	2.7	1.81	2.14	3.33	2.13		
NT2RP3003535	3.14	3.14	4.37	1.92	3.4	2.19		
NT2RP3003536	3.04	3.04	5.95	3.45	5.2	4.97		
NT2RP3003543	2.61	2.61	6.24	3.21	4.81	3.83		
NT2RP3003549	1.43	1.43	6.66	2.18	4.07	1.55		
NT2RP3003552	1.8	1.8	5.76	0.64	0.84	1.58		
NT2RP3003555	4.4	4.4	14.14	12.16	17.43	16.23		
NT2RP3003559	2.81	2.81	6.7	3.88	5.11	5.49		
NT2RP3003564	3.11	3.11	5.9	2.24	4.6	5.25		
NT2RP3003572	2.1	2.1	4.21	1.88	3.02	2.32		
NT2RP3003576	5.88	5.88	10.15	11.32	8.98	9.22		
NT2RP3003587	7.39	7.39	12.41	10.01	12.71	12.75		
NT2RP3003589	15.33	15.33	22.45	23.89	23.75	26.58		

NT2RP3003592	7.77	7.77	10.4	8.42	14.48	9.74		
NT2RP3003593	8.16	8.16	13.62	13.47	13.84	110.49		
NT2RP3003614	2.66	2.66	8.18	3.11	4.48	7.09		
NT2RP3003621	1.64	1.64	3.91	2.1	3.68	2.96		
NT2RP3003625	1.54	1.54	6.94	3.79	5.09	4.96		
NT2RP3003627	6.73	6.73	20.05	16.23	13.97	25.71		
NT2RP3003636	3.3	3.3	7.74	5.99	3.79	10.4		
NT2RP3003642	7.12	7.12	12.2	12.85	13.15	15.83		
NT2RP3003645	2.91	2.91	6.07	2.23	2.42	3.53		
NT2RP3003648	2.88	2.88	3.71	2.17	2.44	3.13		
NT2RP3003649	2.7	2.7	9.28	6.36	5.11	12.04		
NT2RP3003650	2.65	2.65	4.25	4.38	3.16	4.09		
NT2RP3003656	1.69	1.69	3.23	1.94	4.12	3		
NT2RP3003659	2.76	2.76	4.56	2.14	4.8	4.88		
NT2RP3003662	31.39	31.39	53.28	34.35	14.68	34.64		
NT2RP3003664	3.56	3.56	6.5	6.18	5.45	6.55		
NT2RP3003665	1.89	1.89	4.83	2.07	2.8	4.96		
NT2RP3003671	2.88	2.88	4.33	3.03	2.6	4.29		
NT2RP3003672	4.78	4.78	9.8	10.69	14.73	16.35	*	+
NT2RP3003673	4.98	4.98	9.42	5.35	3.05	4.12		
NT2RP3003679	40.1	40.1	95.75	69.92	23.86	83.88		
NT2RP3003680	3.13	3.13	5.38	3.96	4.58	5.88		
NT2RP3003686	2.22	2.22	4.43	2.84	4.85	2.25		
NT2RP3003689	4.05	4.05	9.69	5.94	5.63	8.27		
NT2RP3003697	13.79	13.79	120.74	108.93	77.49	68.74		
NT2RP3003701	2.7	2.7	5.17	2.58	3.05	2.57		
NT2RP3003704	2.99	2.99	6.96	7.09	7.61	6.96		
NT2RP3003714	1.39	1.39	4.25	1.68	0.89	1.14		
NT2RP3003716	2.05	2.05	4.23	3	2.29	2.24		

NT2RP3003721	1.83	1.83	3.27	1.85	3.45	2.18		
NT2RP3003722	3.45	3.45	8.18	8.08	7.79	5.45		
NT2RP3003726	3.5	3.5	4.9	2.77	4.51	2.32		
NT2RP3003729	4.1	4.1	8.53	4.22	5.44	4.6		
NT2RP3003731	5.06	5.06	6.98	4.19	3.54	7.45		
NT2RP3003740	2.58	2.58	5.08	2.42	2.48	2.94		
NT2RP3003746	3.63	3.63	8.14	6.7	5.94	6.59		
NT2RP3003749	0.67	0.67	2.58	1.55	2.08	1.73		
NT2RP3003754	3.32	3.32	7.31	4.66	5.87	5.81		
NT2RP3003759	1.16	1.16	4.44	2.49	4.41	1.43		
NT2RP3003764	3.97	3.97	7.08	6.85	7.41	5.06		
NT2RP3003766	6.93	6.93	7.84	3.3	5.87	3.79	*	-
NT2RP3003767	11.19	11.19	16.8	14.83	21.08	16.97		
NT2RP3003778	3.36	3.36	4.89	4.46	5.55	4.27		
NT2RP3003779	4.05	4.05	15.26	13.02	8.74	10.52		
NT2RP3003783	9.25	9.25	21.72	22.42	13.65	18.76		
NT2RP3003787	2.15	2.15	4.65	4.41	4.74	6.37		
NT2RP3003789	5.12	5.12	10.16	11.63	12.19	14.96	*	+
NT2RP3003795	1.48	1.48	6.48	4.09	2.82	2.24		
NT2RP3003799	2.67	2.67	5.5	3.08	2.38	1.75		
NT2RP3003800	4.36	4.36	5.92	4.14	4.57	6.91		
NT2RP3003805	8.15	8.15	6.78	8.4	5.48	5.89		
NT2RP3003809	1.94	1.94	7.2	5.83	5.4	4.82		
NT2RP3003819	3.39	3.39	6.07	7.3	5.97	6.35		
NT2RP3003824	5.69	5.69	10.69	14.08	14.85	13.32	*	+
NT2RP3003825	9.06	9.06	16.31	12.87	16.88	16.75		
NT2RP3003828	4.7	4.7	14.38	13.36	15.69	14.55		
NT2RP3003831	4.01	4.01	6.38	5.77	6.54	7.23		
NT2RP3003833	5.12	5.12	7.5	6.44	8.88	6.96		

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NT2RP3003836	6.37	6.37	5.05	5.74	6.47	4.31		
NT2RP3003842	2.7	2.7	9.08	6.84	6.51	7.09		
NT2RP3003843	9.26	9.26	26.77	16.67	12.71	16.2		
NT2RP3003844	20.38	20.38	46.56	42.84	27.94	44.32		
NT2RP3003846	4.04	4.04	8.45	8.94	7.18	8.05		
NT2RP3003849	2.27	2.27	2.68	2.67	2.73	1.68		
NT2RP3003862	28.91	28.91	45.63	32	37.58	44.88		
NT2RP3003870	4.76	4.76	4.81	2.54	2.93	2.05	**	-
NT2RP3003874	21.46	21.46	20.88	33.11	47.25	36.44	*	+
NT2RP3003876	1.62	1.62	8.08	5.45	7.49	6.81		
NT2RP3003880	1.74	1.74	4.63	5.31	4.66	4.73		
NT2RP3003889	1.69	1.69	3.04	3.41	3.53	9.53		
NT2RP3003891	1.88	1.88	2.98	2.56	3.19	1.37		
NT2RP3003914	3.1	3.1	7.35	6.88	5.15	7.39		
NT2RP3003915	5.03	5.03	8.44	9.52	11.35	8.6		
NT2RP3003918	6.79	6.79	10.39	10.04	13.71	12.42		
NT2RP3003920	6.9	6.9	9.13	8.31	10.22	8.96		
NT2RP3003924	2.25	2.25	9.57	6.49	5.34	6.91		
NT2RP3003932	1.41	1.41	3.85	5.17	5.26	3.85		
NT2RP3003939	3.48	3.48	11.88	9.86	14.05	11.09		
NT2RP3003940	11.34	11.34	27.33	23.54	20.59	23.06		
NT2RP3003943	2.6	2.6	2.83	2.85	2.78	3.88		
NT2RP3003959	3.52	3.52	6.96	6.54	5.93	5.49		
NT2RP3003963	4.83	4.83	7.59	4.01	4.61	2.52		
NT2RP3003965	11.14	11.14	13.85	18.75	20.67	17.22	**	+
NT2RP3003972	26.1	26.1	40.32	22.13	17.98	38.48		
NT2RP3003973	2.85	2.85	4.33	1.96	3.6	3.96		
NT2RP3003979	5.89	5.89	12.53	6.92	8.49	8.84		
NT2RP3003980	3.52	3.52	9.41	9.34	8.89	7.92		

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NT2RP3003982	4.2	4.2	4.63	2.44	1.6	4.61		
NT2RP3003989	6.24	6.24	4.69	9.61	5.62	16.05		
NT2RP3003992	2.13	2.13	4.89	2.47	5.12	4.8		
NT2RP3004000	2.81	2.81	6	1.72	3.22	2.62		
NT2RP3004001	11.38	11.38	19.94	11.62	11.37	21.11		
NT2RP3004005	2.89	2.89	7.79	4.7	4.48	6.84		
NT2RP3004013	2.23	2.23	7.2	2.66	4.87	3.57		
NT2RP3004016	1.5	1.5	7.1	2.22	3.14	2.88		
NT2RP3004025	4.02	4.02	7.69	7.48	12.19	9.01		
NT2RP3004030	7.05	7.05	12.64	13.97	15.8	17.66	*	+
NT2RP3004041	5.65	5.65	11.38	10.48	9.57	19.81		
NT2RP3004042	15.22	15.22	102.33	97.27	103.6	99.67		
NT2RP3004044	2.13	2.13	6.51	5.14	7.21	4.22		
NT2RP3004051	2.6	2.6	5.79	2.23	5.51	4.69		
NT2RP3004052	7.1	7.1	11.22	5.63	4.98	9.78		
NT2RP3004053	15.87	15.87	35.04	23.12	40.67	40.17		
NT2RP3004055	2.38	2.38	5.33	2.98	3.3	4.47		
NT2RP3004059	4.05	4.05	8.8	8.15	7.03	11		
NT2RP3004063	5.13	5.13	11.23	8.78	11.27	12.33		
NT2RP3004067	4.24	4.24	8.4	6.62	6.42	4.47		
NT2RP3004070	3.58	3.58	9.92	6.26	4.4	5.47		
NT2RP3004075	4.16	4.16	11.23	12.62	11.88	13.3		
NT2RP3004078	2.6	2.6	5.25	4.94	4.19	2.79		
NT2RP3004083	2.93	2.93	6.23	4.57	6.8	11.37		
NT2RP3004084	4.65	4.65	20.29	6.18	8.56	5.32		
NT2RP3004087	4.2	4.2	7.86	7.14	10.81	9.03		
NT2RP3004090	4.11	4.11	6.42	9	8.19	8.61	**	+
NT2RP3004093	2.38	2.38	7.49	4.07	3.51	4.47		
NT2RP3004095	5.02	5.02	13.11	11.57	10.17	18.55		

NT2RP3004102	3.32	3.32	5.59	5.25	4.27	3.21		
NT2RP3004110	12.74	12.74	18.66	22.12	14.31	19.97		
NT2RP3004119	3.3	3.3	7.71	3.91	4.08	3.73		
NT2RP3004125	5.55	5.55	12.05	8.13	10.88	8.38		
NT2RP3004129	4.62	4.62	7.38	3.36	2.95	6.08		
NT2RP3004130	11.81	11.81	28.12	21.92	31.13	21.05		
NT2RP3004133	4.51	4.51	12.95	14.62	8.94	16.81		
NT2RP3004145	1.43	1.43	4.17	2.62	4.87	3.59		
NT2RP3004148	2.67	2.67	7.07	5.26	6.24	4.5		
NT2RP3004155	2.37	2.37	4.82	4.7	4.57	6.59		
NT2RP3004165	17.94	17.94	29.96	29.58	31.82	39.18		
NT2RP3004179	7.34	7.34	6.72	2.71	5.41	3.3	*	-
NT2RP3004185	5.2	5.2	5.53	2.76	2.76	1.95	**	-
NT2RP3004188	4.77	4.77	10.82	7.74	11.35	7		
NT2RP3004189	4.23	4.23	5.91	4.97	4.82	6.28		
NT2RP3004190	2.6	2.6	5.57	5.84	4.36	5.26		
NT2RP3004191	14.09	14.09	23.4	31.41	29.45	30.09	*	+
NT2RP3004202	2.04	2.04	4.56	4.16	4.42	2.3		
NT2RP3004205	8.75	8.75	21.54	21.27	25.35	20.28		
NT2RP3004206	4.5	4.5	9.74	5.14	6.37	9		
NT2RP3004207	5.19	5.19	4.99	3.09	3.25	1.77	**	-
NT2RP3004209	4.74	4.74	7.74	8.2	11.23	9.08	*	+
NT2RP3004215	1.86	1.86	6.7	3.96	2.41	4.55		
NT2RP3004219	5.15	5.15	11.25	10.04	8.81	13.65		
NT2RP3004242	4.65	4.65	10.36	9.8	10.19	14.56		
NT2RP3004246	4.5	4.5	9.39	9.18	10.95	3.8		
NT2RP3004253	1.89	1.89	4.85	3.64	4.99	2.8		
NT2RP3004258	5.45	5.45	10.89	12.77	11.07	11.39		
NT2RP3004262	4.26	4.26	5.71	2.63	2.99	2.01	*	-

NT2RP3004275	5.59	5.59	3.43	1.4	2.97	2.34	*	-
NT2RP3004282	5.45	5.45	68.08	51.29	52.72	53.57		
NT2RP3004289	1.79	1.79	2.95	1.9	2.18	3.99		
NT2RP3004294	2.74	2.74	6.02	6.95	6.93	7.24	*	+
NT2RP3004298	8.76	8.76	48.63	46.33	60.89	50.83		
NT2RP3004309	3.3	3.3	6.46	5.2	5.22	5.31		
NT2RP3004321	3.71	3.71	6.11	3.29	3.74	3.34		
NT2RP3004322	5.61	5.61	6.86	6.06	6.43	6.56		
NT2RP3004332	11.69	11.69	100.11	78.54	102.41	76.72		
NT2RP3004334	1.49	1.49	6.97	8.56	6.06	9.06		
NT2RP3004336	2.11	2.11	6.24	6.02	4.44	5.63		
NT2RP3004338	3.09	3.09	8.41	10.22	9.52	16.47		
NT2RP3004341	1.81	1.81	4.56	6.13	5.17	9.13		
NT2RP3004345	4.1	4.1	8.68	9.3	9.63	8.48		
NT2RP3004348	5.06	5.06	11.25	13.04	10.79	12.54		
NT2RP3004349	5	5	7.5	4.89	7.75	5.76		
NT2RP3004355	5.57	5.57	7.09	7.55	7.07	7.18		
NT2RP3004356	5.76	5.76	21.51	11.29	15.14	15.56		
NT2RP3004360	3.4	3.4	5.26	6.01	5.32	7.85		
NT2RP3004361	2.6	2.6	6.26	7.67	7.3	8.87	*	+
NT2RP3004374	3.06	3.06	10.09	8.8	6.6	5.75		
NT2RP3004378	10.48	10.48	18.57	28.26	24.09	34.81	*	+
NT2RP3004399	3.88	3.88	5.77	3.53	3.17	9.06		
NT2RP3004405	4.07	4.07	6.77	3.03	5.52	3.93		
NT2RP3004406	5.36	5.36	6.23	5.19	6.03	6.12		
NT2RP3004411	5.93	5.93	13.28	8.08	6.39	9.51		
NT2RP3004424	1.53	1.53	2.43	3.27	1.81	2.83		
NT2RP3004428	3.03	3.03	5.36	5.07	3.82	4.09		
NT2RP3004432	3.3	3.3	3.52	3.61	3.11	4.38		

NT2RP3004434	3.42	3.42	8.41	7.28	9.09	7.99
NT2RP3004446	3.29	3.29	4.6	3.29	4.1	2.63
NT2RP3004451	3.2	3.2	6.01	3.89	3.38	2.48
NT2RP3004454	2.96	2.96	4.16	2.69	3.5	2.5
NT2RP3004466	3.5	3.5	7.89	5.25	3.85	5.61
NT2RP3004470	7.42	7.42	24.53	18.4	16.35	24.72
NT2RP3004472	2.49	2.49	4.4	3.97	3.84	3.88
NT2RP3004475	1.71	1.71	5.52	2.72	5.93	3.9
NT2RP3004480	14.12	14.12	17.04	18.94	10.5	18.82
NT2RP3004481	5.42	5.42	11.37	5.04	7.37	12.39
NT2RP3004490	2.66	2.66	8.45	3.92	7.03	8.25
NT2RP3004496	4.8	4.8	14.38	7.22	9.3	11.08
NT2RP3004498	6.39	6.39	21.39	16.86	15.11	18.92
NT2RP3004503	2.78	2.78	9.34	4.85	6.23	5.88
NT2RP3004504	3.91	3.91	11.09	6.05	10.67	11.52
NT2RP3004505	17.38	17.38	28.56	37.35	26.72	37.82
NT2RP3004507	1.57	1.57	6.6	2.52	5.52	1.68
NT2RP3004519	4.9	4.9	7.73	4.93	8.36	8.75
NT2RP3004524	10.04	10.04	29.21	26.88	26.43	29.62
NT2RP3004527	3.03	3.03	3.22	1.29	2.23	2.08
NT2RP3004534	3.08	3.08	10.44	5.58	12	7.38
NT2RP3004539	4.45	4.45	12.17	9.8	8.97	12
NT2RP3004541	2.65	2.65	11.06	5.48	9.44	8.25
NT2RP3004544	3.54	3.54	8.89	6.62	5.24	9.48
NT2RP3004551	3.46	3.46	6.75	6.6	6.6	6.98
NT2RP3004552	2.76	2.76	4.33	2.84	3.22	4.98
NT2RP3004557	5.68	5.68	8.73	9.74	15.44	13.16
NT2RP3004561	1.96	1.96	3.77	2.55	4.46	4.1
NT2RP3004566	3.09	3.09	11.55	7.2	10.05	8.79

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NT2RP3004569	2.21	2.21	7.09	4.63	5.36	6.91		
NT2RP3004572	4.37	4.37	6.83	7.08	5.55	7.07		
NT2RP3004578	2.35	2.35	5.38	4.15	4.27	3.24		
NT2RP3004584	4.76	4.76	28.36	34.99	37.13	30.29		
NT2RP3004588	2.38	2.38	4.89	1.6	3.7	3.28		
NT2RP3004594	2.25	2.25	5.9	5.67	6.49	8.94		
NT2RP3004603	34.16	34.16	99.64	80.2	102.6	97.27		
NT2RP3004612	4.71	4.71	12.17	5.3	3.36	5.34		
NT2RP3004617	1.09	1.09	2.32	2.49	3.3	2.39		
NT2RP3004618	4.61	4.61	5.9	2.49	5.21	5.9		
NT2RP3004625	3.97	3.97	8.17	4.55	6.92	7.1		
NT2RP3004635	4.76	4.76	7.83	1.52	2.86	3.47		
NT2RP3004640	10.61	10.61	62.15	59.33	67.97	48.32		
NT2RP3004642	8.04	8.04	29.31	22.82	26.12	25.12		
NT2RP3004647	3.5	3.5	5.65	5.89	7.35	6.88	*	+
NT2RP3004652	1.76	1.76	10.37	4.2	3.71	4.34		
NT2RP3004669	2.01	2.01	5.36	4.01	5.33	3.46		
NT2RP3004670	5.04	5.04	10.58	12.4	9.19	14.23		
NT2RP4000008	45.17	45.17	71.24	49.77	32.43	48.77		
NT2RP4000018	11.64	11.64	14.61	11.69	14.8	14.87		
NT2RP4000023	6.96	6.96	8.91	4.86	7.38	5.98		
NT2RP4000025	16.2	16.2	22.16	26.22	29.89	24.7	*	+
NT2RP4000035	6.3	6.3	12.01	11.28	15.33	11.01		
NT2RP4000041	14.46	14.46	34.8	22.01	17.41	23.68		
NT2RP4000049	2.64	2.64	6.34	6.59	6.88	5.3		
NT2RP4000050	2.24	2.24	6.87	3.54	4.48	4.05		
NT2RP4000051	4.66	4.66	10.5	10.58	10.02	8.96		
NT2RP4000063	20.51	20.51	33.5	26.77	31	18.33		
NT2RP4000065	7.54	7.54	9.24	11.85	15.01	11.47	*	+

NT2RP4000070	6.63	6.63	5.29	3.79	4.54	3.84	*	-
NT2RP4000074	6.55	6.55	13.63	10.29	15.39	9.52		
NT2RP4000078	3.41	3.41	9.55	12.2	11.66	12.56	*	+
NT2RP4000080	3.52	3.52	7.01	5.06	6.84	6.81		
NT2RP4000099	128.86	128.86	236.22	149.44	161.1	211.56		
NT2RP4000102	3.55	3.55	6.48	5.27	4.97	5.54		
NT2RP4000103	2	2	5.47	2.57	2.85	3.96		
NT2RP4000108	4.66	4.66	7.91	9.33	10.73	10.61	*	+
NT2RP4000109	18.89	18.89	22.84	19.87	24.15	16.14		
NT2RP4000111	4.56	4.56	6.38	4.87	5.27	4.85		
NT2RP4000112	5.62	5.62	10.14	12.45	8.7	11.81		
NT2RP4000115	2.94	2.94	3.62	4.95	7.82	10.93		
NT2RP4000129	2.18	2.18	4.58	3.02	5.04	5.03		
NT2RP4000137	3.36	3.36	10.05	5.34	8.72	11.4		
NT2RP4000138	7.21	7.21	10.91	17.75	20.19	19.17	**	+
NT2RP4000141	3.25	3.25	6.1	5.22	4.9	3.57		
NT2RP4000147	6.21	6.21	4.49	4.27	5.2	3.47		
NT2RP4000150	5.96	5.96	6.93	7.33	10.41	7.06		
NT2RP4000151	2.82	2.82	7.82	5.69	6.24	5.05		
NT2RP4000157	73.27	73.27	222.87	169.53	97.5	173.8		
NT2RP4000159	2.02	2.02	5.03	3.38	5.03	2.92		
NT2RP4000163	5.21	5.21	8.74	10.89	9.18	6.63		
NT2RP4000167	3.26	3.26	4.35	4.32	3.22	3.69		
NT2RP4000171	5.72	5.72	7	5.72	7.45	5.03		
NT2RP4000175	62.48	62.48	94.56	144.06	214.73	147.88	*	+
NT2RP4000180	17.17	17.17	106.15	88.61	123.6	81.8		
NT2RP4000185	7.64	7.64	31.76	31.82	23.23	34.01		
NT2RP4000192	1.04	1.04	4.78	4.19	3.6	3.05		
NT2RP4000194	3.13	3.13	7.53	7.58	4.98	6.36		

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NT2RP4000196	6.81	6.81	43.94	35.57	46.56	41.91		
NT2RP4000210	5.63	5.63	9.71	9.96	8.35	9.27		
NT2RP4000212	5.59	5.59	8.88	8.57	8.41	9.08		
NT2RP4000214	5.53	5.53	10.21	5.72	6.68	11.29		
NT2RP4000216	8.89	8.89	7.36	7	12.63	10.08		
NT2RP4000218	3.45	3.45	9.78	7.25	6.07	5.77		
NT2RP4000223	21.18	21.18	177.28	121.8	125.75	125.3		
NT2RP4000243	16.52	16.52	54.51	42.94	41.61	51.74		
NT2RP4000246	17.75	17.75	37.97	26.43	11.42	27.5		
NT2RP4000250	16.86	16.86	31.23	24.92	23.85	26.39		
NT2RP4000256	4.38	4.38	8.45	4.99	6.44	4.67		
NT2RP4000257	32.45	32.45	44.22	48.67	57.52	39.19		
NT2RP4000259	7.07	7.07	6.96	8.48	13.07	9.08		
NT2RP4000261	4.18	4.18	8.13	4.07	4.55	6.48		
NT2RP4000262	8.36	8.36	11.02	7.11	10.05	7.64		
NT2RP4000263	2.6	2.6	5.14	3.47	3.67	3.78		
NT2RP4000280	5.84	5.84	11.62	9.05	11.58	14.23		
NT2RP4000286	4.73	4.73	10.16	4.38	6.77	11.94		
NT2RP4000290	5.77	5.77	5.42	3.18	3.19	5.5		
NT2RP4000291	42.53	42.53	73.59	62.12	70.23	70.61		
NT2RP4000301	3.31	3.31	20.59	22.93	34.62	26.63	*	+
NT2RP4000312	7.76	7.76	45.27	39.01	43.59	45.92		
NT2RP4000321	3.73	3.73	8.16	7.88	7.14	9.75		
NT2RP4000323	1.44	1.44	4.26	2.27	2.55	2.12		
NT2RP4000324	7.77	7.77	16.76	8.33	10.2	11.08		
NT2RP4000334	20.97	20.97	77.78	63.81	71.76	68.24		
NT2RP4000343	2.48	2.48	5.54	1.57	3.16	2.38		
NT2RP4000348	3.4	3.4	10.81	8.38	6.75	13.2		
NT2RP4000349	1.78	1.78	0.83	0.37	0.72	2.48		

NT2RP4000355	3.98	3.98	14.84	7.18	9.13	9.04		
NT2RP4000356	8.3	8.3	22.64	9.22	11.44	21.13		
NT2RP4000360	3.04	3.04	6.98	5.06	5.43	4.73		
NT2RP4000367	2.18	2.18	3.72	2.04	2.58	2.83		
NT2RP4000370	4.21	4.21	7.51	3.62	7.12	5.99		
NT2RP4000373	3.33	3.33	5.18	3.19	5.23	2.95		
NT2RP4000376	4.2	4.2	5.5	4.85	5.53	6.5		
NT2RP4000381	1.97	1.97	6.46	4.31	7.01	5.59		
NT2RP4000388	85.82	85.82	204.63	128.93	93.38	116.03		
NT2RP4000390	12.16	12.16	94.1	78.97	76.6	82.02		
NT2RP4000393	8.66	8.66	9.77	9.09	5.99	10.79		
NT2RP4000398	5.51	5.51	26.52	22.08	28.3	26.61		
NT2RP4000406	6.68	6.68	15.61	12.95	15.02	10.08		
NT2RP4000407	6.17	6.17	11.52	9.41	14.74	9.13		
NT2RP4000413	1.79	1.79	3.63	1.15	2.35	2.12		
NT2RP4000415	7.59	7.59	26.11	18.6	21.68	21.68		
NT2RP4000417	7.76	7.76	26.64	14.47	12.79	19.19		
NT2RP4000423	3.52	3.52	7.56	7	6.98	6.46		
NT2RP4000424	2.51	2.51	7.2	3.07	5.03	3.27		
NT2RP4000447	10.3	10.3	64.21	64.91	71.82	68.48		
NT2RP4000448	5.59	5.59	6.67	4.32	3.56	6.27		
NT2RP4000449	5.67	5.67	20.48	14.2	19.45	14.67		
NT2RP4000453	3.53	3.53	6.32	9.02	10.32	10.12	**	+
NT2RP4000455	2.64	2.64	3.98	1.81	1.75	2.4		
NT2RP4000456	12.57	12.57	21.7	14.7	9.86	13.58		
NT2RP4000457	1.54	1.54	7.12	3.9	7.55	2.98		
NT2RP4000461	5.7	5.7	9.84	7.65	6.41	4.6		
NT2RP4000462	11.76	11.76	15.32	11.86	11.53	17.37		
NT2RP4000463	10.2	10.2	52.59	50.66	69.3	48.36		

NT2RP4000471	6.36	6.36	10.74	5.74	6.23	4.98		
NT2RP4000472	3.97	3.97	4.41	1.27	1.27	1.66	**	-
NT2RP4000476	27.14	27.14	52.56	74.95	94.93	65.35	*	+
NT2RP4000480	11.56	11.56	29.27	19.08	9.95	26.66		
NT2RP4000481	2.29	2.29	4.76	3.73	4.16	4.33		
NT2RP4000483	1.38	1.38	7.59	7.58	7.85	6.26		
NT2RP4000487	1.54	1.54	4.9	2.26	3.17	0.91		
NT2RP4000496	2.16	2.16	4.98	2.95	4.07	3.65		
NT2RP4000497	17.15	17.15	22.33	34.9	44.46	29.9	*	+
NT2RP4000498	10.46	10.46	21.39	20.15	30.33	24.49		
NT2RP4000500	2.43	2.43	3.21	2.03	1.49	1.39	*	-
NT2RP4000507	5.63	5.63	9.02	12.49	10.62	17.51	*	+
NT2RP4000515	12.85	12.85	88.89	90.3	101.29	96.12		
NT2RP4000516	8.77	8.77	26.09	19.63	21.76	21.82		
NT2RP4000517	3.22	3.22	5.73	4.69	5.89	4.79		
NT2RP4000518	3.42	3.42	7.4	4.47	6.05	3.82		
NT2RP4000519	2.9	2.9	5.76	2.18	2.22	1.77		
NT2RP4000524	4.2	4.2	3.44	2.05	1.72	1.3	**	-
NT2RP4000528	3.67	3.67	3.06	3.01	3.27	8.01		
NT2RP4000537	35.4	35.4	62.6	36.23	30.93	44.52		
NT2RP4000541	2.04	2.04	2.45	3.34	4.33	3.09	*	+
NT2RP4000543	2.93	2.93	8.94	7.96	9.72	8.75		
NT2RP4000545	4.03	4.03	6.38	4.99	6.43	4.78		
NT2RP4000546	3.34	3.34	5.93	5.53	4.9	6.03		
NT2RP4000549	23.81	23.81	56.48	41.6	51.57	38.82		
NT2RP4000556	7.36	7.36	13.04	14.69	15.54	12.07		
NT2RP4000557	6.1	6.1	4.53	1.82	3.97	6.27		
NT2RP4000558	30.12	30.12	94.28	68.16	57.01	73.2		
NT2RP4000560	14.8	14.8	52.31	49.75	58.69	56.12		

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NT2RP4000568	1.72	1.72	3.83	5.6	6.08	4.46	*	+
NT2RP4000583	11.61	11.61	20.2	23.65	14.97	20.56		
NT2RP4000585	3.04	3.04	4.14	3.12	2.55	3.24		
NT2RP4000588	8.65	8.65	12.77	14.58	16.96	13.55	*	+
NT2RP4000590	24.89	24.89	41.97	41.86	50.81	32.65		
NT2RP4000599	4.29	4.29	3.24	2.44	2.23	3.59		
NT2RP4000603	14.08	14.08	33.32	31.06	21.01	29.12		
NT2RP4000607	2.41	2.41	10.04	4.45	7.87	15.35		
NT2RP4000614	6.14	6.14	15.21	15.57	12.53	15.19		
NT2RP4000634	6.61	6.61	11	7.78	9.84	10.31		
NT2RP4000638	3.59	3.59	7.77	8.45	5.8	4.73		
NT2RP4000648	3.13	3.13	4.26	2.54	2.69	2.19		
NT2RP4000657	9.94	9.94	15.38	15.95	18.93	14.49		
NT2RP4000691	5.76	5.76	5.82	4.92	7.47	7.73		
NT2RP4000697	3.74	3.74	8.5	5.55	6.56	6.12		
NT2RP4000704	8.91	8.91	47.2	44.17	54.81	38.14		
NT2RP4000710	40.22	40.22	98.85	90.4	59.28	83.71		
NT2RP4000713	4.35	4.35	19.92	16.67	20.85	15.52		
NT2RP4000724	6.29	6.29	12.5	8.19	9.81	7.83		
NT2RP4000725	3.61	3.61	4	1.88	1.74	2.33	**	-
NT2RP4000728	10.13	10.13	41.12	43.53	66.46	39.83		
NT2RP4000737	4.07	4.07	2.15	3.63	3.09	3.28		
NT2RP4000739	5.07	5.07	7.71	4.61	3.63	5.84		
NT2RP4000749	2.4	2.4	5.29	2.59	3.97	1.68		
NT2RP4000769	4.93	4.93	10.12	4.67	6.27	6.2		
NT2RP4000774	3.34	3.34	8.87	5.12	6.63	4.27		
NT2RP4000781	2.15	2.15	5.12	2.06	2.26	1.55		
NT2RP4000783	6.81	6.81	15.16	13.48	15.44	12.67		
NT2RP4000787	1.45	1.45	2.27	0.31	0.51	0.54	*	-

NT2RP4000788	3.58	3.58	23.26	16	18.3	18.73		
NT2RP4000792	3.68	3.68	5.64	5.5	5.8	9.45		
NT2RP4000809	43.7	43.7	56.09	46.75	50.47	81.62		
NT2RP4000817	3.65	3.65	7.83	7.92	7.25	5.82		
NT2RP4000821	31.34	31.34	38.66	28.32	33.11	25.22		
NT2RP4000822	2.46	2.46	5.91	4.29	6.19	2.6		
NT2RP4000823	697.74	697.74	127.48	923.16	1026.8	947.85		
NT2RP4000831	9.98	9.98	61.97	44.37	68.47	50.69		
NT2RP4000833	3.19	3.19	11.26	6.73	7.19	11.91		
NT2RP4000837	1.41	1.41	4.03	1.56	3.65	2.29		
NT2RP4000839	12.23	12.23	97.13	79.71	85.74	86.06		
NT2RP4000846	3.8	3.8	10.13	4.65	3.46	6.65		
NT2RP4000848	4.63	4.63	10.74	8.65	8.58	6.07		
NT2RP4000855	2.91	2.91	4.7	4	3.85	3.43		
NT2RP4000863	3.08	3.08	4.33	3.11	5.3	3.78		
NT2RP4000865	6.43	6.43	25.36	20.09	39.64	21.24		
NT2RP4000873	9.64	9.64	88.25	63.22	69.65	71.33		
NT2RP4000874	1.76	1.76	3.98	2.37	3.67	2.03		
NT2RP4000875	3.31	3.31	9.24	6.88	6.52	7.19		
NT2RP4000878	24.17	24.17	42.53	28.01	16.35	29.04		
NT2RP4000879	2.56	2.56	5.1	2.95	5.29	2.62		
NT2RP4000880	5.17	5.17	21.59	20.97	27.22	16.8		
NT2RP4000891	81.07	81.07	192.57	252.29	351.53	221.08	*	+
NT2RP4000894	5.16	5.16	9.81	8.53	4.8	6.97		
NT2RP4000898	0.86	0.86	2.74	1.88	2.14	1.64		
NT2RP4000899	9.63	9.63	29.48	24.01	20.85	23.95		
NT2RP4000907	2.14	2.14	3.58	1.74	4.04	0.81		
NT2RP4000908	4.62	4.62	9.67	7.51	5.9	5.87		
NT2RP4000910	14.4	14.4	104.68	124.04	197.74	160.9	*	+

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NT2RP4000918	2.85	2.85	4.76	4.73	4.26	5.35		
NT2RP4000925	3.9	3.9	5.53	2.81	3.15	1.86		
NT2RP4000927	1.99	1.99	2.5	0.46	1.08	0.6	**	-
NT2RP4000928	3.11	3.11	6.8	4.48	4.22	5.18		
NT2RP4000929	1.44	1.44	3.68	1.94	2.86	0.84		
NT2RP4000946	0.92	0.92	3.41	1.78	3.22	1.47		
NT2RP4000947	1.71	1.71	3.51	1.94	3.31	1.79		
NT2RP4000949	4.94	4.94	7.84	3.88	5.48	2.38		
NT2RP4000955	4.17	4.17	6.34	2.07	2.86	0.54	*	-
NT2RP4000959	20.55	20.55	28.14	36.21	42.82	36.14	*	+
NT2RP4000962	3.4	3.4	4.24	8.33	10.09	4.53		
NT2RP4000973	8.6	8.6	16.04	10.31	8.92	9.03		
NT2RP4000975	2.18	2.18	5.84	3.29	3.05	2.62		
NT2RP4000979	3.83	3.83	8.67	5.55	8.13	7.1		
NT2RP4000984	1.61	1.61	4.31	3.15	3.93	1.85		
NT2RP4000986	7.32	7.32	13.27	12.66	12.35	2.52		
NT2RP4000988	5.74	5.74	8.37	4	5.2	2.63		
NT2RP4000989	6.24	6.24	6.55	4.05	3.48	2.89	**	-
NT2RP4000990	3.16	3.16	4	1.92	1.69	2.16	**	-
NT2RP4000994	4.04	4.04	7.67	16.48	10.13	15.95	*	+
NT2RP4000996	3.54	3.54	7.49	6.77	6.52	7.38		
NT2RP4000997	21.59	21.59	36.81	28.52	15.18	34.38		
NT2RP4001001	5.53	5.53	9.17	16.66	18.38	15.09	**	+
NT2RP4001004	1.71	1.71	4.88	2.84	3.09	1.37		
NT2RP4001006	3.46	3.46	8.12	6.85	6.52	6.13		
NT2RP4001009	9.3	9.3	10.45	15.44	20.46	8.25		
NT2RP4001010	7.33	7.33	9.13	7.38	9.75	6.68		
NT2RP4001013	23.29	23.29	50.16	30.87	28.1	30.91		
NT2RP4001029	2.49	2.49	5.95	4.05	2.84	3.63		

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NT2RP4001036	7.55	7.55	13.55	9.11	11.51	13.16		
NT2RP4001041	6.57	6.57	14.4	9.89	12.3	6.35		
NT2RP4001042	4.34	4.34	8.11	9.44	12.5	8.79		
NT2RP4001046	6.98	6.98	9.95	13.24	16.28	15.36	**	+
NT2RP4001050	5.28	5.28	4.81	3.79	4.64	3.35	*	-
NT2RP4001051	6.48	6.48	8.44	5.43	6.82	5.26		
NT2RP4001057	0.76	0.76	2.19	2.34	2.43	1.87		
NT2RP4001063	1.48	1.48	4.39	3.34	3.53	1.8		
NT2RP4001064	3.51	3.51	9.18	12.02	9.13	11.57		
NT2RP4001067	4.42	4.42	9.77	10.96	9.63	6.6		
NT2RP4001078	2.12	2.12	3.43	2.67	2.53	1.82		
NT2RP4001079	5.3	5.3	9.35	8.51	8.02	8.98		
NT2RP4001080	4.1	4.1	5.27	3.52	4.52	2.3		
NT2RP4001086	5.08	5.08	4.19	3.93	6.64	2.85		
NT2RP4001095	2.49	2.49	7.25	7.96	6.49	6.85		
NT2RP4001098	0.92	0.92	3.38	3.87	2.95	3.41		
NT2RP4001100	6.47	6.47	24.34	20.89	20.64	16.99		
NT2RP4001105	3.13	3.13	7.23	6.51	5.58	4.61		
NT2RP4001110	1.75	1.75	3.5	7.07	8.35	5.29	*	+
NT2RP4001115	9.95	9.95	17.68	20.6	18.48	15.31		
NT2RP4001117	19.81	19.81	30.49	35.35	42.53	27.5		
NT2RP4001122	6.06	6.06	6.09	5.17	6.25	3.27		
NT2RP4001123	3.62	3.62	7.76	7.95	5.96	6.27		
NT2RP4001126	4.36	4.36	11.28	10.87	9.09	8.04		
NT2RP4001127	3.25	3.25	4.59	3.39	3.08	2.17		
NT2RP4001138	2.46	2.46	5.8	3.41	2.56	1.62		
NT2RP4001143	2.73	2.73	5.98	6.44	6.54	5.66		
NT2RP4001148	3.72	3.72	6.76	3.77	3.03	2.05		
NT2RP4001149	5.07	5.07	7.28	6.76	9.03	6.37		

NT2RP4001150	3.8	3.8	3.17	3.15	3.7	2.88		
NT2RP4001159	7.08	7.08	11.61	7.69	5.58	10.46		
NT2RP4001162	3.77	3.77	6.14	4.07	6.06	3.41		
NT2RP4001170	1.15	1.15	4.53	1.28	3.2	2.15		
NT2RP4001174	4.16	4.16	12.27	7.91	11.95	5.02		
NT2RP4001175	9.65	9.65	19.14	15.72	21.29	13.28		
NT2RP4001176	99.19	99.19	161.51	174.03	241.92	194	*	+
NT2RP4001184	4.83	4.83	27.1	25.76	32.51	22.85		
NT2RP4001198	21.66	21.66	48.22	29.54	29.17	38.54		
NT2RP4001199	2.52	2.52	6.45	2.59	4.74	3.71		
NT2RP4001206	8.25	8.25	33.2	25.92	32.07	25.48		
NT2RP4001207	2.38	2.38	5.15	2.21	3.11	4.01		
NT2RP4001210	2.73	2.73	5.2	3.62	4.26	2.64		
NT2RP4001213	3.42	3.42	5.11	3.99	4.23	3.63		
NT2RP4001214	3.34	3.34	4.3	3.51	3.76	2.16		
NT2RP4001219	7.4	7.4	12.05	14.35	19.28	13.39	*	+
NT2RP4001228	5.26	5.26	9.63	12.15	15.74	20.07	*	+
NT2RP4001235	2.42	2.42	7.45	3.46	6.02	4.48		
NT2RP4001256	2.11	2.11	4.24	1.66	3.41	2.66		
NT2RP4001257	2.48	2.48	7.27	4.05	4.35	4.05		
NT2RP4001260	3.16	3.16	5.79	2.52	3.86	2.92		
NT2RP4001261	3.84	3.84	6.63	8.42	6.47	5		
NT2RP4001274	22.92	22.92	38.08	25.02	31.56	21.25		
NT2RP4001276	5.24	5.24	10.03	11.38	15.97	11.63	*	+
NT2RP4001283	20.72	20.72	122.55	87.44	93.43	86.47		
NT2RP4001299	9.62	9.62	15.14	14.95	10.52	15.18		
NT2RP4001313	1.45	1.45	3.26	1.72	2.96	0.97		
NT2RP4001315	6.06	6.06	11.14	7.45	9.92	7.74		
NT2RP4001320	14.6	14.6	42.74	32.02	38.13	29.24		

NT2RP4001325	32.53	32.53	146.14	142.88	178.36	128.89		
NT2RP4001336	6.69	6.69	40.75	38.55	46.66	32.11		
NT2RP4001339	4.12	4.12	5.6	3.35	5.56	2.76		
NT2RP4001343	10.46	10.46	83.37	54.71	61.01	60.06		
NT2RP4001344	6.7	6.7	60.08	49.79	55.21	42.62		
NT2RP4001345	1.65	1.65	6.68	5.64	5.7	3.87		
NT2RP4001351	4.1	4.1	15.97	10.01	20.05	11.42		
NT2RP4001353	2.8	2.8	5.91	1.63	2.94	1.86		
NT2RP4001355	2.57	2.57	8.67	1.83	3.12	2.08		
NT2RP4001367	10.64	10.64	17.66	11.92	17.06	13.16		
NT2RP4001372	2.26	2.26	3.82	2.1	2.06	2.07		
NT2RP4001373	8.86	8.86	16.4	10.99	8.59	11.48		
NT2RP4001375	2.71	2.71	6.06	4.91	7.42	2.94		
NT2RP4001379	1.74	1.74	3.52	2.34	4.67	1.38		
NT2RP4001381	5.6	5.6	12.51	12.8	12.66	8.27		
NT2RP4001386	6.39	6.39	14.52	14.77	20.11	12.32		
NT2RP4001389	7.28	7.28	8.66	5.43	9.25	4.09		
NT2RP4001396	5.76	5.76	6.42	2.83	4.61	2.12	*	-
NT2RP4001407	2.92	2.92	2.98	3.07	2.04	1.76		
NT2RP4001409	13.6	13.6	28.28	8.87	5.85	8.84		
NT2RP4001410	33.56	33.56	61.26	40.57	18.92	37.8		
NT2RP4001414	16.59	16.59	37.89	14.29	21.3	16.8		
NT2RP4001424	3.55	3.55	8.85	7.99	10.45	7.41		
NT2RP4001433	3.85	3.85	6	8.39	9.79	3.38		
NT2RP4001438	9.95	9.95	27.94	46.22	53.63	30.76	*	+
NT2RP4001442	4.33	4.33	4.97	3.3	3.41	2.64	*	-
NT2RP4001447	4.42	4.42	4.69	5.08	5.51	3.41		
NT2RP4001466	3.74	3.74	5.45	7.38	3.23	5.57		
NT2RP4001467	21.67	21.67	58.89	54.18	44.07	55.8		

NT2RP4001472	8.05	8.05	12.19	11.7	11.76	11.97		
NT2RP4001474	2.83	2.83	4.81	3.2	5.73	1.98		
NT2RP4001483	1.48	1.48	4.33	2.61	3.7	1.19		
NT2RP4001488	21.03	21.03	32.41	39.07	46.9	33.42		
NT2RP4001492	4.18	4.18	6.73	3.21	3.81	1.91		
NT2RP4001498	4.3	4.3	2.43	2.95	3.52	2.13		
NT2RP4001502	28.2	28.2	57.38	27.65	34.81	41.83		
NT2RP4001503	3.83	3.83	6.74	5.51	4.1	3.37		
NT2RP4001507	2.39	2.39	3.69	5.03	5.95	5.18	**	+
NT2RP4001510	1.74	1.74	4.63	5.64	5.05	3.02		
NT2RP4001516	3.54	3.54	4.16	2.52	1.9	1.27	*	-
NT2RP4001520	25.33	25.33	70.64	73.93	107.21	85.05		
NT2RP4001523	5.57	5.57	9.99	8.4	7.79	6.19		
NT2RP4001524	6.1	6.1	10.17	8.92	11.45	5.98		
NT2RP4001529	29.8	29.8	74.89	59.39	60.69	55.29		
NT2RP4001531	2.88	2.88	10.96	8.63	11.05	7.81		
NT2RP4001546	143.48	143.48	388.31	316.63	215.6	309.45		
NT2RP4001547	9.05	9.05	26.31	28.76	23.06	18.81		
NT2RP4001551	2.27	2.27	3.93	3.87	4.08	2.02		
NT2RP4001555	2.95	2.95	5.8	4.14	3.58	1.74		
NT2RP4001567	6.54	6.54	6.88	5.82	7.12	5.68		
NT2RP4001568	7.58	7.58	11.65	10.02	19.33	12.97		
NT2RP4001569	15.49	15.49	41.42	32.56	40.11	27.18		
NT2RP4001571	5.75	5.75	13.28	9.06	7.43	8.13		
NT2RP4001574	8.5	8.5	19.03	15.54	17.52	15.29		
NT2RP4001575	2.46	2.46	5.86	5.71	5.53	4.24		
NT2RP4001578	17.21	17.21	45.64	52.76	53.63	40.92		
NT2RP4001592	9.76	9.76	13.68	14.13	19.64	11.68		
NT2RP4001593	9.4	9.4	18.11	22.12	27.3	18.04		

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NT2RP4001605	5.97	5.97	4.78	4.1	7.77	4.66		
NT2RP4001606	2.9	2.9	8.34	6.01	3.51	6.75		
NT2RP4001607	2.04	2.04	5.24	4.57	3.26	3.78		
NT2RP4001610	1.74	1.74	2.42	2.6	2.48	1.7		
NT2RP4001614	2.17	2.17	7.19	5.38	4.34	6.86		
NT2RP4001623	2.38	2.38	5.26	2.43	2.65	2.02		
NT2RP4001626	9.48	9.48	11.67	18.67	23.9	19.44	**	+
NT2RP4001634	2.74	2.74	4.93	3.67	5.24	4.26		
NT2RP4001638	3.41	3.41	3.03	2.36	2.11	1.87	**	-
NT2RP4001644	7.86	7.86	33.73	24.36	26.04	24.99		
NT2RP4001646	11.61	11.61	15.02	7.42	10.74	11.21		
NT2RP4001656	3.75	3.75	5.23	2.89	4.51	2.07		
NT2RP4001666	1.99	1.99	4.68	3.26	6.25	2.02		
NT2RP4001670	11.74	11.74	15.51	12.45	7.09	8.31		
NT2RP4001677	28.27	28.27	42.75	42.01	45.48	47.53		
NT2RP4001679	8.82	8.82	33.83	33.23	51.5	29.78		
NT2RP4001695	7.71	7.71	12.76	15.66	20.35	12.87		
NT2RP4001696	2.64	2.64	5.45	3.13	3.92	3.72		
NT2RP4001699	3.58	3.58	8.03	3.18	4.12	4.42		
NT2RP4001717	2.79	2.79	7.03	3.29	5.84	4.15		
NT2RP4001719	3.59	3.59	9.11	7.6	9.27	6.28		
NT2RP4001725	2.27	2.27	4.79	2.28	5.07	1.43		
NT2RP4001726	7.07	7.07	11.18	5.85	6.91	4.98		
NT2RP4001730	3.11	3.11	12.82	11.96	19.81	16.3		
NT2RP4001739	2.83	2.83	5.83	5.79	6.55	4.98		
NT2RP4001741	7.25	7.25	15.93	9.28	12.42	10.97		
NT2RP4001753	3.04	3.04	8.4	4.39	4.64	6.64		
NT2RP4001760	4.32	4.32	6.6	7.79	7.73	12.96		
NT2RP4001787	67.61	67.61	173.05	169.17	187.1	193.22		

NT2RP4001790	2	2	5.29	3.42	2.97	2.58		
NT2RP4001795	9.31	9.31	12.31	14.38	19.76	12.34		
NT2RP4001803	3.35	3.35	3.6	3.94	4.78	3.67		
NT2RP4001805	2.64	2.64	3.57	3.64	2.47	2.95		
NT2RP4001809	4.84	4.84	26.35	18.18	23.17	11.33		
NT2RP4001817	11.55	11.55	19.09	9.5	10.78	12.71		
NT2RP4001822	2.09	2.09	5.36	3.73	5.11	3.33		
NT2RP4001823	1.91	1.91	3.95	1.14	3.34	1.24		
NT2RP4001827	14.88	14.88	25.96	35.78	40.37	29.5	*	+
NT2RP4001828	9.76	9.76	34.37	27.78	34.21	26.3		
NT2RP4001836	7.74	7.74	33.26	27.19	39.14	26.78		
NT2RP4001838	1.59	1.59	7.49	2.09	4.5	2.71		
NT2RP4001841	8.75	8.75	80.37	61.67	50.27	56.46		
NT2RP4001849	1.9	1.9	4.55	2.51	5.08	1.58		
NT2RP4001861	7.27	7.27	34.6	36.09	41.9	34.39		
NT2RP4001877	6.59	6.59	8.44	12.87	9.04	14.1	*	+
NT2RP4001879	9.64	9.64	15.47	11.58	14.24	10.73		
NT2RP4001889	5.09	5.09	10.66	6.68	11.25	8.91		
NT2RP4001893	3.97	3.97	7.34	3.19	6.11	2.72		
NT2RP4001896	3.18	3.18	6.86	5.38	7.87	4.92		
NT2RP4001898	7.83	7.83	26.41	22.98	20.13	20.15		
NT2RP4001901	1.73	1.73	4.69	4.08	5.87	2.69		
NT2RP4001910	39.51	39.51	58.21	53.45	33.59	45.93		
NT2RP4001925	4.1	4.1	10.21	6.69	6.32	6.12		
NT2RP4001926	6.41	6.41	7.22	7.1	9.54	5.52		
NT2RP4001927	6.26	6.26	9.97	5.83	8.13	2.82		
NT2RP4001931	8.64	8.64	14.16	15.49	17.54	11.89		
NT2RP4001933	38.49	38.49	87.13	96.81	133.51	91.22		
NT2RP4001938	2.93	2.93	4.53	4.27	3.31	3.55		

NT2RP4001942	13.44	13.44	27.12	31.34	24.8	18.71		
NT2RP4001945	1.41	1.41	4	1.55	3.67	1.77		
NT2RP4001946	1.97	1.97	5.67	3.04	3.96	1.66		
NT2RP4001947	4.42	4.42	8.93	5.92	9.81	5.16		
NT2RP4001950	4.13	4.13	5	2.25	2.84	1.34	*	-
NT2RP4001953	10.44	10.44	14.15	13.81	19.4	14.36		
NT2RP4001966	2.44	2.44	2.41	2.51	4.26	1.52		
NT2RP4001970	2.26	2.26	5.32	3.91	3.4	2.88		
NT2RP4001975	8.56	8.56	20.03	18.32	13.05	12.02		
NT2RP4001988	6.72	6.72	18.78	22.92	24.78	29.44	*	+
NT2RP4001996	5.27	5.27	12.83	10.65	16.35	12.42		
NT2RP4002014	3.4	3.4	8.14	43.19	37.87	33.17	**	+
NT2RP4002018	6.19	6.19	13.71	10.47	11.39	10.36		
NT2RP4002035	5.35	5.35	5.95	5.4	4.17	2.54		
NT2RP4002043	7.1	7.1	10.8	9.64	12.2	6.5		
NT2RP4002046	9.74	9.74	20.08	21.94	15.28	17.11		
NT2RP4002047	8.37	8.37	19.18	22.28	24.07	28.83	*	+
NT2RP4002052	5.78	5.78	10.36	9.02	9.36	9.37		
NT2RP4002056	32.58	32.58	71.49	58.09	76.58	49.75		
NT2RP4002057	6.37	6.37	11.06	12.13	13.58	7.41		
NT2RP4002058	3.85	3.85	6.6	4.1	4.2	3.22		
NT2RP4002064	5.93	5.93	4.39	2.6	4.16	2.07	*	-
NT2RP4002071	6.67	6.67	7.07	6.95	10.06	6.27		
NT2RP4002075	1.16	1.16	2.11	2.27	2.35	1.27		
NT2RP4002078	2.25	2.25	8.63	6.86	8.24	4.97		
NT2RP4002081	8.11	8.11	26.15	18.73	18.78	19.42		
NT2RP4002083	1.39	1.39	5.25	3.36	3.16	1.88		
NT2RP4002099	3.26	3.26	4.73	2.84	3.56	2.51		
NT2RP4002106	10.35	10.35	20.34	22.36	25.93	20.55		

NT2RP4002111	11.7	11.7	12.37	19.77	30.44	17.72		
NT2RP4002112	6.15	6.15	10.97	8.9	8.34	3.22		
NT2RP4002116	12.6	12.6	47.19	37.43	41.25	28.65		
NT2RP4002122	5.34	5.34	9.29	14.84	14.86	12.67	**	+
NT2RP4002126	6.42	6.42	14.44	16.82	14.35	10.42		
NT2RP4002133	7.56	7.56	20.82	29.17	26.14	21		
NT2RP4002136	3.63	3.63	5.74	4.89	5.38	2.69		
NT2RP4002139	26.89	26.89	31.12	60.65	61.92	32.88		
NT2RP4002174	139.27	139.27	232.64	240.71	275.01	193.19		
NT2RP4002185	7.77	7.77	13.2	12.36	19.06	11.58		
NT2RP4002186	4.5	4.5	9.83	7.82	4.72	6.78		
NT2RP4002187	15.42	15.42	32.13	26.94	19.84	21.17		
NT2RP4002188	3.01	3.01	8.34	8.3	7.75	6.41		
NT2RP4002199	1.85	1.85	3.73	2.6	2.91	3.78		
NT2RP4002206	2.08	2.08	3.39	2.48	2.34	1.29		
NT2RP4002210	3.13	3.13	4.75	2.02	2.86	0.98		
NT2RP4002222	4.2	4.2	6.63	5.56	6.28	4.16		
NT2RP4002241	7.97	7.97	8.24	10.82	11.75	7.19		
NT2RP4002248	5.08	5.08	16.69	10.74	8.9	8.13		
NT2RP4002250	1.54	1.54	3.22	0.73	1.69	0.56		
NT2RP4002259	4.86	4.86	9.82	3.21	4.85	1.75		
NT2RP4002268	16.62	16.62	29.54	28.9	28.18	25.68		
NT2RP4002288	6.42	6.42	12.57	13.29	14.36	11.97		
NT2RP4002290	7.55	7.55	7.61	7.96	7.67	5.87		
NT2RP4002298	3.92	3.92	4.18	5.54	5.03	4.18		
NT2RP4002306	2.38	2.38	5.79	2.97	5.77	2.64		
NT2RP4002308	2.04	2.04	6.03	5.31	5.23	4.1		
NT2RP4002336	2.71	2.71	6.33	3.71	4.19	4.63		
NT2RP4002340	1.09	1.09	3.96	1.28	2.75	0.49		

NT2RP4002361	2.77	2.77	5.78	3.73	4.03	2.48		
NT2RP4002367	2.27	2.27	5.84	3.23	2.48	2.77		
NT2RP4002368	9.87	9.87	17.2	18.26	19.27	16		
NT2RP4002377	3.3	3.3	23.8	25.46	30.75	23.93		
NT2RP4002408	2.22	2.22	3.87	3.75	6.37	4.11		
NT2RP4002425	2.84	2.84	5.81	8.24	7.98	5.23		
NT2RP4002432	12.33	12.33	85.4	61.06	72.53	67.82		
NT2RP4002447	2.97	2.97	7.68	3.96	5.4	4.59		
NT2RP4002451	5.48	5.48	6.2	5.84	5.85	6.83		
NT2RP4002461	9.8	9.8	32.09	32.76	38.91	29.04		
NT2RP4002486	3.5	3.5	6.71	2.47	4.15	2.87		
NT2RP4002517	3.65	3.65	9.11	7.02	8.53	7.18		
NT2RP4002556	4.29	4.29	3.91	5.68	10.03	6.41		
NT2RP4002569	3.36	3.36	7.36	4.93	5.29	3.42		
NT2RP4002587	2.26	2.26	4.19	2.8	3.4	2.02		
NT2RP4002591	2.21	2.21	4.89	2.89	4.5	3.08		
NT2RP4002607	1.43	1.43	3.34	2.87	4.63	1.58		
NT2RP4002627	17.83	17.83	61.9	55.9	76.17	65.3		
NT2RP4002628	7.28	7.28	15.48	14.53	23.95	12.54		
NT2RP4002630	4.19	4.19	5.25	6.72	9.4	7.16	*	+
NT2RP4002639	9.43	9.43	70.25	52.38	77.24	57.28		
NT2RP4002641	1.58	1.58	9.03	3.94	4.07	4.1		
NT2RP4002658	114.62	114.62	166.93	76.49	34.96	109.83		
NT2RP4002669	3.5	3.5	5.67	5.4	5.33	4.68		
NT2RP4002677	6.24	6.24	9.41	10.14	7.99	13.62		
NT2RP4002715	8.42	8.42	34.92	40.1	48.46	32.3		
NT2RP4002750	2.6	2.6	8.29	1.68	2.04	1.33		
NT2RP4002784	3.71	3.71	9.51	9.44	11.22	7.06		
NT2RP4002791	4.91	4.91	9.44	4.88	9.76	5.33		

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NT2RP4002811	1.63	1.63	6.38	3.17	2.95	3.43		
NT2RP4002830	4.26	4.26	7.45	3.9	5.9	5.46		
NT2RP4002832	2.12	2.12	3.13	2.38	5.59	2.54		
NT2RP4002850	5.07	5.07	12.04	14.36	12.63	8.06		
NT2RP4002874	5.17	5.17	6.67	3.41	5.14	1.96		
NT2RP4002884	28.81	28.81	49.75	43.57	74.75	52.87		
NT2RP4002888	5.55	5.55	4.83	3.67	4.32	3.08	*	-
NT2RP4002891	5.48	5.48	15.79	13.16	19.42	11.91		
NT2RP4002894	12.04	12.04	24.47	18.44	12.76	16.4		
NT2RP4002896	5.54	5.54	12.2	8.96	6.18	7.78		
NT2RP4002905	1.71	1.71	4.27	2.32	3.58	1.28		
NT2RP4002907	5.11	5.11	7.62	6.94	10.72	1.41		
NT2RP5003459	68.11	68.11	133.25	154.61	146.15	164.37	*	+
NT2RP5003461	7.34	7.34	10.14	10.85	14.36	8		
NT2RP5003471	106.6	106.6	168.71	124.4	148.85	112.14		
NT2RP5003477	2.71	2.71	2.62	2.59	2.33	1.9		
NT2RP5003487	157.44	157.44	424.89	292.71	256.56	354.93		
NT2RP5003492	3.1	3.1	4.91	5.25	6.17	5.91	*	+
NT2RP5003500	1.5	1.5	3.28	2.38	2.54	2.59		
NT2RP5003506	4.96	4.96	9.3	7.83	10.37	9.04		
NT2RP5003512	2.21	2.21	4.35	2.63	3.46	2.15		
NT2RP5003522	4.1	4.1	5.97	4.62	4.19	2.34		
NT2RP5003524	4.38	4.38	3.86	1.61	1.54	0.84	**	-
NT2RP5003527	24.72	24.72	71.27	76.81	87.24	60.59		
NT2RP5003531	7.16	7.16	17.2	15.58	14.06	14.11		
NT2RP5003534	2.68	2.68	5.49	5.54	6.82	4.55		
NT2RP6000020	8.69	8.69	19.96	14.65	15.13	16.29		
NT2RP6000022	3.19	3.19	4.05	4.06	3.96	2.44		
NT2RP6000050	3.95	3.95	3.99	4.98	5.82	2.88		

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NT2RP6000063	3.91	3.91	6.04	3.61	2.52	2.56		
NT2RP6000074	5.38	5.38	4.88	3.41	3.27	2.17	**	-
NT2RP6000083	7.76	7.76	11.18	11.49	16	9.91		
NT2RP6000100	2.49	2.49	4.58	4.04	4.71	3.3		
NT2RP6000123	1.94	1.94	3.29	5.1	4.26	4.22	*	+
NT2RP6000129	1.9	1.9	4.47	4.06	4.27	2.74		
NT2RP6000147	3.75	3.75	11.74	10.8	11.03	7.48		
NT2RP6000163	2.62	2.62	4.23	2.28	1.95	1.71		
NT2RP6000181	8.03	8.03	12.4	9.44	13.25	9.01		
NT2RP6000182	5.44	5.44	6.42	4.82	5.56	3.88		
OVARC1000001	4.97	4.97	5.24	6.04	7.48	2.35		
OVARC1000003	3.21	3.21	8.31	8.51	7.66	7.05		
OVARC1000004	9.87	9.87	116.19	88.04	109.99	85.44		
OVARC1000006	3.57	3.57	6.58	9.04	7.88	4.73		
OVARC1000013	6.51	6.51	9.19	7.32	8.36	8.33		
OVARC1000014	3.39	3.39	5.02	4.23	5.02	4.17		
OVARC1000017	3.11	3.11	6.81	4.2	4.45	2.72		
OVARC1000026	24.79	24.79	32.1	56.82	69.34	44.53	*	+
OVARC1000035	11.11	11.11	20.26	20.41	23.65	15.36		
OVARC1000037	8.73	8.73	19.12	15.64	9.13	15.9		
OVARC1000058	6.06	6.06	11.69	13.84	7.56	10.6		
OVARC1000060	1.89	1.89	6.28	5.98	5.24	5.13		
OVARC1000068	2.38	2.38	5.33	5.31	3.56	2.42		
OVARC1000069	74.66	74.66	101.53	75.95	84.36	86.42		
OVARC1000071	4.4	4.4	4.77	6.47	5.35	4.04		
OVARC1000075	55.43	55.43	125.63	120.89	150.97	117.03		
OVARC1000083	9.58	9.58	9.24	13.12	12.7	10.64	*	+
OVARC1000085	106.6	90.9	156.14	214.2	177.05	273.14	*	+
OVARC1000086	3.98	6.82	9.23	11.98	11.3	14.09	*	+

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OVARC1000087	1.51	2.83	1.79	4.03	3.57	3.35	*	+
OVARC1000090	1.48	4.1	6.14	10.88	9.58	8.79	*	+
OVARC1000091	4.88	8.33	8.01	7.99	7.76	6.82		
OVARC1000092	2.83	6.81	4.18	4.68	6.25	4.85		
OVARC1000105	9.73	14.86	17.21	26.29	25.62	22.88	*	+
OVARC1000106	26.02	23.03	46.38	66.36	50.1	53.01	*	+
OVARC1000109	9.12	13.08	18.04	16.72	12.91	17.46		
OVARC1000113	4.12	6.25	6.53	6.83	8.19	7.65		
OVARC1000114	2.14	3.44	5.77	5.94	5.86	4.98		
OVARC1000133	2.53	4.96	6.36	4.05	4.97	2.95		
OVARC1000137	6.14	10.05	13.51	13.3	18.59	14.39		
OVARC1000139	14.75	20.77	83.44	71.14	98.1	69.29		
OVARC1000145	0.72	6.64	2.89	1.78	2.42	2		
OVARC1000148	5.09	4.98	7.88	4.91	5.32	7.91		
OVARC1000151	1.41	2.11	2.4	3.58	4.08	3.58	**	+
OVARC1000157	10.99	14.16	17.51	21.21	25.06	22.76	*	+
OVARC1000162	1.22	4.4	2.5	2.93	2.49	2.59		
OVARC1000168	1.98	8.46	6.2	8.01	9.61	9.96		
OVARC1000169	32.03	45.07	49.48	70.63	69.6	89.08	*	+
OVARC1000178	0.84	5.08	2.53	3.37	3.18	2.78		
OVARC1000182	0.8	3.3	1.42	2.02	1.95	1.78		
OVARC1000186	2.51	3.72	3.23	5.95	3.27	4.77		
OVARC1000188	1.04	2.67	2.33	2.48	2.87	1.9		
OVARC1000191	1.01	3.8	2.63	3.12	2.85	2.54		
OVARC1000198	2.09	3.59	4.32	5.62	5.12	5.06	*	+
OVARC1000208	6.49	10.37	22.5	17.79	24.54	22.02		
OVARC1000209	7.99	13.69	22.82	23.42	27.81	29.16		
OVARC1000212	2.47	5.63	3.59	4.76	5.03	4.88		
OVARC1000216	1.72	4.96	4.36	15.43	11.3	12.54	**	+

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OVARC1000240	2.98	3.53	8.13	5.39	5.46	4.87		
OVARC1000241	1.29	2.47	3.18	2.65	3.17	1.4		
OVARC1000249	4.14	5.43	8.17	5.46	5	6.13		
OVARC1000254	33.15	39.39	100.99	100.41	131.42	100.89		
OVARC1000255	0.85	4.83	2.51	2.98	2.45	1.95		
OVARC1000267	2.37	6.41	6.71	6.66	7.16	7.31		
OVARC1000275	79.02	93.7	161.08	199.43	240.76	175.96	*	+
OVARC1000287	226.67	224.66	236.08	433.91	512.76	470.31	**	+
OVARC1000288	3.2	4.25	7.38	6.23	5.32	4.47		
OVARC1000298	8.96	10.09	19.62	13.37	7.19	9.6		
OVARC1000302	1.12	2.14	2.13	2.47	1.85	2		
OVARC1000304	1.09	2.68	3.23	5.02	3.41	6		
OVARC1000307	2.95	6.19	4.74	7.59	4.7	6.29		
OVARC1000309	1.18	7.16	3.22	3.24	2.85	2.4		
OVARC1000312	2.83	11.64	6.03	4.17	5.4	2.46		
OVARC1000313	10.48	19.25	14.81	9.39	17.54	22.17		
OVARC1000321	31.6	24.05	47.79	30.5	31.37	15.43		
OVARC1000326	1.52	2.3	3.9	3.84	3.17	2.79		
OVARC1000327	1.52	3.28	4.24	3.13	1.49	2.46		
OVARC1000331	2.22	4.72	2.41	4.33	4.45	4.58		
OVARC1000335	2.3	5.84	4.02	2.72	5.16	4.75		
OVARC1000347	1.83	8.18	6.24	7.35	9.24	8.44		
OVARC1000348	1.61	10.62	3.73	2.84	4.59	3.05		
OVARC1000363	3.7	9.61	6.51	7.31	11.52	6.83		
OVARC1000377	1.07	2.09	2.43	2.28	2.51	2.45		
OVARC1000382	3.34	3.39	4.33	5.07	2.52	1.03		
OVARC1000384	4.2	5.42	8.35	5.32	4.4	6.04		
OVARC1000401	0.62	3.63	2.09	3.35	4.08	3.64		
OVARC1000406	18.98	23.3	49.12	57.09	74.48	54.63	*	+

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OVARC1000407	1.99	6.28	3.99	4.11	6.42	3.16		
OVARC1000408	27.5	38.45	70.39	74.84	111.17	71.25		
OVARC1000410	6.83	12.72	10.41	4.78	6.65	5.01		
OVARC1000411	0.91	1.5	2.6	3.49	3	2.22		
OVARC1000414	1.31	2.22	3.7	4.5	3.78	3.71		
OVARC1000420	1.44	2.76	3.29	3.3	2.59	2.1		
OVARC1000421	1.42	2.65	3.33	3.96	4.21	4.99	*	+
OVARC1000427	25.78	27.02	130.06	156.9	215.67	142.19		
OVARC1000431	10.51	17.6	19.12	33.66	31.78	25.78	*	+
OVARC1000437	3.14	6.37	7.31	5.97	7.63	6.36		
OVARC1000439	5.81	10.95	13.82	21.81	23.01	21.52	**	+
OVARC1000440	2.56	3.74	5.01	7.47	9.31	7.08	*	+
OVARC1000442	2.34	2.38	6.81	6.66	9.5	8.12		
OVARC1000443	2.09	2.2	2.88	3.29	3.41	2.62		
OVARC1000461	1.11	2.84	2.2	2.55	1.12	2.14		
OVARC1000465	3.27	5.01	3.51	3.94	4.62	3.95		
OVARC1000466	1.94	5.47	5.9	6.54	10.13	6.76		
OVARC1000467	1.01	5.08	2.41	3.65	2.98	3.78		
OVARC1000470	1.13	5.81	3.03	3.18	4.02	3.78		
OVARC1000473	1.81	1.95	2.65	2.44	4.16	1.39		
OVARC1000479	5.67	5.88	9.88	10.35	14.26	6.88		
OVARC1000484	3.99	5.74	6.54	8.66	9.93	6.87		
OVARC1000486	3.17	4.71	4.49	5.74	4.93	4.28		
OVARC1000496	0.93	3.55	0.66	0.31	1.07	0.62		
OVARC1000520	0.84	5.89	1.18	1.32	2.27	2		
OVARC1000522	4.1	7.19	12	13.85	14.03	10.34		
OVARC1000526	1.96	7.04	3.75	5.93	5.48	4.69		
OVARC1000529	2.38	2.57	4.44	3.66	4.16	3.08		
OVARC1000533	3.3	4.66	7.95	8.89	12.29	7.83		

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OVARC1000543	0.84	2.44	2.06	2.57	3.08	2.72		
OVARC1000550	0.75	3.68	2.32	2.82	4.04	2.34		
OVARC1000553	2.1	5.63	7.02	7.72	7.69	6.95		
OVARC1000556	5.77	15.21	11.77	8.95	13.91	8.96		
OVARC1000557	0.83	5.12	1.4	1.61	2.29	1.88		
OVARC1000561	3.48	7.38	9.26	13	17.66	15.09	*	+
OVARC1000564	8.89	9.02	10.44	17.84	11.31	16.69	*	+
OVARC1000573	1.87	3.68	4.86	5.75	5.32	3.83		
OVARC1000576	24.12	29.23	124.94	83.09	93.83	98.58		
OVARC1000578	2.43	4.6	5.53	8.64	4.46	3.93		
OVARC1000581	0.34	3.28	1.15	1.75	1.27	1.23		
OVARC1000586	22.54	28.9	41.17	34.58	43.39	40.93		
OVARC1000588	0.74	5.23	2.03	2.75	3.72	2.05		
OVARC1000605	1.98	2.62	2.88	4.47	4.23	3.87	**	+
OVARC1000622	3.86	4.59	11.57	12.7	11.13	11.6		
OVARC1000636	1.64	3.79	4.58	4.19	4.03	5.09		
OVARC1000640	1.97	4.72	3.93	4.21	3.67	3.09		
OVARC1000649	9.69	14.8	53.54	53.32	64.51	52.67		
OVARC1000661	1.14	9.33	2.99	5.34	5.24	5.24		
OVARC1000677	8.53	10.16	14.87	11.77	10.98	15.47		
OVARC1000678	1.21	4.49	2.71	3.28	4.17	3.26		
OVARC1000679	2.86	3.25	4.09	5.29	5.16	6.25	*	+
OVARC1000681	1.47	1.55	3.2	2.41	2.22	1.71		
OVARC1000682	10.09	11.33	50.91	33.79	47.49	44.31		
OVARC1000689	3.81	7.1	19.94	20.18	22.12	21.83		
OVARC1000700	1.8	10.37	3.18	4.98	4.37	5.14		
OVARC1000703	1.74	7.18	5.35	6.4	6.64	7.77		
OVARC1000722	10.59	11.92	47.93	43.41	60.06	39.34		
OVARC1000726	1.44	3.48	4.62	4.88	5.89	3.58		

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OVARC1000727	1.93	2.09	4.13	3.78	3.79	3.89		
OVARC1000730	5.95	5.86	9.01	4.07	4.16	5.62		
OVARC1000741	4.85	6.13	8.74	15.19	10.58	13.71	*	+
OVARC1000746	0.89	3.61	2.43	2.06	2.9	2.84		
OVARC1000764	1.76	4.93	4.77	5.35	7.01	5.44		
OVARC1000769	1.13	4.3	3.6	3.76	4.42	5.2		
OVARC1000771	2.42	6.28	2.3	4.02	4.81	3.71		
OVARC1000773	19.09	24.7	31.93	44.69	56.24	46.24	*	+
OVARC1000775	11.67	8.94	16.44	12.16	8.7	4.26		
OVARC1000778	2.37	3.89	5.69	4.59	6.23	4.92		
OVARC1000779	0.8	2.02	1.85	2.23	2.45	1.46		
OVARC1000781	1.67	5.05	4.16	6.37	3.45	5.07		
OVARC1000787	1.64	4.79	4.22	2.97	5.44	3.25		
OVARC1000789	7.62	14.23	16.39	24.95	29.69	25.94	**	+
OVARC1000800	2.91	10.72	5.72	6.41	10.65	6.2		
OVARC1000802	1.55	8.77	2.97	2.99	5.34	2.76		
OVARC1000810	3.37	3.54	8.29	6.66	7.99	7.21		
OVARC1000811	2.41	2.73	7.5	4.88	3.67	4.95		
OVARC1000814	3.44	4.55	9.03	7.92	11.3	9.05		
OVARC1000816	7.64	10.41	12.41	10.99	10.58	14.11		
OVARC1000817	1.18	3.38	1.27	1.71	2.14	1.55		
OVARC1000834	2.46	8.3	3.39	4.84	5.81	4.01		
OVARC1000846	2.23	10.02	5.35	7.38	9.66	7.72		
OVARC1000850	1.74	8.37	3.38	3.39	2.51	3.1		
OVARC1000853	23.21	24.23	43.4	30.67	37.81	18.39		
OVARC1000862	2.28	2.66	4.91	3.05	1.61	1.49		
OVARC1000873	2.56	2.98	4.14	4.4	3.79	3.85		
OVARC1000875	1.47	3.07	1.79	2.35	3.09	1.87		
OVARC1000876	3.71	5.67	4.46	5.11	6.06	5.45		

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OVARC1000883	6.06	9.53	9.18	12.43	15.42	13.05	*	+
OVARC1000885	2.84	9.95	3.38	3.74	5.66	4.11		
OVARC1000886	4.31	8.19	4.29	3.74	5.15	4.39		
OVARC1000890	17.47	18.3	91.22	70.97	78.71	51.68		
OVARC1000891	1.28	1.44	3.03	2.85	2.19	3.22		
OVARC1000897	0.48	1.74	1.29	1.21	1.33	0.5		
OVARC1000912	2.06	3.22	4.33	5.21	6.1	5.86	*	+
OVARC1000914	1.48	6.18	1.61	3.68	3.02	2.18		
OVARC1000915	1.71	6.64	4.14	4.87	3.54	4.76		
OVARC1000916	1.91	5.19	2.56	4.05	4.32	3.88		
OVARC1000924	1.45	5.5	3.09	3.28	3.85	3.48		
OVARC1000928	6.05	5.46	8.78	4.22	5.83	5.35		
OVARC1000936	1.37	1.39	2.17	2.04	3.25	2.49		
OVARC1000937	1.69	3.01	1.94	4.17	3.26	3.24		
OVARC1000945	1.55	3.67	3.62	3.83	3.22	2.28		
OVARC1000948	1.57	3.85	2.66	3.15	3.68	1.99		
OVARC1000956	1.41	5.08	4.36	7.56	7.26	5.51		
OVARC1000959	1.8	4.87	3.39	4.88	3.02	3.9		
OVARC1000960	2.64	7.53	9.55	11.64	13.89	12.86	*	+
OVARC1000964	19.89	17.19	103.98	118.41	165.46	96.14		
OVARC1000971	0.42	1.58	1.4	2.53	2.27	2.28	*	+
OVARC1000975	5.93	8.3	36.1	31.27	51.54	30.22		
OVARC1000976	0.65	2.12	1.27	2.17	1.46	1.5		
OVARC1000981	4.06	7.18	4.94	7.97	12.1	8.53		
OVARC1000982	2.83	5.41	2.23	3.13	3.02	3.54		
OVARC1000984	1.78	5.43	3.32	3.01	3.08	2.16		
OVARC1000995	2.94	6.59	4.5	5.98	6.19	6.72		
OVARC1000996	1.68	1.87	4.29	3.58	4.15	4.56		
OVARC1000999	6.02	5.65	15.29	15.61	13.18	13.29		

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OVARC1001000	1.96	4.5	6.2	6.26	7.09	6.86		
OVARC1001004	0.51	3.4	1.45	2.05	3.3	1.47		
OVARC1001010	1.35	3.99	1.66	3.04	1.4	1.54		
OVARC1001011	1.46	5.57	1.13	2.39	3.27	2.45		
OVARC1001030	96.19	101.41	143.98	119.24	154.26	133		
OVARC1001032	1.42	5.34	1.89	1.83	2.82	1.92		
OVARC1001034	4.44	5.58	6.51	3.29	5.21	3.77		
OVARC1001038	3.62	5.03	7.4	10.3	10.88	8.61	*	+
OVARC1001040	2.63	3.77	6.93	5.25	6.51	4.25		
OVARC1001041	4.54	8.03	12.87	8.57	12.25	9.4		
OVARC1001044	1.05	2.92	1.83	1.96	2.43	1.84		
OVARC1001049	3.78	8.78	10.67	10.65	11.87	10.26		
OVARC1001051	40.95	55.97	80.66	66.89	109.71	87.49		
OVARC1001054	1.22	4.06	3.22	2.86	4.19	1.93		
OVARC1001055	2.13	3.38	3.82	4.32	5.61	5.22	*	+
OVARC1001062	5.8	6.15	12.54	8.04	9.94	9.57		
OVARC1001065	8.85	13.63	51.33	51.41	60.3	56.97		
OVARC1001068	2.82	5.62	4.76	4.72	4.02	5.52		
OVARC1001072	0.73	4.18	4.41	3.2	3.71	3.07		
OVARC1001073	0.92	5.7	2.65	2.91	2.54	1.79		
OVARC1001074	0.81	4.66	3.31	1.87	2.95	2.04		
OVARC1001078	2	5.12	2.79	3.57	3.08	2.83		
OVARC1001085	2.41	2.83	3.66	5.54	5.02	6.36	**	+
OVARC1001086	1.97	3.17	2.85	3.98	2.83	4.13		
OVARC1001091	16.24	19.32	92.73	76.48	96.74	77.99		
OVARC1001092	4.62	5.35	7.22	9.69	7.84	6.05		
OVARC1001104	1.05	4.37	2.66	3.16	2.58	2.03		
OVARC1001107	11.59	15.6	40.28	31.21	49.49	42.22		
OVARC1001113	1.04	5.81	1.59	2.46	3.05	2.39		

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OVARC1001117	2.71	6.63	4.31	4.67	5.74	2.67		
OVARC1001118	2.38	3.69	7.08	7.36	6.91	8.28		
OVARC1001125	2.02	2.9	3	5.92	4.97	5.9	**	+
OVARC1001129	2.61	4.58	3.19	8.46	9.43	11	**	+
OVARC1001132	1.7	6.48	2.66	3.69	4.26	4.66		
OVARC1001138	9.52	15.82	23.8	48.95	45.16	44.97	**	+
OVARC1001141	1.68	4.97	3.48	3.77	3.68	3.84		
OVARC1001154	18.31	29.49	68.39	60.43	83.49	65.64		
OVARC1001161	2.49	5.55	6.15	7.03	6.69	5.89		
OVARC1001162	2.2	3.13	5.34	5.09	4.86	5.26		
OVARC1001163	0.69	3.59	2.77	2.2	3.98	2.54		
OVARC1001167	3.03	4.57	7.69	10.19	12.95	9.3	*	+
OVARC1001169	0.74	4.87	2.68	2.47	1.91	2.06		
OVARC1001170	7.81	15.04	17.59	14.61	19.45	14.99		
OVARC1001171	15.57	17.71	24.31	16.12	23.34	22.51		
OVARC1001173	2.09	5.08	5.1	4.32	6.75	5.49		
OVARC1001176	22.57	21.48	89.96	76.74	102.3	70.7		
OVARC1001180	3.01	4.58	12.7	11.81	10.77	9.56		
OVARC1001188	2.66	3.7	3.95	3.62	3.44	4.16		
OVARC1001200	1.52	4.56	3.62	3.47	2.9	2.96		
OVARC1001202	3.75	6.65	6.53	9.26	7.79	10.23	*	+
OVARC1001206	1.52	5.52	1.15	1.59	1.13	1.9		
OVARC1001209	4.89	8.92	27.46	24.69	30.38	24.27		
OVARC1001219	1.81	6.36	4.71	5.33	3.95	3.62		
OVARC1001222	2.5	8.36	5.01	3.2	4.34	5.63		
OVARC1001232	2.91	4.18	7.74	6.75	6.02	5.65		
OVARC1001240	2.05	3.27	6.84	5.55	5.06	5.4		
OVARC1001243	0.94	2.59	1.76	3.64	2.64	1.86		
OVARC1001244	9.07	12.05	18	21.61	18.57	26.62		

OVARC1001246	30.48	50.95	48.51	80.54	100.83	101.88	**	+
OVARC1001247	3.64	9.86	7.7	6.57	7.02	4.49		
OVARC1001260	1.05	9.07	1.85	2.62	2.65	1.85		
OVARC1001261	4.23	10.5	6.99	3.46	2.08	2.94		
OVARC1001268	24.4	19.69	52.37	32.58	35.32	14.16		
OVARC1001270	14.46	15.1	20.83	9.69	9.8	8.65	*	-
OVARC1001271	2.62	3.62	3.88	3.95	7.02	4.26		
OVARC1001282	0.88	3.02	3.09	1.37	1.59	2		
OVARC1001296	3.02	8.06	2.3	3.04	4.11	5.41		
OVARC1001306	1.48	8.27	2.4	2.04	2.29	3.82		
OVARC1001314	0.49	8.47	1.57	1.06	1.79	1.32		
OVARC1001316	2.77	7.17	4.81	5.48	8.11	5.36		
OVARC1001329	6.12	6.18	21.11	17.09	19.29	16.22		
OVARC1001330	0.2	1.89	1.38	1.22	1.35	1.42		
OVARC1001336	1.92	3.7	3.59	5.67	4.09	4.02		
OVARC1001338	0.26	2.87	0.86	2.49	1.71	1.07		
OVARC1001339	12.07	18.29	22.73	33.65	32.72	37.29	**	+
OVARC1001340	0.72	4.83	1.23	1.33	2.44	1.3		
OVARC1001341	4.35	9.25	6.77	7.94	11.38	9.69		
OVARC1001342	90.37	98.53	136.12	129.68	163.22	127.78		
OVARC1001344	2.1	2.51	6.27	6.52	6.89	6.2		
OVARC1001357	5.61	8.93	16.02	15.52	11.34	11.69		
OVARC1001359	8.96	12.4	16.15	21.66	13.84	10.6		
OVARC1001360	0.44	2.52	0.99	1.97	2.6	1.62		
OVARC1001369	1.56	5.66	1.89	3.41	1.88	3.1		
OVARC1001372	0.96	4.23	3.33	1.52	2.77	1.95		
OVARC1001376	1.82	5.1	3.62	5.79	5.79	4.18		
OVARC1001381	4.51	6.44	9.94	10.95	12.91	11.21		
OVARC1001391	0.5	1.62	1.44	1.88	1.27	1.26		

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OVARC1001392	2.12	4.69	6.14	11.96	12.7	7.79	*	+
OVARC1001399	0.98	3.59	2.16	1.77	2.54	1.1		
OVARC1001417	1.01	3.07	1.76	2.39	3.61	2.81		
OVARC1001419	2.47	5.4	3.06	4.39	4.03	3.16		
OVARC1001425	2.29	5.58	5.15	8.76	8.5	8.07	*	+
OVARC1001436	1.37	5.85	2.54	2.9	3.57	3.18		
OVARC1001442	0.64	4.84	1.39	2.27	1.52	0.69		
OVARC1001451	3.09	2	3.89	5.18	5.98	4.75	*	+
OVARC1001452	1.35	2.41	2.87	2.96	4.69	3.13		
OVARC1001453	1.21	2.84	1.88	2.3	1.82	1.57		
OVARC1001476	10.67	14.38	16.52	17.22	12.9	13.09		
OVARC1001480	0.93	4.73	1.5	3.1	2.98	2.21		
OVARC1001489	0.97	6.89	2.51	3.01	2.83	2.09		
OVARC1001493	2.09	6.59	3.75	7.38	8.78	10.48	*	+
OVARC1001496	4.65	9.58	8.63	10.74	7.37	11.03		
OVARC1001499	1.24	1.18	2.6	3.47	2.68	2.84		
OVARC1001506	2.9	2.7	5.31	5.33	6.73	5.48		
OVARC1001509	1.73	3.89	3.69	4.07	4.59	3.07		
OVARC1001510	0.16	3.69	1.42	1.94	1.73	0.86		
OVARC1001516	2.57	5.78	3.85	6.04	4.97	4.39		
OVARC1001525	0.53	4.76	2.12	1.94	2.01	1.81		
OVARC1001542	8.8	12.86	13.01	15.91	13.63	17.23		
OVARC1001544	2.14	6.6	6.72	7.54	8.33	6.22		
OVARC1001546	4.08	4.32	4.6	6.12	5.31	7.23	*	+
OVARC1001547	1.29	2.53	1.68	2.44	1.85	2.22		
OVARC1001555	10.39	16.51	68.77	48.66	65.39	56.39		
OVARC1001560	3.35	4.91	5.52	5.36	4.93	5.34		
OVARC1001569	1.63	4.75	4.79	5.92	5.19	5.1		
OVARC1001570	3.96	7.9	6.93	7.72	10.7	8.55		

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OVARC1001577	1.68	5.89	5.41	8.61	6.9	10.2		
OVARC1001578	0.25	3.47	-0.19	-0.47	0.24	0.15		
OVARC1001596	12.13	11.65	14.23	13.51	14.82	27.15		
OVARC1001600	1.13	2.9	1.48	2.81	2.67	3.67		
OVARC1001607	6.22	7.72	10.91	13.42	14.01	13.45	*	+
OVARC1001610	1.81	5.25	2.84	4.25	2.66	2.7		
OVARC1001611	0.13	5.11	1.24	1.48	2.89	1.79		
OVARC1001615	0.58	5.42	1.93	1.54	2.56	1.74		
OVARC1001636	1.09	3.75	1.05	2.39	2.05	2.15		
OVARC1001668	3.77	6.75	10.04	10.5	11.4	10.48		
OVARC1001702	1.18	2.21	2.42	3.86	2.07	2.25		
OVARC1001703	2.82	3.18	2.97	2.64	4.71	4.65		
OVARC1001710	3.58	7.03	8.67	8.01	6.28	9.55		
OVARC1001711	1.96	7.3	3.36	5.01	4.15	5.4		
OVARC1001713	9.17	11.54	44.65	36.47	51.48	43.79		
OVARC1001725	1.01	5.45	6.11	2.56	3.77	4.01		
OVARC1001726	1.64	4.48	3.23	4.97	5.6	5.18		
OVARC1001727	1.4	2.41	1.52	1.43	2.35	1.14		
OVARC1001731	120.62	110.86	255.43	140.73	139.03	74.2		
OVARC1001735	1.29	3.44	3.54	3.75	3.25	2.89		
OVARC1001741	3.3	4.73	15.28	13.09	12.93	13.17		
OVARC1001745	2.72	5.39	6.83	9.17	10.23	8.89	*	+
OVARC1001759	3.31	9.01	6.31	7.61	7.61	11.95		
OVARC1001762	3.96	7.78	6.38	10.3	11.01	13.4	*	+
OVARC1001766	5.33	7.8	11.99	15.56	16.86	15.33	*	+
OVARC1001767	0.94	3.76	1.18	1.97	1.96	2.41		
OVARC1001768	3.31	3.86	3.76	5.35	4.59	3.54		
OVARC1001770	3.04	6.58	9.98	11.46	9.08	9.46		
OVARC1001776	2.11	4.7	3.5	4.72	3.64	2.92		

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OVARC1001791	1.13	4.77	3.54	3.07	3.12	3.42		
OVARC1001795	0.89	6.19	1.24	2.31	2.87	2.11		
OVARC1001798	2.81	12.11	7.57	9.72	11.93	9.04		
OVARC1001802	1.73	11.64	4.9	5.6	5.93	4.01		
OVARC1001805	1.92	6.96	2.58	3.62	4.59	3.51		
OVARC1001807	1.9	2.53	4.18	3.06	3.12	2.46		
OVARC1001809	12.38	14.06	76.32	55.87	81.41	52.83		
OVARC1001812	1.44	3.39	3.15	3.23	4.63	3.71		
OVARC1001813	1.61	4.29	2.33	2.93	3.98	2.51		
OVARC1001820	1.67	7.15	3.21	3.47	3.76	3.22		
OVARC1001828	0.78	6.85	2.36	1.91	3.23	2.2		
OVARC1001833	1.07	8.12	2.02	2.4	2.1	1.92		
OVARC1001839	1.56	8.43	2.98	2.91	3.59	1.15		
OVARC1001846	1.91	1.38	2.9	2.15	2.11	1.8		
OVARC1001849	1.21	2.52	2.42	5.79	3.69	4.03	*	+
OVARC1001861	1.46	3.56	2.73	2.78	2.5	2.09		
OVARC1001873	3.09	3.78	4.68	5.47	4.42	4.73		
OVARC1001879	1.44	6.08	3.48	2.35	2.93	2.22		
OVARC1001880	0.91	7.84	2.94	3.63	5.78	3.8		
OVARC1001883	0.99	7.61	3.12	2.61	3.42	2.52		
OVARC1001900	1.11	7.07	4.03	2.57	3.61	2.89		
OVARC1001901	0.54	1.84	1.21	2.42	1.37	2.43		
OVARC1001911	0.59	1.57	1.66	1.51	1.39	1.55		
OVARC1001916	1.86	3.13	3.35	4.16	4.61	3.51		
OVARC1001928	1.45	3.53	1.55	1.58	1.62	1.72		
OVARC1001937	5.12	11.69	8.13	17.41	11.63	15.16		
OVARC1001940	1.1	4.51	3.13	3.72	3.14	2.78		
OVARC1001942	3.85	7.4	8.03	11.47	13.91	12.77	*	+
OVARC1001943	7.16	10.07	11.08	9.62	13.85	11.87		

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OVARC1001949	1.69	3.34	4.15	5.35	4.01	5.55		
OVARC1001950	1.53	2.41	3.79	6.3	4.35	3.98		
OVARC1001952	11.3	11.38	53.57	52.33	78.84	38.05		
OVARC1001954	1.12	2.99	2.2	3.09	2.67	2.05		
OVARC1001963	1	4.91	2.89	4.5	3.39	3.21		
OVARC1001983	3.62	14.16	14.25	20.96	19.21	21.67		
OVARC1001987	3.12	6.54	5.94	6.08	8.39	8.02		
OVARC1001989	1.41	5.2	4.96	4.54	5.59	5.26		
OVARC1001991	1.74	3.27	4.08	4.57	3.86	3.27		
OVARC1002005	4.14	3.55	7.66	10.01	9.06	8.2	*	+
OVARC1002044	3.73	3.94	6.17	6.57	8.32	6.99	*	+
OVARC1002046	10.28	16.21	20.07	29.4	37.78	37.02	**	+
OVARC1002050	1.7	5.6	2.43	3.96	3.82	2.53		
OVARC1002058	4.23	6.11	4.02	4.69	5.55	5.43		
OVARC1002066	11.47	13.5	25.49	26.02	28.69	22.63		
OVARC1002082	3.6	8.55	8.81	9.6	8.89	6.49		
OVARC1002091	3.17	5.67	8.37	9.49	5.49	7.64		
OVARC1002092	1.38	2.72	2.2	4	3.97	1.88		
OVARC1002093	1.79	3.1	4.51	5.01	4.44	3.88		
OVARC1002094	1.55	6.24	4.17	36.42	27.25	28.35	**	+
OVARC1002107	1.42	4.63	2.69	4.86	5.48	3.6		
OVARC1002112	6.17	11.59	8.5	13.47	17.48	11.92		
OVARC1002126	2.66	6.35	6.68	7.95	6.44	8.79		
OVARC1002127	0.73	5.04	1.86	1.92	2.61	1.52		
OVARC1002138	1.4	1.79	1.86	3.16	4.82	2.75	*	+
OVARC1002143	0.73	1.51	1.55	1.29	3.03	2.09		
OVARC1002156	2.42	3.87	4.19	4.43	3.9	3.65		
OVARC1002158	0.88	2.63	1.6	2.36	1.57	1.51		
OVARC1002165	4.85	6.3	9.83	10.73	14.03	10.87		

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OVARC1002176	0.86	5.08	3.59	2.01	3.46	2.64		
OVARC1002178	0.83	5.35	3.12	3.8	5.02	4.25		
OVARC1002182	1.29	2.89	3.77	2.45	4.64	3.12		
OVARC1002185	11.45	13.19	62.79	43.91	53.43	55.56		
PLACE1000004	1.42	3.23	2.35	3.87	4.25	4.05	*	+
PLACE1000005	1.18	3.06	3.3	5.27	5.31	4.83	*	+
PLACE1000006	2.01	8.33	3.23	4.2	5.44	4.67		
PLACE1000007	0.97	5.13	2.89	3.03	2.47	2.56		
PLACE1000014	2.9	8.06	6.26	6.67	8.18	6.55		
PLACE1000031	0.88	4.81	0.45	2.61	2.71	2.79		
PLACE1000033	1.23	2.15	2.75	2.42	3.17	2.56		
PLACE1000040	3.08	4.43	6.18	7.11	5.54	7.37		
PLACE1000048	1.83	3.24	2.14	3.32	3.96	3.74		
PLACE1000050	2.12	5.36	9.1	9	6.55	8.25		
PLACE1000061	138.29	147.36	249.77	165.55	233.98	230.37		
PLACE1000066	14.23	15	19.46	15.86	15.62	18.52		
PLACE1000075	3.03	6.24	9.08	4.98	6.93	7.11		
PLACE1000078	2.1	5.75	5	6.07	6.93	5.19		
PLACE1000081	1.08	1.88	1.52	1.13	1.89	1.27		
PLACE1000086	4.97	6.55	11.25	8.1	9.16	7.75		
PLACE1000094	0.7	4.18	1.72	1	3.44	2.96		
PLACE1000101	4.67	8.44	7.7	11.69	10.38	13.65	*	+
PLACE1000121	0.87	6.29	2.02	1.95	2.85	2.39		
PLACE1000133	6.65	11.93	17.66	15.19	17.59	21.71		
PLACE1000142	1.79	6.03	5.66	2.64	4.77	4.24		
PLACE1000146	1.95	4.51	2.89	3.71	5.02	2.82		
PLACE1000163	4.52	5.99	10.71	16.27	10.95	13.78		
PLACE1000172	1.12	2.63	1.48	1.81	3.21	2.29		
PLACE1000181	1.06	3	2.98	2.63	3.75	2.86		

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PLACE1000184	1.17	3.08	1.48	1.87	3.28	2.27		
PLACE1000185	2.99	6.52	8.47	9.53	9.99	12.03		
PLACE1000198	0.78	4.09	2.49	2.19	2.17	1.93		
PLACE1000213	3.3	5.87	7.36	4.35	5.38	8.09		
PLACE1000214	1.37	4.29	4.54	5.22	6.72	4.22		
PLACE1000220	9.61	7.84	16.78	7.48	5.77	4.1		
PLACE1000231	2.48	4.1	4.92	4.57	4.65	3.91		
PLACE1000236	0.66	3.33	2.43	2.8	3.63	2.37		
PLACE1000245	2.92	5.88	6.34	9.34	11.24	10.55	*	+
PLACE1000246	5.15	8.27	9.95	3.29	2.55	2.86	*	-
PLACE1000258	5.4	12.61	13.52	14.88	16.7	14.95		
PLACE1000288	1.68	7.22	2.96	2.83	4.02	2.48		
PLACE1000292	3.72	9.02	8.85	10.23	20.58	9.21		
PLACE1000302	0.56	1.01	1.39	1.07	0.92	0.62		
PLACE1000304	1.13	3.26	3.17	3.75	2.32	3.05		
PLACE1000308	2.54	4.35	4.17	4.42	3.87	1.34		
PLACE1000309	2.29	4.02	4	6.72	5.23	7.88	*	+
PLACE1000312	1.33	3.44	2.48	2.74	3.99	2.5		
PLACE1000330	0.46	5.76	3.02	1.32	1.93	1.35		
PLACE1000332	1.02	8.82	2.01	3.01	3.78	1.68		
PLACE1000347	2.3	9.48	3.89	2.59	5.81	3.22		
PLACE1000351	1.2	1.5	2.87	2.2	2.4	2		
PLACE1000374	2.01	3.03	7.02	8.89	6.55	6.85		
PLACE1000380	2.39	4.27	3.95	4.9	2.12	2.38		
PLACE1000383	1.03	2.62	1.9	2.53	3.64	2.4		
PLACE1000397	0.63	4.06	1.89	2.82	3.34	3.47		
PLACE1000401	1.22	6.39	2.24	2.23	3.05	2.36		
PLACE1000406	1.08	8.76	3.4	3.72	4.08	3.64		
PLACE1000412	1.61	6.38	1.56	1.62	3.45	1.46		

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PLACE1000420	2.59	3.51	4.6	8.95	7.28	5.6	*	+
PLACE1000421	0.99	1.3	2.32	2.97	2	1.7		
PLACE1000423	16.6	23.29	32.85	10.67	8.02	8.09	*	-
PLACE1000424	1.36	3.09	2.12	3.35	2.65	1.97		
PLACE1000430	0.77	4.36	1.95	3.51	2.94	3.77		
PLACE1000433	1.06	5.9	1.65	1.89	2.6	1.8		
PLACE1000435	1.39	7.21	4.77	6.22	6.29	4.22		
PLACE1000437	6.06	10.65	10.14	17.29	20.07	18.79	**	+
PLACE1000442	3.75	3.85	6.27	7.81	5.7	6.7		
PLACE1000444	2.14	3.94	8.96	11.14	11.55	9.8		
PLACE1000453	5.57	11.03	14.16	10.42	7.4	2.99		
PLACE1000456	1.25	2.21	1.97	1.33	2.18	1.07		
PLACE1000465	2.09	5.63	6.62	12.97	11.8	10.69	**	+
PLACE1000481	2.32	8.1	3.73	6.89	6.64	6.45		
PLACE1000492	1.15	4.45	2.95	3.27	3.06	2.81		
PLACE1000508	1.36	4.64	4	3.91	4.24	3.71		
PLACE1000512	4.91	4.29	6.39	8.12	7.8	4.6		
PLACE1000540	5.18	3.93	7.84	5.44	6.9	5.57		
PLACE1000541	13.59	15.07	48.84	60.62	81.24	41.96		
PLACE1000546	0.86	3.61	2.82	4.72	4.63	2.5		
PLACE1000547	2.16	4.61	3.83	6.31	5.64	5.92	*	+
PLACE1000560	2.08	5.97	2.1	1.62	2.8	1.72		
PLACE1000562	2.8	6.23	6.04	8.86	11.26	8.61	*	+
PLACE1000564	1.54	6.4	3.07	3.16	4.41	3.43		
PLACE1000583	3.75	3.28	6.32	6.78	11.53	6.8		
PLACE1000587	8.52	9.32	12.99	13.64	14.69	9.43		
PLACE1000588	1.92	4.36	3.99	8.79	8.15	4.48		
PLACE1000596	1.99	5.34	4.39	7.8	6.74	4.51		
PLACE1000599	2.39	5.51	7.05	7.92	7.79	6.46		

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PLACE1000605	5.12	11.43	7.06	14.2	15.1	12.67	*	+
PLACE1000610	2.01	6.08	3.54	5.26	4.48	2.94		
PLACE1000611	13.18	19.13	24.68	16.45	20.37	22.79		
PLACE1000626	3.19	4.04	8.04	5.71	9.93	8.12		
PLACE1000633	1.32	2.12	3.95	4.8	6.06	3.59		
PLACE1000636	1.15	2.54	1.43	2.72	4.25	2.94		
PLACE1000653	5.07	8.56	9.29	11.07	11.87	14.08	*	+
PLACE1000656	4.2	12.9	25.22	16.66	16.71	12.92		
PLACE1000663	2	6.43	3.59	2.39	6.61	4.03		
PLACE1000706	2	6.3	5.04	5.37	7.27	6.26		
PLACE1000712	3.9	9.52	10.82	10.49	10.07	9.11		
PLACE1000716	0.98	2.75	3.44	2.44	3.2	2.82		
PLACE1000740	2.74	5.28	6.24	8.83	8.13	9.69	*	+
PLACE1000748	3.35	3.51	6.81	3.12	5.02	4.23		
PLACE1000749	3.49	6.35	5.94	4.61	4.65	6.02		
PLACE1000751	2.71	5.34	4.07	7.81	8.32	8.36	**	+
PLACE1000755	1.39	6.14	1.93	2.55	5.1	2.96		
PLACE1000769	2.29	6.8	3.45	3.33	4.58	2.6		
PLACE1000778	0.87	1.48	1.99	2.05	2.94	2.38		
PLACE1000785	9.56	12.21	27.18	28	24.34	29.54		
PLACE1000786	2.68	4.22	3.63	3.09	3.77	3.7		
PLACE1000793	4.05	7.21	6.7	6.06	7.6	9.1		
PLACE1000795	2.15	5.5	3.99	4.44	5.29	4.31		
PLACE1000798	0.88	8.44	3.24	3.13	3.8	3.72		
PLACE1000812	2.13	5.08	4.46	5.06	5.16	6.03		
PLACE1000823	1.71	5.2	4.89	5.67	7.28	4.84		
PLACE1000825	1.6	2.86	2.02	3.77	3.96	3.76	*	+
PLACE1000838	16	15.77	23.73	13.88	15.6	15.65		
PLACE1000841	1.22	3.78	3.31	3.97	10.65	3.77		

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PLACE1000843	2.14	6.2	5.68	5.79	7.7	5.38		
PLACE1000849	2.79	8.82	6.72	7.24	6.78	10.02		
PLACE1000856	2.01	5.3	3.59	3.42	4.79	4.19		
PLACE1000863	5.2	7.58	9.56	8.97	12.34	11.53		
PLACE1000876	3.65	7.6	6.02	6.7	9.95	9.06		
PLACE1000899	1.36	2.24	3.12	4.12	5.14	4.22	*	+
PLACE1000907	4.82	5.53	9.59	6.77	8.44	5.83		
PLACE1000909	1.18	3.31	2.45	3.65	3.88	3.44		
PLACE1000912	0.42	4.55	1.77	1.76	2.72	1.46		
PLACE1000914	1.05	4.41	3.5	3	6.09	4.22		
PLACE1000918	0.54	4.49	1.61	1.82	3.13	1.98		
PLACE1000927	10.48	12.41	16.9	20.91	23.21	25.47	*	+
PLACE1000931	0.69	3.44	2.12	2.44	3.94	3.3		
PLACE1000944	2.55	2.24	4.78	3.84	3.32	2.09		
PLACE1000948	0.52	2.31	2.96	2.21	2.72	1.72		
PLACE1000958	0.12	2.2	1.73	1.11	1.77	2.27		
PLACE1000972	1.01	3.43	2.89	4.49	5.33	3.75		
PLACE1000977	2.33	5.67	4.42	2.71	5.33	5.25		
PLACE1000979	1.63	8.01	3.93	4.24	5.92	4.57		
PLACE1000986	3.37	16.51	6.63	6.97	8.75	7.69		
PLACE1000987	1.76	10.13	4.79	4.17	4.74	5.11		
PLACE1001000	4.85	4.62	7.76	6.02	4.25	3.02		
PLACE1001007	7	6.94	14.66	5.39	3.76	3.47		
PLACE1001010	0.61	2.04	2.45	2.56	2.73	2.84		
PLACE1001015	0.88	2.55	1.84	2.36	1.72	2.42		
PLACE1001016	1.79	4.54	4.29	6.37	9	6.57	*	+
PLACE1001022	0.68	6.5	2.45	1.9	2.39	1.29		
PLACE1001024	1.05	8.89	1.83	1.34	2.49	2.35		
PLACE1001036	2.63	10.55	5.42	3.62	5.49	5.43		

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PLACE1001038	50.16	49.81	118.83	82.67	64.83	52.8		
PLACE1001048	1.07	1.82	0.92	2.39	2.09	1.21		
PLACE1001054	9.95	10.74	63.88	62.96	79.44	66.71		
PLACE1001062	1.45	4.19	3.71	3.12	4.17	3.05		
PLACE1001063	1.35	3.74	2.2	4.06	3.65	2.74		
PLACE1001076	0.46	6.48	1	1.86	2.18	1.62		
PLACE1001081	1.53	7.95	3.33	3.65	5.24	4.8		
PLACE1001088	1.32	5.24	1.22	1.42	2.81	1.37		
PLACE1001092	2.31	2.47	4.68	5.8	4.18	3.9		
PLACE1001098	0.93	2.62	4.53	5.49	4.05	3.17		
PLACE1001100	1.31	2.58	2.48	4.27	4.17	3.37	*	+
PLACE1001104	1.95	4.09	4.54	3.39	3.42	4.47		
PLACE1001114	1.56	6.54	4.33	5.17	3.78	3.27		
PLACE1001118	2.52	5.77	6.12	6.21	6.14	5.1		
PLACE1001123	2.86	5.3	7.53	7.08	8.51	7.63		
PLACE1001136	1.58	4.39	5.13	5.29	5.95	5.85		
PLACE1001144	6.27	5.67	13.43	10.34	11	10.08		
PLACE1001147	2.11	2.98	6.03	6.13	5.15	4.83		
PLACE1001148	1.72	1.31	1.89	1.76	2.39	2.31		
PLACE1001159	0.86	2.37	2.05	2.27	3.73	1.43		
PLACE1001168	8.87	14.52	15.09	25.46	23.18	30.79	*	+
PLACE1001171	0.69	3.89	1.23	2.53	1.42	1.53		
PLACE1001183	0.24	3.61	1.81	1.57	2.78	1.38		
PLACE1001185	3.13	7.43	3.76	5	6.4	5.64		
PLACE1001201	1.77	2.8	3.29	6.32	6.94	6.32	**	+
PLACE1001229	7.51	8.56	12.64	15.24	11.45	10.42		
PLACE1001231	1.83	2.73	3.07	4.09	5.1	2.3		
PLACE1001238	1.52	4.35	3.74	3.65	4.52	4.57		
PLACE1001241	1.63	5.58	2.92	5.73	8.13	7.04		

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PLACE1001242	22.28	29.54	30.28	46.43	48.89	62.65	*	+
PLACE1001247	2.43	7.02	4.07	5.03	5.91	4.52		
PLACE1001250	1.01	5.36	3.61	4.68	4.39	4.81		
PLACE1001257	2.99	3.06	7.06	7.89	9.21	7.69		
PLACE1001272	3.19	4.27	5.68	7.13	6.43	5.14		
PLACE1001279	0.96	3.12	2.74	3.08	3.81	3.29		
PLACE1001280	1.08	4.75	2.68	4.98	4.45	2.86		
PLACE1001294	1.91	7.23	6.91	4.88	5.57	6.18		
PLACE1001295	4.16	9.94	7.53	8.55	11.85	8.43		
PLACE1001300	2.46	7.9	4.31	4.65	14.73	4.95		
PLACE1001304	3	8.27	10.47	8.57	10.81	10.64		
PLACE1001311	3.95	3.34	5.67	6.85	9.14	7.6	*	+
PLACE1001323	2.17	2.95	5.12	5.66	8.43	5.5		
PLACE1001325	0.88	1.95	3.71	2.84	3.56	3.27		
PLACE1001340	5.18	6.99	9.8	8.69	12.02	10.48		
PLACE1001344	1.52	3.49	1.77	2.34	2.06	1.75		
PLACE1001351	3.23	6.39	8.39	6.4	8.62	6.1		
PLACE1001366	1	4.49	4.02	4.19	4.6	3.72		
PLACE1001377	3.02	4.97	5.1	7.91	7.28	5.83	*	+
PLACE1001383	2.31	4.13	3.53	2.62	5.5	5.72		
PLACE1001384	1.81	3.23	2.89	2.05	3.43	3.15		
PLACE1001387	1.65	3.64	3.7	3.03	4.83	3		
PLACE1001395	3.72	6.64	6.54	7.01	7.61	7.73		
PLACE1001399	3.71	6.58	9.31	7.37	8.61	9.22		
PLACE1001401	0.83	5.25	2.33	1.55	1.76	0.87		
PLACE1001407	11.65	21.8	24.47	22.63	18.09	26.24		
PLACE1001412	1.6	4.98	4.53	4.08	4.42	3.83		
PLACE1001414	2.3	3.02	5.86	7.57	5.13	6.83		
PLACE1001416	2.99	4.71	3.29	5.62	4.04	7.08		

PLACE1001433	33.62	33.05	51.64	49.1	58.33	55.88		
PLACE1001440	1.95	3.99	3.96	3.6	3.53	2.1		
PLACE1001456	1.64	5.5	4.26	4.15	4.87	4.49		
PLACE1001464	32.76	28.05	47.41	53.22	68.42	61.32	*	+
PLACE1001468	0.85	5.04	1.17	1.56	2.55	2.27		
PLACE1001484	1.31	4.85	2.96	4.25	5.8	3.04		
PLACE1001500	0.92	2.22	2.14	2.72	3.34	3.26	*	+
PLACE1001502	1.36	3.6	3.9	3.54	5.9	4.54		
PLACE1001503	1.7	4.58	6.72	7.47	8.2	8.05		
PLACE1001505	6.34	14.13	16.16	39.97	27.14	46.65	*	+
PLACE1001513	4.09	10.82	8.17	5.87	8.53	14.61		
PLACE1001516	0.61	4.33	1.33	1.71	3.49	1.99		
PLACE1001517	5.56	8.58	14.77	14.14	14.96	14.28		
PLACE1001523	12.83	14.09	20.42	22.79	19.74	32.9		
PLACE1001526	5.12	4.89	8.42	9.51	9.11	6.89		
PLACE1001534	2.12	5.12	3.58	3.62	5.55	3.99		
PLACE1001536	0.61	2.5	1.52	2.11	3.2	1.9		
PLACE1001545	17.97	23.9	38.46	33.78	45.13	66.08		
PLACE1001551	2.55	6.26	6.15	4.72	6.59	6.71		
PLACE1001564	1.37	4.87	2.88	4.01	3.57	3.7		
PLACE1001570	2.62	5.95	4.18	2.19	3.82	4.32		
PLACE1001571	2.04	4.51	6.07	5.69	6.27	5.81		
PLACE1001595	4.73	4.64	10.04	11.6	8.27	5.28		
PLACE1001602	7.23	8.39	18.65	20.38	18.68	19.71		
PLACE1001603	2.01	3.83	5.37	6.86	5.86	4.56		
PLACE1001608	3.44	7.22	5.9	5.82	7.73	8.7		
PLACE1001610	3.77	8.4	8.22	9.26	9.49	9.85		
PLACE1001611	1.94	7.34	3.65	2.28	3.85	1.88		
PLACE1001629	0.78	6.77	2.24	3.62	3.36	3.52		

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PLACE1001632	1.66	8.26	4.04	4.3	4.14	4.37		
PLACE1001634	7.4	9.92	39.12	23.85	32.41	18.38		
PLACE1001637	0.84	2.16	1.25	1.41	2.4	1.1		
PLACE1001640	1.33	3.27	4.66	2.68	4.85	4.49		
PLACE1001655	0.83	2.93	2.06	2.82	2.14	2.02		
PLACE1001672	1.84	7.04	4.01	3.3	4.41	4.09		
PLACE1001676	1.38	8.49	3.54	4.63	4.77	3.85		
PLACE1001683	12.79	23.62	24.61	25.33	30.22	27.13		
PLACE1001691	3.41	12.29	6.72	9.03	8.96	9.83		
PLACE1001692	1.47	2.96	5.25	5.87	5.6	5.13		
PLACE1001705	3.02	3.75	9.88	10.06	9.21	8.32		
PLACE1001716	1.68	3	2.61	2.24	3.79	3.58		
PLACE1001720	1.49	2.62	2.21	1.56	2.45	1.71		
PLACE1001728	1.43	6.19	4.24	1.96	2.04	2.51		
PLACE1001729	2.12	8.13	4.44	3.8	4.52	4.36		
PLACE1001739	2.61	9.55	4.04	4.95	7.24	6.16		
PLACE1001740	0.92	5.36	2.09	1.92	2.1	1.69		
PLACE1001745	1.15	0.98	3.22	1.87	2.48	2.31		
PLACE1001746	1.04	2.25	2.55	4.64	3.4	2.82		
PLACE1001748	4.74	7.01	8.18	8.19	6.58	5.96		
PLACE1001753	2.06	3.54	3.29	7.44	5.57	5.82	*	+
PLACE1001756	5.6	11.31	38.07	31.78	44.99	35.99		
PLACE1001760	6.54	12.23	12.85	16.36	16.96	16.66	*	+
PLACE1001767	11.26	14.98	59.72	45.37	61.46	45.39		
PLACE1001771	1.96	6.64	4.03	4.32	5.22	4.54		
PLACE1001775	2.23	2.81	6.72	5.1	3.11	4.79		
PLACE1001777	83.34	145.9	190.82	142.92	71.27	59.69		
PLACE1001781	1.9	3.86	4.91	8.72	3.39	2.3		
PLACE1001783	0.76	3.21	2.06	4.84	2.09	1.54		

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PLACE1001786	1.77	6.61	2.72	3.7	3.32	2.6		
PLACE1001788	5.16	9.07	7.14	10.52	8.74	9.32		
PLACE1001795	1.92	4.4	4.82	5.42	4.61	5.42		
PLACE1001799	0.69	3.62	2.11	1.86	2.83	1.97		
PLACE1001810	0.89	1.52	1.76	2.73	3.91	1.73		
PLACE1001817	5.53	6.12	10.88	10.56	9.4	6.38		
PLACE1001821	4.68	6.07	7.11	8.37	9.92	4.99		
PLACE1001836	0.91	3.12	2.38	2.69	4.12	2.63		
PLACE1001844	1.55	5.1	3.48	4.42	4.36	4.09		
PLACE1001845	3.62	8.38	7.39	7.88	7.55	9.93		
PLACE1001858	2.56	6.58	3.52	5.26	7.48	6.05		
PLACE1001869	3.13	7.15	4.85	6.09	6.46	5.66		
PLACE1001890	11.74	11.92	21.45	173.44	255.31	125.13	*	+
PLACE1001897	9.19	13.85	16.44	22.22	23.13	12.95		
PLACE1001902	10.13	12.6	21.53	22.74	27.67	12.77		
PLACE1001904	1.38	3.72	1.51	2.45	2.53	2.35		
PLACE1001907	3.36	6.76	5.71	7.67	5.67	5.59		
PLACE1001910	83.6	82.16	135.34	301.29	325.42	244.59	**	+
PLACE1001912	1.53	6.6	3.36	5.54	5.48	4.85		
PLACE1001918	17.31	22.95	30.16	31.14	40.44	40.02	*	+
PLACE1001920	2.07	3.51	5.43	11.97	13.8	11.4	**	+
PLACE1001928	3.06	2.96	4.67	5.29	9.7	5.31		
PLACE1001930	1.17	3.92	2.2	2.9	4.73	3.22		
PLACE1001949	1.16	3.67	1.78	3.84	4.24	3.18		
PLACE1001959	1.36	4.7	3.16	2.63	3.17	2.26		
PLACE1001969	2.09	7.83	7.21	6.56	10.73	6.57		
PLACE1001974	7.39	11.98	11.87	11.43	16.09	16.06		
PLACE1001981	0.77	4.38	3.22	1.77	3.88	2.36		
PLACE1001983	3.81	4.12	5.32	5.92	6.16	5.72	*	+

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PLACE1001989	2.34	4.15	5.02	4.37	5.91	3.72		
PLACE1002004	3.07	4.06	8.05	9.22	9.69	7.18		
PLACE1002008	8.4	11.76	17	23.36	22.19	22.42	*	+
PLACE1002015	26.96	30.92	67.62	105.75	88.42	94.15	*	+
PLACE1002044	3.79	8.07	5.86	4.64	6.39	6.4		
PLACE1002046	1.78	5.68	1.9	4.3	5.79	4.97		
PLACE1002052	1.09	4.98	2.26	1.38	2.41	2.32		
PLACE1002066	4.79	6.3	8.29	10.24	10.77	9.93	*	+
PLACE1002072	2.55	3.91	4.86	6	5.48	6	*	+
PLACE1002073	0.51	2.83	2.29	2.35	4.06	2.91		
PLACE1002080	1.81	6.49	6.13	4.76	6.82	5.72		
PLACE1002081	1.66	6.13	4.06	3.74	4.86	4.3		
PLACE1002090	7.74	16.55	13.87	12.53	14.4	19.41		
PLACE1002095	2.97	6.22	8.45	10.01	10.18	11.32	*	+
PLACE1002102	4.26	8.56	8.81	9.47	9.56	10.67		
PLACE1002109	2.57	5.08	3.81	4.66	6.17	6.32		
PLACE1002115	1.75	3.57	2.48	2.78	4.26	2.59		
PLACE1002119	15.65	15.3	35.78	37.28	32.59	38.23		
PLACE1002140	5.25	8.45	14.05	19.93	17.14	17.19	*	+
PLACE1002150	1.54	8.26	4.25	3.23	5.36	4.12		
PLACE1002153	1.6	5.75	2.58	3.47	5.76	4.48		
PLACE1002157	0.87	2.96	1.72	1.76	3.28	3.73		
PLACE1002163	2.13	4.67	4.55	6.21	8.81	6.03		
PLACE1002168	2.39	4.04	4.42	4.68	6.28	3.22		
PLACE1002170	2.73	3.53	7.35	4.89	5.33	3.74		
PLACE1002171	3.09	6.11	10.02	18.44	14.63	13.93	*	+
PLACE1002180	3.16	6.23	6.77	4.63	8.54	8.39		
PLACE1002184	9.2	15.58	18.42	124.63	250.27	333.14	*	+
PLACE1002200	1.35	5.67	2.38	2.97	2.89	2.26		

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PLACE1002205	3.3	6.47	18.07	17.08	18.38	14.61		
PLACE1002213	2.2	4.16	4.93	5.52	8.03	6.03		
PLACE1002219	1.05	1.91	2.23	3.33	3.53	1.96		
PLACE1002227	0.68	2.65	1.7	1.5	3.03	1.67		
PLACE1002253	0.32	2.67	1.28	1.47	0.76	0.43		
PLACE1002256	1.16	4.78	3.31	3.54	3.01	4.79		
PLACE1002259	1.46	5.69	4.48	3.22	2.98	2.31		
PLACE1002285	1.16	10.74	2.29	1.55	2.38	1.24		
PLACE1002301	9.42	17.5	14.68	12.7	10.48	11.7		
PLACE1002310	4.28	10.16	9.86	8.82	7.87	9.94		
PLACE1002311	1.84	2.94	3.87	2.96	2.87	2.03		
PLACE1002319	2.31	2.64	2.94	3.21	3.23	3.92	*	+
PLACE1002329	0.56	2.54	2.5	4.07	3.58	3.07		
PLACE1002333	1.34	3.1	1.96	1.22	2.44	2		
PLACE1002342	4.19	9.04	9.44	5.06	8.52	8.17		
PLACE1002343	0.49	6.98	2.94	2.08	1.9	2.52		
PLACE1002355	1.31	9.39	2.36	3.33	4.35	2.63		
PLACE1002358	1.15	7.94	3.3	2.6	2.65	2.13		
PLACE1002359	1.91	2.17	3.47	4.7	3.91	3.42		
PLACE1002374	29.69	28.18	54.19	53.9	34.73	36.14		
PLACE1002376	3.58	5.91	7.86	6.23	6.82	6.56		
PLACE1002379	6.24	7.66	6.63	10.13	9.68	10.9	**	+
PLACE1002386	0.86	5.32	1.35	1.87	2.05	1.51		
PLACE1002395	3.69	9.97	17.13	16.43	20.62	16.16		
PLACE1002399	2.38	11.09	3.42	5.31	10.38	7.39		
PLACE1002407	1.09	5.22	2.31	2.3	4.01	3.66		
PLACE1002433	1.63	2.17	2.97	2.96	4.35	3.66		
PLACE1002437	0.79	1.4	1.47	1.41	3.28	1.35		
PLACE1002438	0.74	2.38	1.96	1.8	2.43	3.38		

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PLACE1002446	4.64	8.42	5.95	10.27	8.88	11.99	*	+
PLACE1002447	1.26	6.06	2.05	3.92	3.14	4.32		
PLACE1002450	1.19	5.92	3.24	4.32	4.21	5.05		
PLACE1002462	0.81	4.02	2.94	3.51	2.99	3.13		
PLACE1002465	0.96	4.69	2.2	2.69	4.31	2.24		
PLACE1002474	1.61	2.26	3.23	3.85	4.41	3.6	*	+
PLACE1002477	11.11	14.51	32.39	44.06	41.42	26.68		
PLACE1002493	3.39	4.1	10.1	14.39	16.66	9.49		
PLACE1002497	0.68	2.81	0.67	1.45	0.93	0.99		
PLACE1002499	2.12	4.73	3	5.98	6.44	5.28	*	+
PLACE1002500	2.61	6.52	7.36	7.58	10.45	7.25		
PLACE1002514	0.3	4.49	1.84	1.74	2.47	1.75		
PLACE1002518	2.86	7.65	6.9	5.62	7.55	4.67		
PLACE1002529	1.14	1.56	2.21	3.19	3.4	1.44		
PLACE1002532	1.31	1.82	3.18	5.75	4.94	5.59	**	+
PLACE1002536	3.59	3.75	3.44	5.84	6.07	3.85		
PLACE1002537	1.63	4.06	2.7	2.69	4.07	3.08		
PLACE1002539	1.86	5.68	2.75	4.53	5.29	4.78		
PLACE1002547	6.09	8.06	7.3	12.32	11.02	11.26	**	+
PLACE1002571	2.84	6.85	5.19	6.84	8.65	6.23		
PLACE1002578	3.57	8.34	8.35	11.11	12.19	8.11		
PLACE1002583	1.33	1.61	2.32	3.18	4.02	2.46		
PLACE1002591	0.82	1.62	2.34	3.25	4.43	1.92		
PLACE1002598	6.56	10.95	12.39	11.93	9.04	7.74		
PLACE1002604	1.73	3.57	2.69	3.75	5.38	3.51		
PLACE1002612	2.89	8.47	5.95	11.25	10.88	8.06		
PLACE1002625	1.25	4.79	3.18	2.7	3.25	1.82		
PLACE1002638	2.94	8.01	6.66	7.78	6.81	7.29		
PLACE1002655	1.39	6.51	5.57	7.19	7.62	6.46		

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PLACE1002665	4.57	3.88	5.4	7.47	12.16	10.75	*	+
PLACE1002685	0.58	1.12	1.3	0.67	2.43	0.98		
PLACE1002692	7.42	8.56	16.7	19.27	22.67	16.29		
PLACE1002714	1.8	3	2.11	2.43	3.14	2.24		
PLACE1002721	2.94	4.37	3.88	5.88	7.1	4.28		
PLACE1002722	0.92	5.42	1.97	1.37	3.28	1.85		
PLACE1002726	1.6	6.24	3.66	4.6	5.7	5.26		
PLACE1002756	1.57	4.5	7.04	5.92	9.63	7.78		
PLACE1002768	1.05	3.72	2.16	2.1	2.34	1.71		
PLACE1002772	0.54	2.15	1.32	2.49	2.86	2.3		
PLACE1002775	4.33	4.71	9.15	7.05	7.08	8.67		
PLACE1002780	185.63	218.72	325.36	272.21	244.38	305.38		
PLACE1002782	0.4	3.76	1.1	1.62	1.69	1.14		
PLACE1002794	1.5	6.71	3.27	2.26	4.59	4.36		
PLACE1002795	1.92	6.45	0.81	2.37	3.63	2.77		
PLACE1002811	0.6	1.57	1.34	1.9	1.46	1.16		
PLACE1002815	6.39	7	10.49	7.24	3.16	9.21		
PLACE1002816	8.5	9.72	9.05	7.22	8.2	7.97	*	-
PLACE1002822	0.58	2.51	2.06	2.2	2.87	1.94		
PLACE1002833	9.98	15.11	16.78	15.42	15.99	16.56		
PLACE1002834	3.2	8.08	6.57	6.23	6.79	8.41		
PLACE1002835	0.62	4.14	1.72	0.85	1.83	1.79		
PLACE1002839	1.13	5.75	2.72	2.89	4.72	2.81		
PLACE1002851	1.52	1.87	1.41	1.98	2.15	2.7		
PLACE1002853	4.18	6.23	9.15	6.26	5.6	7		
PLACE1002881	3.42	5.2	11.04	8.35	11.57	10.26		
PLACE1002901	9.66	12.66	20.09	24.14	25.51	30.67	*	+
PLACE1002904	0.89	7.35	1.41	1.98	1.95	3.09		
PLACE1002905	1.36	5.46	3.26	4.04	4.46	3.4		

PLACE1002908	1.6	5.19	3.18	3.84	5.27	3.81		
PLACE1002911	3.91	6.96	6.9	4.66	7.89	6.75		
PLACE1002941	1.57	2.2	2.48	3.94	2.02	2.31		
PLACE1002950	9.59	9.15	14.74	5.31	8.02	14.51		
PLACE1002955	47.83	40.69	72.7	82.17	62.5	84.64		
PLACE1002958	19.36	26.92	35.27	35.6	35.35	59.02		
PLACE1002962	1.03	4.03	2.2	1.41	2.63	1.67		
PLACE1002967	1.34	4.83	3.19	4.37	3.52	2.81		
PLACE1002968	1.2	5.14	2.7	2.55	3.05	1.81		
PLACE1002976	8.94	12.08	24.23	24.5	36.89	30.05		
PLACE1002991	2.68	3.05	6.66	3.49	4.56	3.6		
PLACE1002993	2.72	3.86	5.52	8.21	6.92	5.56		
PLACE1002996	2.02	3.03	3.43	5.54	3.52	3.01		
PLACE1003010	1.91	3.69	4.27	4.31	3.86	3.32		
PLACE1003025	2.85	7.01	6.1	8.57	11.37	10.11	*	+
PLACE1003027	5.02	13.08	9.31	8.55	12.45	12.76		
PLACE1003044	1.95	8.24	2.61	3.64	4.16	2.74		
PLACE1003045	1.41	7.75	1.77	1.88	2.64	1.01		
PLACE1003052	2.19	3.16	5.74	4.44	3.6	1.99		
PLACE1003083	1.59	3.04	3.23	3.06	1.61	2.25		
PLACE1003085	3.91	6.19	5.6	9.46	5.89	3.33		
PLACE1003092	3.94	4.87	6.25	7	5.6	6.17		
PLACE1003097	0.37	3.06	1.44	2.12	1.88	1.63		
PLACE1003100	1.65	7.1	4.2	3.88	4.74	4.29		
PLACE1003108	1.26	10.37	2.91	3.32	4.44	2.39		
PLACE1003115	11.39	18.3	58.59	73.64	99.24	69.1	*	+
PLACE1003120	3.1	3.08	9.71	11.34	8.32	10.19		
PLACE1003135	0.72	2.04	1.09	1.56	2.89	1.08		
PLACE1003136	3.95	5.82	6.05	9.03	6.55	7.34		

PLACE1003141	2.04	2.97	2.1	1.97	2.49	1.8		
PLACE1003145	1.21	4.17	2.52	6.24	6.88	7.67	*	+
PLACE1003147	2.87	7.85	5.71	5.02	5.25	6.28		
PLACE1003153	0.54	7.63	2.14	1.66	3.2	1.82		
PLACE1003163	6.09	13.55	8.19	8.39	14.09	12.26		
PLACE1003172	23.21	21.74	44.19	47.78	43.17	39.52		
PLACE1003174	2.31	2.49	3.75	4.3	3.55	1.68		
PLACE1003176	0.47	2	1.89	2.88	1.27	1.46		
PLACE1003181	1.72	4.19	2.72	2.5	2.76	2.36		
PLACE1003184	0.76	3.92	1.53	1.91	1.49	2.06		
PLACE1003190	2.39	9.81	8.67	10.73	7.98	10.34		
PLACE1003200	0.29	4.48	1.84	0.72	1.92	1.16		
PLACE1003205	3.94	7.07	9.68	6.82	10.38	7.2		
PLACE1003209	1.43	2.18	2.62	2.28	1.82	2.89		
PLACE1003214	0.83	1.3	2	2.15	2.44	1.81		
PLACE1003229	2.08	2.78	2.9	2.78	3.35	3.48		
PLACE1003238	0.46	2.34	1.24	1.35	2	0.75		
PLACE1003249	1.87	5.04	4.7	7.33	7.56	5.89		
PLACE1003256	3.47	7.69	7.94	8.82	7.68	6.08		
PLACE1003258	1.03	3.81	3.48	2.42	2.19	0.87		
PLACE1003279	3.09	7.19	9.02	11.15	13.56	11.58	*	+
PLACE1003294	0.95	1.54	1.59	1.57	1.25	2.64		
PLACE1003296	1.49	2.6	2.45	2.59	3.11	2.4		
PLACE1003297	7.52	10.15	31.88	23.01	23.49	19.3		
PLACE1003302	3.92	5.16	6.99	5.8	4.72	5.47		
PLACE1003334	1.51	4.41	1.91	2.4	3.59	3.09		
PLACE1003337	13.69	16.3	29.83	28.53	34.27	25.76		
PLACE1003342	1.05	4.07	1.89	2.15	2.35	1.97		
PLACE1003343	1.07	4.98	1.61	2.02	2.75	2.12		

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PLACE1003344	6.25	5.33	12.83	11.18	11.35	11.98		
PLACE1003353	19.67	16.04	40.09	37.78	42.55	40.26		
PLACE1003361	1.82	3.64	3.72	5.85	5.31	4.6	*	+
PLACE1003366	1.45	4.35	3.63	3.22	3.33	2.97		
PLACE1003369	2.75	4.51	3.49	3.29	3.25	4.62		
PLACE1003372	2.08	5.73	2.68	5.45	4.72	3.39		
PLACE1003373	2.85	7.37	6.62	8.8	11.81	9.89		
PLACE1003375	1.42	4.91	1.92	2.59	2.95	3.21		
PLACE1003378	0.94	0.94	0.98	0.7	1.66	1.08		
PLACE1003383	0.87	1.55	2.33	1.59	3.15	1.57		
PLACE1003394	10.55	12.49	24.08	11.75	22.99	17.27		
PLACE1003401	0.79	3.91	1.34	1.03	2.13	1.04		
PLACE1003405	1.5	3.97	2.22	2.54	2.46	2.04		
PLACE1003407	2.39	6.06	5.16	3.96	6.3	4.02		
PLACE1003420	3.26	7.69	6.19	6.8	10.92	8.7		
PLACE1003428	0.63	3.3	2.62	2.07	2.94	1.96		
PLACE1003432	6.14	5.81	8.2	6.64	7.05	5.42		
PLACE1003438	0.45	2.66	0.93	2.41	2.34	1.99		
PLACE1003452	1.87	5.02	5.08	4.53	3.43	3.84		
PLACE1003454	2.49	5.59	7.34	7.31	6.95	5.61		
PLACE1003455	2.58	4.26	2.35	2.97	3.01	3.17		
PLACE1003456	3.22	7.74	8.62	6.9	7.2	7.79		
PLACE1003460	6.39	13.35	14.87	13.02	16.76	12.86		
PLACE1003478	1.15	1.71	0.86	2.33	2.07	1.24		
PLACE1003484	12.06	12.21	45.33	28.12	31.5	34.2		
PLACE1003493	1.61	4.72	4.9	3.84	5.96	5.08		
PLACE1003503	85.45	87.35	107.79	115.17	111.85	172.81		
PLACE1003505	1.99	6.77	4.78	7.44	6.63	8.87		
PLACE1003516	0.86	6.78	2.7	2.8	3.95	2.39		

PLACE1003519	17.58	26.29	50.41	45.77	36.97	58.75		
PLACE1003520	14.18	25.48	35.96	25.73	31.4	32.19		
PLACE1003521	2.71	3.64	4.93	5.97	4.71	7.4		
PLACE1003525	8.45	11.81	45.05	33.94	43.71	36.88		
PLACE1003528	39.18	44.68	136.4	106.04	122.76	127.22		
PLACE1003529	1.46	4.26	3.29	2.4	3.94	3.83		
PLACE1003537	4.41	9.05	11.05	11.36	13.77	13.3		
PLACE1003549	1.1	5.02	4.59	5.61	6.01	5.93		
PLACE1003553	1.6	5.89	3.88	4.02	4.17	4.23		
PLACE1003566	5.93	9.8	17.51	13.03	19.09	14.58		
PLACE1003568	3.01	2.71	5.76	5.69	4.43	4.04		
PLACE1003573	0.98	2.43	1.19	2.16	1.87	1.48		
PLACE1003575	2.16	3.09	3.44	3.34	3.5	4.15		
PLACE1003583	0.97	3.45	3.34	2.29	4.16	2.23		
PLACE1003584	1.23	4.46	4.01	3.56	3.8	2.65		
PLACE1003592	4.4	8.48	9.48	7.11	10.48	9.53		
PLACE1003593	0.84	5.55	2.4	2.23	3.02	1.55		
PLACE1003594	4.24	6.76	6.01	5.78	6.68	7.36		
PLACE1003596	13.77	11.31	22.53	15.68	17.69	8.25		
PLACE1003598	2.83	3.63	5.02	4.89	3.7	2.95		
PLACE1003602	1.8	4.24	6.36	4.37	3.54	2.68		
PLACE1003605	17.43	21.72	45.86	94.65	95.6	91.55	**	+
PLACE1003611	2.34	5.18	6.07	5.65	7.14	6		
PLACE1003618	0.67	7.39	2.09	1.58	2.4	1.32		
PLACE1003625	1.78	10.41	2.75	3.33	5.48	2.8		
PLACE1003626	8.77	15.99	17.14	10.87	14.46	13.19		
PLACE1003630	1.8	2.57	5.8	7.05	4.67	5.86		
PLACE1003635	2.15	1.83	3.19	2.96	2.82	2.44		
PLACE1003638	1.3	2.58	3	5.21	4.19	3.13		

PLACE1003644	4.01	5.7	7.25	7.81	9.13	8.76	*	+
PLACE1003654	2.56	6.14	4.04	3.54	6.96	6.4		
PLACE1003656	2.69	7.79	6.12	6.54	5.63	4.77		
PLACE1003660	0.26	9.54	3.5	3.08	4.92	4.11		
PLACE1003669	2.43	9.05	3.67	2.59	4.26	3.08		
PLACE1003670	5.37	5.7	9.44	11.01	8.26	8.76		
PLACE1003671	1.66	1.22	3.57	3.11	2.57	1.57		
PLACE1003697	7.27	7.99	9.8	8.23	6.06	6.42		
PLACE1003704	3.12	3.97	5.17	5.96	7.25	5.97	*	+
PLACE1003709	0.89	2.63	0.8	1.19	1.24	2.44		
PLACE1003711	0.74	5.48	1.35	1.87	1.8	1.39		
PLACE1003723	1.07	6.99	4.7	4.2	5.31	4.16		
PLACE1003724	3.31	10.74	9.1	9.11	11.79	10.49		
PLACE1003737	2.14	2.21	4.72	3.35	3.1	3.29		
PLACE1003738	1.06	1.94	3.13	3.96	3.92	3.41		
PLACE1003742	2.25	3.58	5.71	6.81	6.18	2.85		
PLACE1003744	6.13	8.86	14.6	16.21	17.96	19.13	*	+
PLACE1003758	0.85	4.55	0.96	2	1.46	1.16		
PLACE1003760	13.44	18.68	27.23	31.82	20.52	22.79		
PLACE1003762	1.45	4.97	3.7	3.77	3.78	3.49		
PLACE1003765	1.18	5.23	3.45	2.01	3.1	2.11		
PLACE1003768	0.36	1.14	1.36	1.45	2.75	1.07		
PLACE1003771	1.28	1.94	2.07	1.84	3.13	1.43		
PLACE1003772	34.15	38.19	97.86	62.42	64.06	52.43		
PLACE1003783	1.48	3.02	2.22	18.65	19.53	16.61	**	+
PLACE1003784	0.69	3.92	0.87	2.09	2.19	2.68		
PLACE1003788	0.4	4.92	1.06	1.85	1.71	0.32		
PLACE1003795	1.01	4.1	3.57	4.73	4.38	3.54		
PLACE1003827	13.83	20.46	20.72	22.48	30.84	25.92		

PLACE1003833	0.98	1.49	3.9	3.65	4.33	3.31		
PLACE1003839	22.55	19.18	52.95	50.39	56.11	43.86		
PLACE1003845	6.09	6.88	11.72	24.98	19.99	10.6		
PLACE1003850	3.16	4.84	7.19	5.45	5.95	6.39		
PLACE1003852	0.25	3.36	1.09	0.99	1.58	1.05		
PLACE1003858	1.34	4.42	1.99	2.04	1.85	2.92		
PLACE1003861	0.95	4.51	1.63	2.98	2.78	1.73		
PLACE1003864	0.94	5.5	2.74	2.88	3.86	2.69		
PLACE1003870	3.84	3.4	13.2	10.71	16.12	12.03		
PLACE1003885	1.33	1.42	1.59	3.07	3.76	2.38	*	+
PLACE1003886	4.56	6.01	5.75	9.27	6.87	4.3		
PLACE1003888	0.75	3.79	1.96	2.87	3.42	2.68		
PLACE1003892	4.93	6.91	20.79	17.21	22.33	14.87		
PLACE1003900	2.27	5.92	7.17	6.34	9.75	6.6		
PLACE1003902	1.91	7.39	5.25	5.43	8.07	6.29		
PLACE1003903	0.42	5.07	2.94	2.55	3.5	2.59		
PLACE1003915	8.15	7.04	10.78	8.31	9.79	9.84		
PLACE1003918	1.88	2.45	4.75	3.47	6.26	3.75		
PLACE1003923	2.06	3.73	5.63	2.7	5.54	3.32		
PLACE1003932	3.99	5.16	5.47	4.06	7.58	5.09		
PLACE1003936	1.02	3.82	2.81	3.63	2.42	2.78		
PLACE1003966	3.11	7.43	7.76	4.89	7.32	4.21		
PLACE1003968	1.68	5.68	5.94	3.33	4.26	4.57		
PLACE1004018	25.49	33.73	48.16	32.56	40.53	28.62		
PLACE1004020	8.91	10.18	13.26	11.42	18.03	24.15		
PLACE1004028	0.41	2.55	1.3	1.38	1.23	1.91		
PLACE1004034	3.56	4.53	5.22	8.42	9.03	13.04	*	+
PLACE1004042	17.25	20.19	68.35	79.51	93.32	79.44	*	+
PLACE1004078	1.14	4.1	3.3	4.95	6.51	4.45		

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PLACE1004103	5.54	10.93	13.98	13.77	15.09	14.14		
PLACE1004104	5.94	12.29	27.78	24.18	34.98	29.71		
PLACE1004113	1.37	3.7	3.28	2.75	3.27	1.29		
PLACE1004114	1.12	2.55	2.23	2.84	2.49	2.93		
PLACE1004118	1.58	3.52	2.09	2.74	3.64	2.5		
PLACE1004128	4.4	6.84	5.66	6.61	8.13	9.01		
PLACE1004130	2.25	4.83	8.35	6.86	9.26	6.73		
PLACE1004149	3.59	7.3	9.86	10.23	13.29	10.12		
PLACE1004156	3.61	7.91	10.12	11.66	17.62	13.31		
PLACE1004160	5.45	9.54	14.36	13.1	19.65	14.53		
PLACE1004161	2.2	4.86	3.54	4.85	5.73	7.48		
PLACE1004166	5.61	5.81	9.91	8.3	8.66	11.2		
PLACE1004168	3.35	4.97	3.73	4.73	6.65	6.79		
PLACE1004170	0.78	3.28	1.93	2.98	3.42	2.76		
PLACE1004178	0.83	5.23	2.37	2.4	2.59	2.36		
PLACE1004183	0.89	7.99	4.41	3.53	4.32	4.84		
PLACE1004197	0.64	5.14	1.55	1.73	3.54	1.65		
PLACE1004199	1.66	4.52	4.09	3.78	5.88	4.35		
PLACE1004203	1.8	3.57	4.17	2.43	3.62	2.83		
PLACE1004242	3.8	5.64	11.04	8.55	8.14	8.64		
PLACE1004249	31.4	56.31	117.88	127.93	152.54	151.22	*	+
PLACE1004255	0.79	2.65	1.26	2.59	2.15	1.93		
PLACE1004256	9.06	11.68	13.63	14.66	14.18	23.37		
PLACE1004257	2.63	7.95	6.48	7.89	8.8	8.64		
PLACE1004258	1.87	5.21	3.13	4.59	3.15	3.11		
PLACE1004270	0.72	3.8	2.5	2.7	4.01	1.65		
PLACE1004272	1.34	3.68	3.73	3.86	5.38	6.15		
PLACE1004273	92.91	89.59	212.62	212.05	129.56	99.82		
PLACE1004274	2.09	3.61	6.51	6.42	7.14	6.74		

PLACE1004277	2.3	4.4	5.76	6.45	7.7	6.04		
PLACE1004279	0.54	3.39	2.23	3.16	2.64	2.02		
PLACE1004282	2.43	8.25	6.62	4.22	5.56	4.49		
PLACE1004284	4.59	11.31	7.84	7.38	8.16	7.15		
PLACE1004289	1.28	7.85	2.46	3.06	3.63	2.1		
PLACE1004299	0.33	6.41	1.38	1.54	2.67	1.83		
PLACE1004302	1.01	2.98	3.27	2.41	2.45	1.12		
PLACE1004305	1.11	2.09	1.9	1.9	1.82	1.78		
PLACE1004316	2.3	4.48	5.4	6.06	3.85	4.52		
PLACE1004322	2.49	3.41	5.25	6.35	7.14	5.75	*	+
PLACE1004325	2.43	6.38	3.84	3.85	3.66	4		
PLACE1004332	1.21	7.18	2.8	3.72	3.46	3.01		
PLACE1004336	2.87	9.6	5.36	6.88	9.21	6.71		
PLACE1004346	0.47	7.22	2.58	1.87	2.54	1.69		
PLACE1004358	1.3	2.41	2.41	2.46	2.09	2.03		
PLACE1004376	11.07	10.15	23.35	19.16	17.04	16.46		
PLACE1004384	0.65	3.46	1.46	1.92	2.48	2.1		
PLACE1004385	1.4	2.89	1.69	3.52	1.88	2.67		
PLACE1004388	1.79	5.73	4.27	3.44	4.87	3.04		
PLACE1004405	2.16	8.39	4.42	13.36	14.48	16.74	**	+
PLACE1004407	5.05	13.12	13.37	11.2	16.24	11.85		
PLACE1004424	0.37	5.78	0.85	1.7	1.81	1.58		
PLACE1004425	1.14	1.94	3.57	3.28	3.27	3.44		
PLACE1004427	1.96	3.31	4.56	4.67	4.22	3.24		
PLACE1004428	0.88	2.05	2.17	2.66	2.08	2.62		
PLACE1004433	5.7	8.3	10.82	12.94	15.67	12.05	*	+
PLACE1004435	0.72	4.17	1.43	1.95	1.9	2.15		
PLACE1004437	4.05	7.68	14.2	11.07	13.01	12.37		
PLACE1004441	7.82	11.68	34.06	30.75	43.19	26.41		

PLACE1004446	1.5	4.36	0.9	1.03	1.35	1.39		
PLACE1004450	0.33	1.46	1.34	2.57	1.71	0.7		
PLACE1004451	0.51	1.45	2.14	1.89	2.69	0.88		
PLACE1004456	8.22	9.7	10.97	16.68	10.4	4.18		
PLACE1004458	3.39	4.81	3.66	7.77	7.05	8.24	**	+
PLACE1004460	0.84	4.58	2.1	2.91	2.69	1.75		
PLACE1004467	5.31	6.81	10.65	7.67	10.14	10.48		
PLACE1004471	2.65	5.93	6.64	6.79	7.34	6.14		
PLACE1004473	1.16	4.66	3.5	3.18	3.23	3.21		
PLACE1004475	14.03	16.41	32.49	31.09	32.51	18.17		
PLACE1004482	8.37	6.7	10.79	10.04	9.76	9.15		
PLACE1004491	0.39	2.51	1.49	1.19	2.68	1.3		
PLACE1004492	61.52	74.8	127.94	129.92	127.64	123.82		
PLACE1004506	10.71	14.35	14.4	8.45	11.13	10.03		
PLACE1004507	2.9	7.37	5.09	7.15	6.87	6.18		
PLACE1004510	2.51	6.23	6.33	6.59	7.8	8.16		
PLACE1004516	0.98	7.36	2.12	2.79	3.78	2.22		
PLACE1004518	1.64	1.78	3.03	2.41	3.88	2.83		
PLACE1004519	0.17	0.82	0.62	1.43	2.79	1.51	*	+
PLACE1004520	6.08	8.09	10.06	7.44	9.11	2.52		
PLACE1004530	33.19	43.86	68.13	41.86	27.72	38.09		
PLACE1004545	1.13	3.83	2.12	3.03	3.31	3.65		
PLACE1004547	5	7.61	7.82	8.66	11.2	10.28		
PLACE1004548	1.69	6.73	4.43	6.93	8.48	6.5		
PLACE1004550	2.27	6.24	6.67	5.92	6.78	6.15		
PLACE1004551	0.8	2.16	1.62	2.14	2.21	1.95		
PLACE1004559	2.9	2.89	5.11	4.45	6.75	4.82		
PLACE1004562	8.67	11.27	16.07	13.01	14.38	13.34		
PLACE1004564	1.84	5.19	4.36	4.64	5.98	4.49		

PLACE1004604	1.69	4.21	9.88	2.49	4.34	1.97		
PLACE1004611	2.73	5.87	4.89	3.86	4.17	3.99		
PLACE1004629	9.42	15.75	19.92	23.93	30.49	29.01	*	+
PLACE1004630	16.66	20.82	35.1	16.76	23.04	19.17		
PLACE1004637	5.03	8.82	10.34	6.61	9.17	8.29		
PLACE1004645	36.5	39.28	92.04	85.16	87.94	74.59		
PLACE1004646	1.07	2.91	2.87	3.68	2.19	2.28		
PLACE1004648	0.8	3.42	2.52	2.53	3.15	1.22		
PLACE1004655	45.95	58.09	130.94	112.14	126.25	99.01		
PLACE1004658	2.4	7.34	6.31	6.64	8.37	6		
PLACE1004664	1.26	4.83	1.3	3.02	2.65	1.89		
PLACE1004672	2.32	6.79	8.02	6.3	7.51	7.14		
PLACE1004674	9.4	11.97	14.7	8.3	9.75	15.25		
PLACE1004681	1.97	3.84	5.62	5.05	5.69	4.39		
PLACE1004686	2.74	4.33	7.46	9.22	10.77	8.59	*	+
PLACE1004690	10.64	13.43	19.62	21.75	19.21	31.72		
PLACE1004691	1.14	6.71	3.71	2.92	4.13	2.75		
PLACE1004693	1.34	7.54	4.89	3.91	4.59	5.97		
PLACE1004701	13.01	18.45	24.24	25.21	24.46	25.1		
PLACE1004705	1.29	3.33	2.27	1.8	1.96	1.47		
PLACE1004708	37.69	46.37	80.19	41.34	39.66	50.98		
PLACE1004716	6.37	8.81	11.08	4.22	12.55	14.26		
PLACE1004722	1.31	3.05	2.6	2.26	3.28	2.51		
PLACE1004736	5.25	7.71	7.6	9.16	8.89	11.63		
PLACE1004737	5.42	12.71	16.14	8.15	11.23	13.78		
PLACE1004740	4.88	9.06	8.22	7.37	7.93	8.2		
PLACE1004743	1.31	4.04	3.1	1.97	4	3.55		
PLACE1004751	0.98	2.89	2.88	2.75	3.74	3.06		
PLACE1004757	3.45	4.34	10.53	8.4	9.6	7.22		

PLACE1004761	6.41	7.32	12.59	9.99	10.44	9.72		
PLACE1004773	1.05	2.34	1.7	1.94	2.31	2.72		
PLACE1004775	0.35	3.26	1.37	1.29	2.14	1.07		
PLACE1004777	2.1	7.57	2.97	3.68	4.25	4.4		
PLACE1004793	0.83	4.58	1.37	1.9	2.06	1.25		
PLACE1004796	6.65	8.7	13.08	7.79	8.57	7.88		
PLACE1004804	0.99	4.46	3.25	2.44	2.38	3.22		
PLACE1004813	4.55	7.11	9.84	6.45	5.19	5.45		
PLACE1004814	7.16	11.76	17.62	15.83	11.39	10.1		
PLACE1004815	0.7	2.81	2.43	3.12	2.61	3.44		
PLACE1004816	1.16	2.63	2.04	2.36	2.26	1.84		
PLACE1004824	3.25	7.37	5.27	8.1	9.13	8.85		
PLACE1004827	1.4	10.89	3.17	2.57	3.05	1.3		
PLACE1004836	1.72	12.95	4.26	6.25	7.99	4.49		
PLACE1004838	1.35	8.81	2.2	2.49	2.34	1.68		
PLACE1004840	1.59	2.06	2.21	1.85	2.08	1.37		
PLACE1004842	0.86	1.98	1.89	1.98	1.78	2.33		
PLACE1004850	0.81	2.35	1.63	1.83	2.76	2.36		
PLACE1004868	0.81	2.97	2.04	1.62	2.23	2		
PLACE1004885	1.5	7.09	3.51	3.4	6.03	4.77		
PLACE1004886	1.87	8.53	2.76	3.33	5.12	4.93		
PLACE1004887	18.14	34.01	58.51	36.9	38.66	30.33		
PLACE1004896	8.39	14.15	15.4	9.39	11.14	14.03		
PLACE1004900	1.75	2.7	6.69	5.66	5.74	4.44		
PLACE1004902	5.42	6.25	9.27	6.39	4.2	3.6		
PLACE1004904	1.7	4.66	2.52	6.49	4.78	3.03		
PLACE1004911	0.69	2.5	1.12	5.95	4.82	6.09	**	+
PLACE1004913	3.63	5.72	7.38	4.49	5.45	4.79		
PLACE1004918	1.3	6.69	2.05	2.39	3.24	2.64		

PLACE1004930	2.74	8.84	5.93	10.63	16.57	14.71	*	+
PLACE1004934	1.14	4.3	3.34	2.97	2.03	2.5		
PLACE1004937	2.1	4.03	4.91	2.74	3.59	2.36		
PLACE1004949	4.32	4.98	7.67	8.53	8.48	6.04		
PLACE1004969	0.74	1.74	1.99	1.39	2.34	1.4		
PLACE1004970	0.45	2.18	1.2	1.43	1.31	1.01		
PLACE1004972	1.63	6.56	2.69	5.66	3.17	4.76		
PLACE1004974	1.27	5.21	4.2	5.6	5.7	5.62		
PLACE1004975	0.59	2.84	1.11	1.94	1.98	1.24		
PLACE1004979	1.58	4.06	4.26	4.91	5.69	4.75		
PLACE1004982	5.66	6.45	9.74	10.03	10.67	5.65		
PLACE1004985	1.4	1.47	1.46	2.5	2.17	1.2		
PLACE1005003	2.85	4.22	6	6.05	6.37	5.78		
PLACE1005004	0.47	3.36	0.92	1.5	0.73	0.85		
PLACE1005005	3.35	6.9	5.32	6.67	9.65	7.17		
PLACE1005011	6.03	11.12	35.8	37.66	56.97	36.62		
PLACE1005026	0.79	4.18	2.29	2.44	2.49	2.16		
PLACE1005027	2.46	6.72	6.69	5.36	6.92	5.68		
PLACE1005031	1.21	1.47	3.69	5.72	7.1	4.6	*	+
PLACE1005036	2.27	3.6	6.83	9.08	8.91	7.53	*	+
PLACE1005041	2.5	2.84	2.84	5.05	4.41	3.25	*	+
PLACE1005046	2.23	4.11	4.56	6.04	3.92	4.33		
PLACE1005047	0.23	3.19	2.6	1.43	1.23	2.1		
PLACE1005052	4.24	8.53	6.36	8.08	8.15	8.1		
PLACE1005055	2.54	7.45	4.66	7.2	6.45	5.62		
PLACE1005066	4.33	8.26	7.58	12.9	14.14	16.49	**	+
PLACE1005077	1.17	0.68	1.2	2.1	2.43	1.54	*	+
PLACE1005085	1.41	1.97	3.06	3.34	4.14	3.45		
PLACE1005086	1.93	3.77	5.17	5.62	7.78	4.79		

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PLACE1005088	24.66	32.47	46.03	43.45	31.47	27.46		
PLACE1005089	1.57	4.78	3.15	2.52	3.67	3.14		
PLACE1005101	3.37	8.11	5.46	6.11	8.96	6.39		
PLACE1005102	2.56	7.14	5.01	4.11	5.51	3.8		
PLACE1005108	2	6.08	5.87	6.58	6.19	5.09		
PLACE1005110	1.34	1.89	3.08	1.75	2.75	2.15		
PLACE1005111	1.31	1.34	1.23	1.45	2.17	1.54		
PLACE1005123	26.23	26.21	47.58	34.26	49.34	34.98		
PLACE1005124	3.2	4.66	4.18	4.2	6.91	5.44		
PLACE1005128	9.54	8.89	18.22	16.37	16.36	16.13		
PLACE1005130	2.65	6.57	5.54	2.84	4.98	3.58		
PLACE1005141	6.3	9.92	11.25	16.15	20.75	18.95	**	+
PLACE1005146	1.3	2.71	3.03	2.17	2.53	2.29		
PLACE1005152	1.85	3.9	4.56	4.13	4.23	4.79		
PLACE1005157	2.66	5.19	5.3	4.38	4.09	7.01		
PLACE1005162	2.79	3.72	9.31	6.57	7.45	7.1		
PLACE1005170	17.34	18.92	29.76	21.38	18.18	23.73		
PLACE1005176	0.57	5.6	1.7	2.33	2.47	1.94		
PLACE1005181	0.53	5.14	0.96	0.89	1.36	0.37		
PLACE1005184	4.06	9.09	10.4	8.97	12.82	11.26		
PLACE1005186	3.5	3.41	8.56	8.05	5.79	5.73		
PLACE1005187	2.85	4	4.13	6.1	4.99	4.25		
PLACE1005189	6.12	7.71	5.34	10.84	10.65	12.22	**	+
PLACE1005193	1.48	3.78	1.71	3.84	2.91	2.61		
PLACE1005200	1.35	4.68	2.61	2.47	3.75	3.1		
PLACE1005206	2.43	6.48	4.26	3.35	3.95	2.95		
PLACE1005216	1.53	5.46	4.44	5.6	6.51	4.12		
PLACE1005223	1.43	6.21	5	4.38	5.66	3.27		
PLACE1005225	1.36	3.01	3.49	3.33	3.32	4.65		

PLACE1005232	1.86	3.31	4.87	5.63	6.19	3.88		
PLACE1005239	1.06	4.3	2.32	2.84	2.86	2.41		
PLACE1005243	4.35	7.32	5.41	8.48	7.49	10.75		
PLACE1005250	4.24	10.31	7.98	4.38	5.9	8.88		
PLACE1005261	3.21	7.43	4.74	4.78	5.82	3.51		
PLACE1005266	1.05	4.47	2.82	2.28	4.43	2.76		
PLACE1005271	4.66	5.31	8.79	5.87	11.16	7.95		
PLACE1005277	2.06	3.48	2.35	2.62	1.98	2.64		
PLACE1005287	3.63	4.31	5.87	2.98	5.06	6.91		
PLACE1005299	24.16	22.75	48.29	35.17	24.24	41.06		
PLACE1005305	6.81	8.46	11.13	10.67	11.85	16.25		
PLACE1005307	1.59	5.44	4.14	3.15	5.42	4.84		
PLACE1005308	2.41	4.96	3.95	5.32	5.99	5.79		
PLACE1005313	1.08	3.83	1.6	1.8	2.05	1.8		
PLACE1005320	1.36	3.65	3.34	3.39	4.05	2.26		
PLACE1005327	10.78	8.74	16.8	10.36	7.95	4.43		
PLACE1005331	2.28	4.92	5.28	4.66	4.97	3.33		
PLACE1005335	1.53	3.8	2.24	2.03	3.22	2.42		
PLACE1005336	9.12	12.58	16.58	16.39	16.99	20.15		
PLACE1005351	2.62	8.18	10.17	9.28	8.66	9.52		
PLACE1005366	2.04	6.93	3	2.99	3.71	4.23		
PLACE1005373	1.77	6.34	4.44	3.91	5.36	3.37		
PLACE1005374	3.29	9.47	11.4	7.35	10.22	12.41		
PLACE1005383	8.16	7.54	12.81	7.21	5.93	4.03		
PLACE1005388	0.33	2.04	1.56	1.92	3.67	2.2		
PLACE1005409	2.97	5.02	4.99	3.9	4.23	2.97		
PLACE1005410	12.41	16.44	18.89	24.38	20.98	27.1	*	+
PLACE1005426	5.16	7.48	9.06	5.51	7.67	5.45		
PLACE1005431	12.6	15.65	22.53	19.64	26.25	23.75		

PLACE1005453	1.4	10.38	3.93	4.85	4.45	3.28
PLACE1005467	3.09	11.87	7	5.57	11.63	7.28
PLACE1005471	1.6	1.94	1.66	2.29	1.52	1.28
PLACE1005476	0.42	1.73	1.24	1.6	1.57	1.46
PLACE1005477	1.58	2.26	2.51	3	2.93	2.74
PLACE1005480	0.77	2.01	1.86	1.93	1.4	0.53
PLACE1005481	0.44	4.81	2.3	2.77	3.62	2.44
PLACE1005494	0.27	6.66	1.68	1.21	1.73	1.06
PLACE1005495	3.86	12.83	8.31	6.85	9.25	7.62
PLACE1005497	2.27	7.72	3.95	4.24	5.68	5.91
PLACE1005499	5.71	5.86	11.07	10.82	7.9	6.49
PLACE1005502	1.59	2.87	3.43	4.07	3.45	1.49
PLACE1005513	1.77	4.14	3.35	1.86	2.85	1.98
PLACE1005515	2.89	4.76	4.22	4.58	5.29	3.78
PLACE1005519	1.04	4.53	3.29	2.85	2.85	2.83
PLACE1005526	0.58	5.55	1.38	1.3	1.59	0.71
PLACE1005528	2.08	7.71	5.57	5.94	7.12	5.33
PLACE1005530	2.16	7.09	4.32	5.17	8.23	4.67
PLACE1005536	1.74	1	2.74	3.12	2.43	2.88
PLACE1005539	10.1	11.64	23.77	8.65	8.66	5.22
PLACE1005543	1.7	3.57	5.62	3.54	4.32	2.57
PLACE1005544	0.86	3.26	3.15	2.49	2.68	2.27
PLACE1005550	4.32	7.61	7.85	10.16	7.25	6.86
PLACE1005554	1.15	5.47	2.67	2.17	2.17	1.17
PLACE1005557	1.76	7.21	4.95	8.22	7.64	7.7
PLACE1005563	0.51	4	1.89	1.45	2.07	1.06
PLACE1005569	0.6	0.5	1.56	1.59	1.81	1.09
PLACE1005574	1.07	1.88	2.49	2.48	4.43	2.22
PLACE1005584	1.3	2.68	3.91	3.91	5.58	3.03

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PLACE1005590	4.28	5.14	8.4	9.87	10.73	8.02		
PLACE1005595	3.08	4.03	2.89	3.65	3.81	3.89		
PLACE1005601	2	5.66	4.22	3.77	4	4.02		
PLACE1005603	1.08	4.9	1.04	2.49	0.95	1.94		
PLACE1005604	1.2	6.71	2.42	3.6	4.2	3.46		
PLACE1005611	2.22	2.3	3.98	5.15	5.65	2.89		
PLACE1005622	0.65	1.71	1.98	2.94	3.88	1.26		
PLACE1005623	1.42	3.08	3.27	3.71	3.65	1.61		
PLACE1005630	3.31	5.81	7.75	87.83	72.15	89.12	**	+
PLACE1005639	0.75	4.36	1.28	1.66	2.02	1.18		
PLACE1005646	2.13	5.41	4.31	5.4	5.08	2.55		
PLACE1005647	2.77	9.69	6.72	7.34	9.11	6.25		
PLACE1005648	3	8.11	9.21	8.34	10.59	8.22		
PLACE1005653	1.99	1.43	2.74	2.74	2.13	2.67		
PLACE1005656	0.92	2.48	2.24	1.68	2.78	1.58		
PLACE1005659	0.87	2.64	1.01	1.62	1.84	1.32		
PLACE1005660	3.91	8.03	5.77	8.87	8.88	8.34		
PLACE1005664	2.69	6.57	6.14	3.39	4.27	3.19		
PLACE1005666	0.89	5.91	3.55	4.63	4.93	3.97		
PLACE1005669	4.46	10.41	11.39	11.64	13.9	14.6		
PLACE1005682	1.94	5.27	4.49	6.2	5.2	5.47		
PLACE1005698	0.6	2.7	2.92	2.01	2.67	2.38		
PLACE1005708	25.32	34.08	53.46	53.89	59.98	53.76		
PLACE1005725	3.25	3.75	6.41	5.64	5.82	7.29		
PLACE1005727	2.97	4.54	4.15	3.9	3.49	4		
PLACE1005730	0.77	4.29	3.26	1.1	1.54	1.28		
PLACE1005736	5.37	7.55	5.73	9.25	12.55	10.19	*	+
PLACE1005739	0.81	4.96	1.38	2.46	3.17	1.74		
PLACE1005745	8.03	7.11	11.52	11.98	6.97	11.44		

PLACE1005752	1.31	3.15	2.96	2.55	2.24	1.25		
PLACE1005755	0.8	2.79	3.02	1.72	3.28	2.27		
PLACE1005756	10.79	12.06	17.2	18.22	19.3	21.47	*	+
PLACE1005760	10.22	15.24	68.06	49.69	68.81	53.09		
PLACE1005763	1.47	7.04	3.58	3.79	4.63	3.02		
PLACE1005768	1.25	5.63	3.69	4.58	5.13	4.19		
PLACE1005771	5.71	13.63	13.7	11.28	17.49	17.27		
PLACE1005783	1.82	2.44	3.64	3.05	3.71	3.47		
PLACE1005799	4.79	5.25	8.37	6.12	8.78	8.62		
PLACE1005802	1.07	3.78	3.64	2.7	3.64	1.96		
PLACE1005803	3.06	6.15	4.78	5.6	4.94	7.36		
PLACE1005804	0.92	8.41	1.33	2	1.91	2.44		
PLACE1005813	17.23	18.71	78.06	70.01	94.17	74.89		
PLACE1005815	1.43	5.6	4.38	3.8	5.01	4.1		
PLACE1005828	2.11	3.62	4.42	5.34	6.24	3.56		
PLACE1005833	119.17	92.82	182.22	122	114.37	107.96		
PLACE1005834	2.04	4.33	3.95	3.55	3.56	2.56		
PLACE1005835	22.7	19.1	51.52	72.32	60.34	68.56	*	+
PLACE1005836	2.39	4.21	4.97	2.61	3.83	2.55		
PLACE1005845	0.97	5.42	2.66	2.67	3.05	3.65		
PLACE1005850	1.82	3.91	3.04	2.84	2.85	2.15		
PLACE1005851	1.03	3.44	1.46	1.2	2.01	1.11		
PLACE1005856	0.92	4.01	2.42	2.24	3.37	3.37		
PLACE1005875	1.78	3.89	4.77	3.3	3.48	3.17		
PLACE1005876	1.33	3.99	4.76	6.87	6.34	6.9	*	+
PLACE1005878	1.3	2.67	2.08	3.54	4.46	2.79		
PLACE1005880	2.36	4.09	4.31	4.16	3.07	3.45		
PLACE1005884	1.6	4.87	1.89	2.48	2.21	2.73		
PLACE1005890	1.9	9.57	3.7	2.26	3.09	1.88		

PLACE1005898	3.29	10.87	5.34	7.36	8.12	6.36		
PLACE1005913	1.46	9.31	8.05	4.99	6.47	4.33		
PLACE1005921	0.99	1.92	2.03	1.49	2.22	0.79		
PLACE1005923	0.74	1.61	1.17	1.47	2.42	1.43		
PLACE1005925	0.83	2.67	3.18	2.19	2.14	1.68		
PLACE1005927	1.26	2.49	1.93	1.95	2.56	2.3		
PLACE1005932	2.04	5.66	2.44	2.53	2.32	2.52		
PLACE1005934	0.88	7.91	3.16	3.9	5.61	4.19		
PLACE1005936	1.31	8.96	3.02	2.02	2.84	2.3		
PLACE1005939	54.61	68.58	111.22	157.61	194.58	212.18	**	+
PLACE1005951	2.36	3.39	4.98	5.56	4.48	2.35		
PLACE1005953	1.5	1.64	2.64	2.59	2.43	3.03		
PLACE1005955	1.64	2.01	3.8	4.07	3.43	2.55		
PLACE1005966	0.76	3.42	1.69	1.75	2	2.19		
PLACE1005968	1.52	4.96	3.2	4.71	5.15	6.12		
PLACE1005975	2.58	7.11	5.42	6.18	7.01	6.49		
PLACE1005990	0.7	7.7	1.54	2.1	1.87	0.88		
PLACE1005997	88.15	118.52	196.48	189.6	226.97	172.1		
PLACE1006002	3.38	3.97	8.87	8.4	7.71	9.18		
PLACE1006003	1.55	3.02	4.83	5.09	4.44	5.33		
PLACE1006011	1.85	3.63	3.46	4.48	2.68	1.91		
PLACE1006017	0.84	2.74	2.81	3.4	3.4	3.58		
PLACE1006037	2.99	7.05	2.48	6.14	3.64	4.29		
PLACE1006040	2.2	7.87	3.97	6.64	6.9	7.77		
PLACE1006063	0.94	4.64	2.59	2.11	3.15	2.25		
PLACE1006071	3.06	6.52	4.97	5.36	4.03	4.47		
PLACE1006073	2.74	3.53	6.43	7.19	6.81	6.93		
PLACE1006074	1.4	2.22	3.34	2.62	3.23	1.69		
PLACE1006076	1.36	2.51	2.98	3.15	2.47	2.75		

PLACE1006079	1.38	4.32	1.78	2.1	1.1	1.11		
PLACE1006093	0.49	3.76	1	3.56	3.85	1.83		
PLACE1006116	2.99	6.44	4.04	5.28	5.01	4.91		
PLACE1006119	3.15	6.81	7.07	9.22	10.4	8.03		
PLACE1006129	2.12	5.6	3.98	6.59	7.62	5.65		
PLACE1006139	3.44	2.98	6.03	7.77	8.85	5.58		
PLACE1006143	0.5	1.48	1.87	3.18	4.13	3.17	*	+
PLACE1006157	1.55	2.54	4.82	2.96	3.9	2.44		
PLACE1006159	0.69	3.61	0.94	2.68	1.98	1.04		
PLACE1006164	0.35	3.18	1.37	1.73	1.85	1.21		
PLACE1006167	2.18	6.5	3.37	3.95	4.52	3.13		
PLACE1006170	2.79	6.09	6.09	4.34	5.31	3.68		
PLACE1006181	2.75	7.34	2.84	5.8	5.51	5.22		
PLACE1006187	0.76	1.3	2.15	2.01	2.41	1.48		
PLACE1006195	0.11	1.24	1.73	1.93	1.93	0.87		
PLACE1006196	1.8	4.01	4.15	4.32	5.77	2.19		
PLACE1006197	2.12	5.6	5.24	4	3.47	3.39		
PLACE1006198	0.27	3.68	1.21	0.84	1.63	0.5		
PLACE1006205	0.89	5.59	0.99	2.43	2.18	1.28		
PLACE1006208	7.28	13.32	13.46	14.09	14.99	12.5		
PLACE1006211	2.6	8.05	7.92	6.07	9.08	9.35		
PLACE1006219	6.77	5.77	8.94	14.88	22.25	15.35	*	+
PLACE1006223	1.55	1.46	3.19	1.39	3	1.64		
PLACE1006225	0.56	2.27	1.3	1.04	2.3	0.99		
PLACE1006236	1.53	3.2	2.92	3.06	5.01	2.29		
PLACE1006239	0.67	3.62	1.97	2.61	3.66	3.41		
PLACE1006245	3.86	7.13	5.45	4.43	7.44	3.28		
PLACE1006246	1.66	6.56	6.19	5.59	7.66	6.33		
PLACE1006248	1.58	4.47	5.6	2.77	3.1	2.82		

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PLACE1006262	0.93	2.24	1.49	2.08	1.61	1.4		
PLACE1006269	2.28	4.71	3.42	2.06	2.47	2.33		
PLACE1006275	1.6	3.57	3.37	4.12	3.68	3.53		
PLACE1006277	1.01	2.42	1.4	1.79	3.01	0.88		
PLACE1006288	9.32	13.59	22.49	26.85	18.4	25.21		
PLACE1006290	1.79	6.81	5.99	8.87	7.56	9.13		
PLACE1006298	1.93	5.52	2.47	3.87	5.08	4.55		
PLACE1006311	0.65	3.38	1.75	225.97	161.43	251.12	**	+
PLACE1006318	3.52	4.03	4.17	4.04	3.17	4.01		
PLACE1006325	5.43	6.73	6.31	8.09	8.38	8.08	**	+
PLACE1006331	1.87	3.36	3.21	4.44	3.59	2.56		
PLACE1006335	1.76	3.64	2.55	4.45	2.98	2.92		
PLACE1006357	0.27	4.51	1.59	1.7	1.49	1.2		
PLACE1006360	1.1	5.11	1.79	2.46	2.74	2.62		
PLACE1006364	4.51	8.06	7.29	7.37	9.19	5.75		
PLACE1006365	1.68	4.65	1.97	1.8	2.12	0.97		
PLACE1006368	1.53	3.11	2.57	3.01	3.04	4.27		
PLACE1006371	1.38	3.2	1.46	1.68	3.01	1.67		
PLACE1006373	2.21	5.21	5.75	7.83	8.02	7.56	*	+
PLACE1006382	0.9	4.67	2.81	3.3	1.92	2.95		
PLACE1006385	1.59	6.33	1.86	2.68	2.59	2.71		
PLACE1006391	1.19	5	1.95	1.96	2.79	1.63		
PLACE1006412	1.88	5.53	5.92	7.07	9.93	5.27		
PLACE1006414	0.63	3.42	0.95	1.22	1.87	1.6		
PLACE1006419	7.79	9.8	11.93	5.19	7.29	5.32	*	-
PLACE1006438	0.99	6.07	3.42	3.29	4.56	5.14		
PLACE1006443	2.05	5.01	5.12	5.01	5.31	6.44		
PLACE1006445	0.84	5.76	3.65	3.53	3.27	3.55		
PLACE1006447	1.34	5.81	3.28	2.95	3.26	3.96		

PLACE1006466	0.75	4.38	1.35	1.49	1.66	1.08		
PLACE1006469	0.67	4.66	2.31	1.65	2.26	1.67		
PLACE1006470	2.47	3.71	3.74	5.25	7.02	4.35		
PLACE1006472	24.4	23.44	52.17	26.23	28.52	9.36		
PLACE1006476	2.52	4.31	8.67	6.21	7.23	5.93		
PLACE1006482	1.64	3.35	4.43	4.25	4.67	4.98		
PLACE1006488	14.12	19.42	32.69	40.76	34.77	41.4	*	+
PLACE1006492	2.03	6.41	4.38	4.04	4.98	3.02		
PLACE1006506	1.78	6.67	4.04	4.41	5.71	4.17		
PLACE1006515	1.65	5.7	3.08	3.19	2.84	4.08		
PLACE1006516	1.1	7.32	7.05	4.89	5.69	7.28		
PLACE1006520	1.02	2.74	2.12	1.19	3	1.54		
PLACE1006521	2.4	3.54	6.38	6.49	6.86	5.08		
PLACE1006529	5.96	7.35	6.96	10.56	8.2	7.93		
PLACE1006531	1.01	4.31	3.33	1.84	2.05	2.43		
PLACE1006534	1.68	6.04	2.59	3.01	3.86	3.19		
PLACE1006540	2.68	9.7	7.77	8.71	11.21	4.46		
PLACE1006549	0.6	9.45	2.09	1.6	2.28	1.65		
PLACE1006550	1.76	8.82	4.07	2.77	2.94	4.14		
PLACE1006552	1.3	2.48	2.14	1.97	1.3	0.81		
PLACE1006557	2.38	4.01	3.79	2.84	2.51	2.45		
PLACE1006563	2.49	3.44	5.7	4.23	4.15	4.3		
PLACE1006579	1.53	7.5	4.82	4.88	5.38	5.78		
PLACE1006594	236.53	241.11	397.64	122.37	278.58	324.29		
PLACE1006598	0.72	8.53	2.4	1.53	1.58	2.07		
PLACE1006607	1.47	7.69	4.18	3.45	5.86	4.29		
PLACE1006610	9.46	13.73	38.26	27.65	32.76	22.64		
PLACE1006615	6.22	9.09	18.78	20.25	15.74	15.86		
PLACE1006617	0.91	1.54	2.66	1.87	2.49	2.09		

PLACE1006618	5.42	8.01	9.24	5.33	8.59	5.76		
PLACE1006626	1.53	4.11	1.3	2.47	2.78	1.16		
PLACE1006629	0.99	5.05	1.36	2.22	2.56	1.76		
PLACE1006637	1.29	6.54	3.97	3.77	4.23	4.87		
PLACE1006640	0.59	5.14	1.17	0.85	2.54	0.94		
PLACE1006644	1.66	4.46	2.12	2.79	2.49	2.39		
PLACE1006657	1.28	2.09	2.31	4.55	3.09	2.19		
PLACE1006673	2.29	4.73	10.34	11.06	10.89	6.45		
PLACE1006678	2.54	2.98	1.44	1.37	1.96	1.39		
PLACE1006682	3.5	5.93	2.58	15.44	20.96	23.99	**	+
PLACE1006684	1.12	4.8	1.81	1.64	2.54	1.65		
PLACE1006698	1.54	5.86	4.52	2.15	3.57	1.9		
PLACE1006704	1.81	5.41	2.71	2.93	2.92	2.97		
PLACE1006708	1.69	5.07	3.49	3.46	4.11	3.7		
PLACE1006711	14.21	16.18	29.77	24.34	26.25	22.42		
PLACE1006714	2.27	3.26	4.74	4.57	5.23	3.53		
PLACE1006716	1.51	2.75	3.7	6	7.05	3.99		
PLACE1006731	1.65	3.77	2.83	2.71	4	3.09		
PLACE1006754	0.43	3.94	1.73	1.8	1.81	0.99		
PLACE1006760	7.56	10.98	10.08	8.58	8.89	11.31		
PLACE1006779	1.44	4.12	2.88	3.19	3.79	2.97		
PLACE1006782	0.44	5.17	2.42	2.95	1.57	1.15		
PLACE1006783	9.34	11.46	18.65	157.98	223.05	66.46	*	+
PLACE1006786	3.31	4.08	6.07	5.9	6.24	3.34		
PLACE1006792	1.61	3.31	5.38	5.66	3.33	4.18		
PLACE1006795	0.89	2.43	0.74	0.81	1.27	1.01		
PLACE1006800	1.62	4.94	2.53	4.7	4.56	3.93		
PLACE1006805	3.94	7.79	5.5	10.83	9.8	8.79	*	+
PLACE1006809	3.55	5.7	5.94	9.58	10.61	8.97	**	+

PLACE1006815	1.7	7.57	4.1	5.12	5.23	5.8		
PLACE1006819	0.33	0.88	0.95	0.89	1.76	0.63		
PLACE1006820	2.35	2.01	4.91	4.84	6.72	4.18		
PLACE1006826	2.28	6.22	4.84	7.68	7.62	5.58		
PLACE1006829	3.76	5.51	6.54	9.49	8.66	8.69	*	+
PLACE1006853	1.2	4.21	1.97	2.25	2.93	2.88		
PLACE1006860	1	4.29	1.62	1.61	2.1	1		
PLACE1006867	5.65	9.36	11.34	7.04	8.33	7.63		
PLACE1006875	1.15	6.19	5.66	4.84	4.53	4.63		
PLACE1006878	1.59	2.84	3.09	2.99	3.22	2.39		
PLACE1006883	3.21	5.08	6.78	6.83	7.38	6.19		
PLACE1006898	1.67	4.23	3.67	3.54	4.77	4.59		
PLACE1006901	2.59	4.75	4.03	3.71	3.28	4.14		
PLACE1006904	0.91	3.59	2.7	3.26	2.92	2.04		
PLACE1006917	3.63	7.13	6.1	5.8	7.21	7.03		
PLACE1006932	0.54	5.85	1.29	0.92	1.34	1.19		
PLACE1006935	1.3	5.46	2.54	1.59	4.03	1.6		
PLACE1006956	0.92	2.55	3.4	2.55	2.41	2.09		
PLACE1006958	0.78	2.41	1.35	1.76	4.2	3.39		
PLACE1006959	4.97	8.48	9.98	11.46	9.58	13.62		
PLACE1006961	8.03	9.85	14.42	13.73	11.57	14.2		
PLACE1006962	2.97	7.44	6.56	5.04	7.26	6.22		
PLACE1006966	2.02	6.94	3.46	3.15	3.89	2.89		
PLACE1006979	0.95	4.44	2.03	1.46	2.64	1.77		
PLACE1006989	2.19	5.05	3.02	3.27	3.9	5.06		
PLACE1007001	4.98	6.79	10.71	4.03	7.43	7.38		
PLACE1007014	1.37	3.03	3.45	1.79	2.18	2.2		
PLACE1007021	0.74	3.03	2.11	0.75	2.2	1.73		
PLACE1007026	2.1	9.23	3.93	4.15	4.27	5.42		

PLACE1007028	4.12	8.5	10.56	7.89	8.34	9.35		
PLACE1007038	237.33	267.91	446.14	406.27	622.67	671.17		
PLACE1007040	1.55	3.14	2.85	1.57	3.31	2.45		
PLACE1007045	1.08	3.74	2.85	2.9	5.03	2.74		
PLACE1007048	147.06	149.67	259.53	121.61	211.26	109.43		
PLACE1007053	4.9	6.69	10	3.59	4.91	4.71		
PLACE1007068	7.56	10.33	62.76	39.52	45.9	36.69		
PLACE1007070	5.97	10.85	10.28	8.65	9.6	14.3		
PLACE1007076	8.22	14.4	14.19	16.53	23.62	24.67	*	+
PLACE1007077	2.65	6.45	4.01	5.2	5.28	5.43		
PLACE1007081	0.36	4.47	1.94	1.92	1.92	1.37		
PLACE1007082	1.23	4.66	4.95	4.32	4.5	3.99		
PLACE1007092	2.49	4.12	7.26	4.77	5.22	4.34		
PLACE1007096	0.72	2.19	0.74	1.35	1.63	0.97		
PLACE1007097	0.54	2.49	1.35	1.61	1.28	1.04		
PLACE1007099	1.58	4.66	2.56	2.77	3.64	3.72		
PLACE1007105	1.18	6.51	3.44	2.65	4.13	2.21		
PLACE1007108	3.55	13.02	7.41	5.03	6.87	5.75		
PLACE1007111	1.33	9.51	1.52	1.74	2.37	1.52		
PLACE1007112	1.23	7.26	1.79	2.09	3.12	2.36		
PLACE1007130	0.54	2.02	1.92	0.87	1.47	0.33		
PLACE1007132	1.46	3.32	4.63	3.58	3.38	2.88		
PLACE1007140	0.61	2.58	2.41	1.98	1.98	1.32		
PLACE1007143	2.79	6.32	4.62	4.9	5.34	5.33		
PLACE1007169	2.21	8.59	3.46	5.44	8.46	7.99		
PLACE1007178	0.82	8.66	2.48	3.28	6.28	4.1		
PLACE1007190	3.31	10.9	6.7	10.51	13.57	11.14		
PLACE1007201	0.81	5.82	1.41	1.72	3.04	2.51		
PLACE1007202	37.76	34.95	76.28	58.23	34.42	37.86		

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PLACE1007226	2.01	2.39	2.73	1.89	3.14	2.29		
PLACE1007238	1.64	3.07	1.83	2.39	2.73	2.2		
PLACE1007239	1.81	3.68	2.99	1.76	2.72	2.44		
PLACE1007242	0.61	5.18	1.87	1.54	1.14	1.67		
PLACE1007243	2.21	7.36	2.29	2.24	3.27	3.31		
PLACE1007247	0.36	6.17	1.71	1.11	1.36	1.34		
PLACE1007257	1.67	5.33	3.34	3.3	5.27	4.25		
PLACE1007274	1.46	2.18	4.43	4.38	4.03	4.06		
PLACE1007276	0.93	2.02	1.1	2.13	2.1	1.74		
PLACE1007282	2.51	4.2	5.72	4.28	3.62	4.66		
PLACE1007286	2.97	4.8	7.85	10.14	12.47	8.79	*	+
PLACE1007296	10.55	19.45	24.46	31.43	17.57	27.05		
PLACE1007301	0.65	5.17	1.55	1.19	1.54	1.11		
PLACE1007314	3.11	6.61	8.64	7.98	8.96	10.24		
PLACE1007317	1.19	3.34	1.27	1.88	1.62	1.79		
PLACE1007329	0.89	0.73	1.78	2.38	2.35	2.09	*	+
PLACE1007338	3.96	6.47	9.58	11.59	8.93	2.32		
PLACE1007342	0.71	1.8	1.3	1.1	1.1	0.7		
PLACE1007345	1.72	4.57	2.54	2.72	3.6	3.29		
PLACE1007346	1.43	4.61	3.89	5.77	4.53	4.1		
PLACE1007359	0.74	4.55	2.16	2.59	2.44	3.53		
PLACE1007367	4.53	8.63	15.16	12.49	13.49	11.75		
PLACE1007375	0.36	3.24	2.02	1.75	2.56	1.59		
PLACE1007377	1.49	2.01	3.18	3.29	3.96	2.36		
PLACE1007386	1.55	1.75	1.47	2.37	1.68	1.36		
PLACE1007392	1.57	2.99	2.49	2.79	4.48	3.51		
PLACE1007402	2.41	5.66	3.08	1.52	2.91	1.8		
PLACE1007409	1.05	4.57	1.04	2.51	2.68	2.02		
PLACE1007416	3.45	6.97	6.5	7.05	9.14	6.52		

PLACE1007420	12.12	12.66	20.8	25.26	23.9	22.88	*	+
PLACE1007431	1.87	7.4	5.51	7.17	5.28	5.91		
PLACE1007450	0.79	1.22	2.65	3	2.99	2.39		
PLACE1007452	0.42	2.36	1.76	2.09	2.98	1.45		
PLACE1007454	23.74	28.02	76.56	59.97	75.95	46.61		
PLACE1007460	0.75	3.52	2.35	2.34	1.93	2.58		
PLACE1007478	0.41	3.07	1.33	1.35	2.18	1.92		
PLACE1007484	0.6	4.8	2.57	2.56	1.45	1.69		
PLACE1007488	0.4	6.24	1.64	1.74	2.61	1.46		
PLACE1007507	2.91	6.36	4.49	5.31	8.29	8.11		
PLACE1007511	0.53	1.29	1.06	1.06	1.29	0.42		
PLACE1007513	10.57	10.43	24.05	12.24	16.88	16.9		
PLACE1007524	1.55	3.33	3.53	3.96	4.72	2.96		
PLACE1007525	1.24	2.95	3.14	2.38	2.85	2.24		
PLACE1007537	8.6	9.68	49.88	43.78	63.66	40.1		
PLACE1007544	1.55	6.45	4.97	3.2	3.92	4.61		
PLACE1007547	1.36	5.03	4.15	2.37	2.84	2.4		
PLACE1007557	1.12	3.16	3.14	3.07	3.9	3.41		
PLACE1007560	9.38	8.86	12.57	11.03	9.62	17.59		
PLACE1007565	0.37	2.27	1	1	1.16	0.91		
PLACE1007580	1.06	3.71	3.06	10.8	11.15	13.74	**	+
PLACE1007583	0.76	3.88	1.78	2.51	2.37	1.09		
PLACE1007591	0.79	4.62	1.7	2.2	2.53	2.07		
PLACE1007598	1.13	6.98	3.86	2.71	3.46	4.71		
PLACE1007610	0.41	5.63	1.28	1.33	3.18	1.5		
PLACE1007618	1.57	1.91	2.01	1.75	2.2	2.41		
PLACE1007621	1.78	2.83	3.64	3.33	3.57	4.38		
PLACE1007626	23.99	25.61	32.78	30.53	30.94	13.53		
PLACE1007632	2.03	3.26	2.52	2.65	3.81	4.63		

PLACE1007635	1.61	4.62	6.42	2.8	4.19	3.37
PLACE1007645	10.59	11.55	15.06	9.99	11.58	11.95
PLACE1007649	1.7	5.88	3.47	2.78	4.95	3.13
PLACE1007659	1.33	5.85	3.61	4.88	6.22	4.9
PLACE1007669	2.01	2.1	3.74	2.97	4.63	4.4
PLACE1007677	1.25	2.29	2.81	2.68	3.07	2.91
PLACE1007688	3.4	5.69	5.43	1.98	4.53	4.98
PLACE1007690	1.4	4.03	2.12	3.74	3.37	4.61
PLACE1007697	0.69	7.13	1.37	1.84	2.56	1.8
PLACE1007702	2.03	7.08	5.7	4.03	3.91	4.08
PLACE1007705	1.38	3.93	1.59	1.74	4.45	2.75
PLACE1007706	3.11	6.08	4.69	5.25	8.84	7.49
PLACE1007725	3.41	4.69	6.65	5.1	3.29	5.39
PLACE1007729	0.98	2.65	1.8	2.7	3.11	1.99
PLACE1007730	1.25	4.29	3.07	3.66	3.75	4.32
PLACE1007737	1.43	4.79	3.39	3.79	4.7	4.17
PLACE1007743	1.38	4.26	2.29	2.3	2.83	2.03
PLACE1007746	6.56	9.02	10.42	9.65	13.29	12.97
PLACE1007753	0.53	4.48	1.71	1.35	2.86	1.94
PLACE1007769	1.31	4.31	3.5	3.27	4.51	4.58
PLACE1007780	5.77	4.63	7.11	6.51	3.75	2.17
PLACE1007791	1.82	3.29	3.38	3.16	3.69	2.87
PLACE1007807	0.67	2.79	1.72	2.33	1.76	1.29
PLACE1007810	0.39	4.45	2.63	4.11	4.08	3.27
PLACE1007814	3.57	5.98	5.04	4.2	4.62	6.3
PLACE1007828	2.01	7.64	3.34	2.69	4.64	3.44
PLACE1007829	1.32	6.9	2.88	2.87	4.87	3.06
PLACE1007841	1.64	7.26	1.87	2.25	3.14	3.39
PLACE1007842	1.1	3.32	2.44	2.09	3.96	1.39

PLACE1007843	1.2	1.92	1.43	2.13	1.48	1.86		
PLACE1007845	1.76	3	4.11	3.45	3.42	2.36		
PLACE1007846	0.99	3.26	1.64	2.02	2.73	1.5		
PLACE1007848	1.09	3.51	2.23	2.39	2.62	2.25		
PLACE1007852	2.26	7.88	3.82	2.94	4.61	3.24		
PLACE1007858	3.65	11.57	5.81	61.71	80.46	57.09	**	+
PLACE1007866	19.42	25.98	40.48	43	80.39	56.73		
PLACE1007871	8.1	7.9	15.45	16.17	12.35	11.08		
PLACE1007877	1.09	2.09	1.45	1.4	2.39	1.53		
PLACE1007878	5.98	9.75	14.61	13.65	7.49	8.9		
PLACE1007881	0.43	2.66	1.34	1.59	1.94	1.93		
PLACE1007885	4.35	7.85	6.76	5.57	6.53	7.01		
PLACE1007897	0.27	6.51	1.85	1.72	1.53	1.41		
PLACE1007908	3.14	12.29	5.73	5.96	7.9	8.24		
PLACE1007922	6.08	11.75	8.75	5.24	7.15	4.54		
PLACE1007946	1.07	2.03	1.86	2.71	2.28	1.94		
PLACE1007950	6.98	7.6	18.21	16.17	19.34	12.63		
PLACE1007954	-0.03	2.45	1.15	2.46	1.57	1.51		
PLACE1007955	0.92	4.01	2.17	2.05	2.52	3.05		
PLACE1007956	0.6	3.61	2.91	2.35	2.1	2.22		
PLACE1007958	0.75	6.31	1.34	0.79	1.21	0.8		
PLACE1007965	0.64	5.88	3.25	3.38	2.91	2.17		
PLACE1007969	1.09	6.37	3.06	2.35	3.29	2.21		
PLACE1007971	2.73	4.17	5.21	6.1	4.41	5.92		
PLACE1007990	1.95	2.33	2.31	3.22	3.09	1.88		
PLACE1008000	0.32	2.16	1.98	1.85	1.27	0.66		
PLACE1008002	0.99	3.38	1.7	1.81	2.04	0.51		
PLACE1008037	0.57	4.19	1.7	4.59	2.86	2.02		
PLACE1008044	1.42	5.81	2.46	4.18	4.93	4.16		

PLACE1008045	0.4	4.07	1.54	1.75	2	1.65		
PLACE1008080	2.05	6.08	3.22	4.23	4.03	4.78		
PLACE1008092	1.56	1.56	1.48	1.48	2.98	1.86		
PLACE1008095	0.59	2.14	1.48	2.38	2.73	1.23		
PLACE1008105	0.95	1.76	1.71	2.24	2.71	0.74		
PLACE1008107	0.27	2.33	0.7	1.72	1.44	1.68		
PLACE1008111	1.73	5.01	2.12	4.57	5.4	4.04		
PLACE1008113	5.88	9.24	12.48	16.57	20.29	19.24	*	+
PLACE1008122	1.22	5.54	2.55	1.61	1.57	1.5		
PLACE1008129	1.5	5.64	2.8	2.43	5.36	2.91		
PLACE1008132	5.51	4.47	8.34	6.61	11.2	7.63		
PLACE1008137	0.96	1.82	1.02	2.12	3.88	0.8		
PLACE1008174	0.77	3.16	2.43	5.12	4.39	2.46		
PLACE1008177	1.62	4.87	3.09	3.79	3.26	3.77		
PLACE1008181	1.76	3.87	1.6	2.06	2.43	1.43		
PLACE1008195	2.66	6.08	2.97	4.34	4.14	3.9		
PLACE1008198	1.06	5.56	2.52	2.55	3.31	1.54		
PLACE1008201	1.22	4.45	3.58	5.92	7.69	5.64	*	+
PLACE1008209	2.35	2.29	4.46	2.51	5.31	4.44		
PLACE1008226	1.8	2.35	5.25	4.72	5.68	7.08		
PLACE1008227	0.77	2.67	3.02	2.38	4.6	3.54		
PLACE1008231	1.26	3.85	1.85	1.05	1.83	0.78		
PLACE1008238	1.22	3.21	2.9	2.47	2	1.72		
PLACE1008244	1.01	4.69	1.56	1.68	3.2	1.56		
PLACE1008249	0.8	4.94	2.55	1.22	2.17	2.01		
PLACE1008266	11.31	18.61	43.04	60.04	82.48	59.04	*	+
PLACE1008273	1.47	3.95	3.81	3.53	3.8	4.47		
PLACE1008275	1.59	3.67	2.17	2.62	2.57	2.34		
PLACE1008280	0.85	2.6	1.84	2.42	2.48	2.36		

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PLACE1008282	4.71	8.19	6.89	7.27	9.02	6.38
PLACE1008297	2.32	4.7	3.36	2.89	3.42	3.21
PLACE1008303	1.65	6.68	1.24	4.12	3.83	2.65
PLACE1008309	0.43	6.52	0.82	1.77	1.5	1.29
PLACE1008315	5.3	5.93	8.61	4.92	4.79	9.83
PLACE1008329	0.47	2.23	2.06	2.32	2.8	2.49
PLACE1008330	0.72	4.06	3.16	2.48	3.36	2.96
PLACE1008331	0.84	5.01	2.1	4.5	2.17	2.91
PLACE1008351	4.34	8.66	7.41	7.91	7.31	7.1
PLACE1008356	1.56	8.23	1.93	2.86	4.16	3.35
PLACE1008359	1.57	4.11	2.89	2	2.97	2.94
PLACE1008368	2.27	6.38	7.43	5.72	7.33	6.95
PLACE1008369	0.57	2.46	1.45	1.12	1.59	1.68
PLACE1008392	0.8	3.09	2.54	2.44	3.22	3.24
PLACE1008394	2.08	4.84	3.75	3.98	5.03	4.76
PLACE1008398	5.32	9.36	11.44	11.36	11.3	12.33
PLACE1008401	1.19	7.06	3.21	2.82	3.43	3.33
PLACE1008402	3.21	6.45	7.2	7.23	10.15	9.26
PLACE1008405	10.3	10.95	18.42	17.17	18.82	20.4
PLACE1008409	1.88	5.19	5.69	4.97	5.41	5.65
PLACE1008420	1.4	1.87	1.96	2.67	2.69	2.27 * +
PLACE1008424	0.88	2.69	2.54	1.69	2.34	1.71
PLACE1008426	0.98	2.58	1.58	1.7	2.66	2.32
PLACE1008429	0.92	3.17	2.14	1.91	3.4	1.84
PLACE1008430	1.63	4.85	3.04	2.93	3.52	3
PLACE1008437	0.87	3.64	3.01	2.83	1.82	1.57
PLACE1008453	1.16	4.8	1.02	1.64	2.06	1.17
PLACE1008454	2.14	6.46	9.23	5.46	9.02	5.92
PLACE1008455	2.06	4.33	7.2	5.26	6.68	4.87

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PLACE1008457	0.51	2.6	2.01	2.28	2.43	2.47
PLACE1008465	0.49	2.41	1.72	1.56	2.13	0.48
PLACE1008469	2.42	4.36	5.32	5.16	4.75	7.1
PLACE1008488	0.81	5.48	1.97	2.44	2.03	1.8
PLACE1008519	1.48	10.85	6.17	4.41	4.99	4.51
PLACE1008524	1.04	11.09	1.72	2	3.22	2.02
PLACE1008531	0.64	8.37	1.92	1.33	2.05	1.72
PLACE1008532	2.12	3	5.51	5.66	4.72	4.19
PLACE1008533	2.01	4	4.07	5.53	5.18	3.77
PLACE1008542	1.61	2.36	0.96	2.05	2.1	1.72
PLACE1008549	0.96	3.06	0.67	1.45	2.1	1.53
PLACE1008560	1.18	4.23	2.28	2.29	3.93	3.47
PLACE1008567	0.87	7.26	1.85	2.33	3.67	2.38
PLACE1008568	2.37	10.67	5.49	2.97	7.47	4.21
PLACE1008569	3.94	10.32	6.74	6.1	8.6	7.6
PLACE1008584	0.88	1.4	1.58	2.86	3.38	1.31
PLACE1008585	4.96	4.8	7.56	11.08	4.84	3.57
PLACE1008603	5.9	7.25	31	30.55	43.67	29.76
PLACE1008621	0.55	2.28	0.95	0.72	1.89	1.16
PLACE1008625	0.64	4.01	0.9	1.18	1.41	2.03
PLACE1008626	0.55	6.06	0.9	1.03	0.83	0.95
PLACE1008627	0.46	8.32	1.86	1.87	3.34	2.7
PLACE1008629	3.22	9.18	5.84	5.44	6.75	4.41
PLACE1008630	1.68	3.39	4.23	4.21	3.01	3.51
PLACE1008643	1.31	0.93	1.98	1.72	2.34	1.94
PLACE1008650	0.25	3.05	1.62	2.23	1.63	1.24
PLACE1008657	1.17	2.39	2.51	2.34	4.04	2.91
PLACE1008664	0.91	5.93	2.37	2.91	2.51	1.13
PLACE1008693	0.97	4.93	3.09	2.53	3.81	2.2

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PLACE1008696	0.88	3.84	2.21	2.26	2.11	1.47		
PLACE1008715	1.05	4.71	2.11	1.34	2.65	2.65		
PLACE1008716	2.48	3.94	4.19	5.75	6.9	7.07	*	+
PLACE1008722	3.85	4.34	7.37	7.64	7.19	3.45		
PLACE1008738	5.17	9.13	12.7	9.49	5.83	4.8		
PLACE1008742	6.57	6.87	14.66	14.94	15.06	12.41		
PLACE1008744	3.52	6.98	5.61	5.83	4.55	2.74		
PLACE1008748	0.63	4.39	2.75	2.44	1.67	1.61		
PLACE1008757	0.99	4.74	4.51	2.77	5.74	2.17		
PLACE1008766	2.66	6.75	3.77	3.51	6.47	4.06		
PLACE1008785	1.39	1.68	2.6	3.26	3.8	3.89	*	+
PLACE1008790	1.57	1.8	2.29	3.5	5.39	2.96		
PLACE1008798	1.71	3.82	4.45	6	5.93	3.32		
PLACE1008807	1.34	3.95	1.61	2.54	2.62	1.8		
PLACE1008808	1.6	4.53	3.01	4.24	3.69	5.04		
PLACE1008813	1.38	4.85	1.97	1.9	1.95	2.3		
PLACE1008836	1.34	5.81	3.68	3.89	6.17	4.1		
PLACE1008851	1.21	6.65	3.94	4.85	10.04	4.54		
PLACE1008854	0.56	0.48	1.14	1.16	1.41	1.6		
PLACE1008864	1.98	1.92	2.96	2.73	2.65	2.49		
PLACE1008867	1.2	6.57	6.22	6.43	5.71	4.82		
PLACE1008876	11.7	16.5	27.29	26.74	20.94	23.24		
PLACE1008887	1.37	4.31	1.44	3.26	2.07	3.28		
PLACE1008902	1.33	5.62	2.93	3.17	4.58	2.06		
PLACE1008911	4.04	8.56	10.48	11.31	13.99	15.66		
PLACE1008917	0.6	4.53	2.72	1.7	2.9	1.71		
PLACE1008920	0.75	0.77	0.87	0.61	1.58	1.44		
PLACE1008925	0.25	0.9	1.04	0.94	1.91	0.84		
PLACE1008930	4.12	7.32	9.83	5.11	10.36	7.17		

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PLACE1008934	0.9	3.42	2.9	2.89	2.28	1.7		
PLACE1008941	1.57	4.14	2.8	2.06	2.59	4.05		
PLACE1008947	2.3	5.41	5.51	3.96	5.84	5.16		
PLACE1008984	1.26	6.31	3.25	3.1	3.93	3.19		
PLACE1008985	0.94	2.75	2.74	2.84	2.43	2.7		
PLACE1008994	0.27	1.72	0.65	1.11	0.78	0.68		
PLACE1009020	0.46	3.49	2.42	2.49	3.1	2.16		
PLACE1009027	0.89	2.7	1.59	2.24	1.75	2.09		
PLACE1009039	-0.06	3.31	3.42	2.39	1.59	1.49		
PLACE1009045	1.53	6.33	6.05	23.13	20.76	22.2	**	+
PLACE1009048	0.41	5.97	2.3	0.61	1.04	0.54		
PLACE1009050	0.97	4.9	1.68	1.07	1.47	1.55		
PLACE1009060	5.61	8.4	9.51	10.74	8.55	11.96		
PLACE1009067	1.14	2.8	2.03	1.6	2.34	3.4		
PLACE1009071	1.44	4.05	3.9	3.79	7.24	9.82		
PLACE1009090	1.27	6.46	2.35	3.11	4.73	2.86		
PLACE1009091	5.58	10.22	38.11	38.77	49.35	36.29		
PLACE1009094	0.26	5.68	1.88	1.67	5.04	1.71		
PLACE1009099	1	5.52	3.47	3.49	3.36	3.84		
PLACE1009110	1.59	5.82	1.16	1.68	4.3	4.39		
PLACE1009111	1.88	5.24	2.65	3.95	3.77	2.88		
PLACE1009113	2.24	3.52	3.62	6.14	4.87	7.29	*	+
PLACE1009130	4.46	6.8	7.84	6.68	9.36	10.47		
PLACE1009150	0.88	3.54	1.95	3.23	3.3	3.01		
PLACE1009155	1.11	5.06	2.98	4.46	4.43	3.87		
PLACE1009158	1.06	5.77	1.95	1.77	2.35	2.88		
PLACE1009166	0.76	4.8	1.53	1.59	2.16	1.3		
PLACE1009172	1.43	3.96	2.45	2.26	5.85	2.61		
PLACE1009174	1.13	3.45	2.42	1.67	3.02	2.38		

PLACE1009183	1.62	3.54	4.47	4.1	6.33	8.06		
PLACE1009186	1.04	5.07	2.3	2.46	2.86	2.91		
PLACE1009190	0.75	2.32	1.44	1.53	1.9	1.65		
PLACE1009196	0.81	4.01	2.73	2.24	2.38	1.99		
PLACE1009200	1.01	4.44	2.94	2.84	4.39	2.91		
PLACE1009217	2.55	4.91	3.43	4.46	7.29	7.23		
PLACE1009230	1.9	5.55	6.63	5.63	9.16	9.46		
PLACE1009236	4.97	7.07	12.6	8.21	10.79	7.13		
PLACE1009246	11.71	11.96	24.75	14.59	16.36	9.05		
PLACE1009265	6.95	7.82	14.01	15.61	5.19	12.17		
PLACE1009279	0.67	2.07	2.46	1.93	2.54	1.63		
PLACE1009298	5.54	9.92	9.52	10.21	11.25	17.55		
PLACE1009308	1.13	6.82	2.04	2.48	2.48	2.34		
PLACE1009319	2.04	9.25	3.15	2.92	3.54	2.5		
PLACE1009328	1.04	5.78	1.81	2.98	3.39	2.17		
PLACE1009335	1.38	6.55	4.72	2.24	3.21	3.01		
PLACE1009338	2.56	4.14	5.1	3.24	4.3	1.57		
PLACE1009344	0.73	2.45	1.08	1.31	1.55	0.84		
PLACE1009355	5.41	7.37	9.95	13.44	10.76	13.55	*	+
PLACE1009368	1.3	2.56	2.41	2.43	2.32	2.19		
PLACE1009375	1.21	6.41	3.05	3.04	4.46	2.53		
PLACE1009388	1.18	8.68	3.01	3.46	4.53	2.72		
PLACE1009398	1.19	9.2	3.74	3.17	4.28	3.96		
PLACE1009404	2.78	9.18	4.51	5.33	6.73	6.94		
PLACE1009410	1.27	2.35	2.33	2.51	2.31	1.44		
PLACE1009417	0.95	2.25	4.34	2.55	3.08	1.71		
PLACE1009424	1.88	3.61	3.18	2.85	3.24	3.93		
PLACE1009434	0.84	3.94	2.91	1.29	1.82	2.19		
PLACE1009443	1.21	7.2	2.55	2.42	3.43	3.17		

PLACE1009444	1.33	7.71	4.05	2.51	3.17	3.79		
PLACE1009459	0.23	7.99	1.55	1.71	1.83	0.86		
PLACE1009460	1.75	6.84	3.26	5.15	4.31	4.08		
PLACE1009468	0.99	2.83	3.42	4.43	4.42	2.97		
PLACE1009476	0.21	1.21	0.73	1.05	0.67	1.33		
PLACE1009477	1.35	3.13	2.67	3.06	2.35	2.2		
PLACE1009493	0.87	3.35	0.94	1	1.87	1.41		
PLACE1009502	0.76	4.64	2.13	1.19	1.89	1.66		
PLACE1009524	1.32	4.22	1.63	0.94	2.14	1.6		
PLACE1009527	0.95	4.51	2.11	1.64	2.55	1.28		
PLACE1009531	20.82	28.24	41.52	46.25	43.25	49.96		
PLACE1009535	1.1	1.56	2.68	2.42	2.15	1.11		
PLACE1009539	2.15	3.41	4.18	3.88	2.65	2.57		
PLACE1009540	5.89	8	11.66	14.8	4.47	3.84		
PLACE1009542	1.11	3.37	1.42	1.51	2.06	1.44		
PLACE1009546	0.62	5.27	0.97	2.24	1.64	1.25		
PLACE1009556	0.35	4.46	3.46	3.36	2.86	3.16		
PLACE1009569	0.05	3.93	2.46	3.34	2.7	3.11		
PLACE1009571	1.67	4.27	2.52	3.04	2.85	2.67		
PLACE1009573	3.81	2.97	6.73	6.92	8.12	6.49		
PLACE1009576	1.92	2.51	4.3	2.73	3.66	2.08		
PLACE1009580	1.42	1.81	1.74	2.73	3.47	2.33	*	+
PLACE1009581	0.89	4.25	2.03	2.91	4.38	2.74		
PLACE1009587	0.96	4.91	2.29	2.43	3.2	1.99		
PLACE1009593	2.71	6.73	4.37	4.94	6.85	5.03		
PLACE1009595	1.81	5.44	2.66	2.67	5	2.79		
PLACE1009596	1.57	6.83	2.6	3.44	3.97	2.7		
PLACE1009600	3.03	4.27	4.48	5.48	9.14	4.42		
PLACE1009604	2.32	4.64	5.02	4.22	6.11	3.23		

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PLACE1009607	1.29	2.48	3.18	3.19	4.17	3.18		
PLACE1009613	1.94	5.23	2.94	2.65	3.08	2.23		
PLACE1009621	1.66	6.72	3.32	8.21	8.67	8.06	*	+
PLACE1009622	1.78	5.93	3.78	3.9	4.1	3.9		
PLACE1009624	1.16	5.77	3.42	3.2	3.65	3.5		
PLACE1009637	2	6.88	3.36	3.07	4.59	3.91		
PLACE1009639	1.94	1.76	4.15	3.44	3.67	4.99		
PLACE1009654	20.88	17.13	34.95	14.94	24.53	20.64		
PLACE1009659	2.77	6.78	7.45	6.38	8.38	6.55		
PLACE1009665	1.04	4.21	1.93	1.19	2.72	1.93		
PLACE1009669	7.73	9.64	14.54	9.85	16.89	8.82		
PLACE1009670	1.76	5.36	2.54	2.77	4.47	4.01		
PLACE1009708	2.1	5.57	5.09	3.64	6.54	5.84		
PLACE1009721	1.34	4.28	3.56	5.78	5.81	3.01		
PLACE1009731	1.36	3.59	3	3.58	6.53	5		
PLACE1009735	1.94	3.94	3.21	5.16	7.52	4.78		
PLACE1009737	1.89	4.29	2.95	4.83	5.61	5.47	*	+
PLACE1009741	1.3	4.32	3.45	2.09	5.03	3.07		
PLACE1009752	1.34	5.64	2.65	2.3	3.33	1.68		
PLACE1009763	3.95	9.73	6.82	7.13	7.44	8.39		
PLACE1009766	1.46	6.98	3.32	3.07	5.19	3.75		
PLACE1009772	0.48	5.19	0.6	1.01	2.46	0.89		
PLACE1009782	0.91	2.39	2.03	2.88	2.91	3.74		
PLACE1009794	2.58	4.45	5.11	3.54	3.66	5.03		
PLACE1009798	1.59	5.37	4	6.26	5.57	5.67		
PLACE1009845	1.05	6.02	2.92	2.79	3.39	3.92		
PLACE1009849	0.96	6.61	2.35	1.79	3.41	2.59		
PLACE1009857	0.79	4.86	1.45	1.19	1.27	1.56		
PLACE1009861	1.43	4.67	3.87	4.1	3.47	3.11		

PLACE1009872	53.53	52.43	88.5	74.95	49.47	81.73
PLACE1009877	5.45	7.59	12.08	10.03	10.3	12.32
PLACE1009879	0.82	3.28	1.59	1.55	2.99	1.34
PLACE1009886	0.68	4.04	1.53	1.62	3.04	1.72
PLACE1009888	1.03	7.4	3.23	5.34	5.84	7.94
PLACE1009908	1.56	7.63	8.64	3.37	6.71	5.9
PLACE1009919	4.5	7.53	8.26	5.84	10.72	10.15
PLACE1009921	0.96	3.94	3.32	1.63	4.28	2.47
PLACE1009923	3.82	5.56	6.85	6.32	8.13	5.57
PLACE1009924	3.01	2.49	4.53	4.43	4.31	1.04
PLACE1009925	0.61	2.77	1.84	2.51	2.2	2.5
PLACE1009931	2.78	5.21	9	8.71	6.93	8.09
PLACE1009935	0.74	3.71	2.1	1.19	1.08	1.5
PLACE1009947	0.47	3.83	1.64	1.51	2.46	2.03
PLACE1009961	0.43	4.08	1.39	1.69	2.18	1.9
PLACE1009971	0.92	4.9	1.98	1.35	1.74	1.45
PLACE1009982	40.34	48.71	89.8	53.8	57.87	66.96
PLACE1009992	0.94	1.9	2.59	1.47	2.52	0.68
PLACE1009995	6.47	10.83	15.72	7.79	9.03	11.23
PLACE1009997	0.55	3.7	3.03	2.76	3.2	2.64
PLACE1010002	1.4	4.14	2.82	2.89	3.04	3.46
PLACE1010011	2.09	8.13	3.85	4.4	5.21	4.68
PLACE1010013	0.18	12.85	1.74	0.92	1.81	0.68
PLACE1010021	3.18	11.98	5.42	4.12	4.13	6.06
PLACE1010023	2.15	8.45	5.16	5.62	6.52	6.14
PLACE1010031	4.6	4.35	7.23	6.79	4.91	1.82
PLACE1010039	1.17	3.3	1.45	1.28	1.23	1.19
PLACE1010045	1.1	2.83	3.66	2.52	3.55	2.64
PLACE1010053	1.42	3.56	1.65	2.21	2.76	2.37

PLACE1010060	1.63	6.1	4.13	4.11	4.6	4.05		
PLACE1010069	0.41	7.96	2.32	1.48	2.91	1.3		
PLACE1010070	0.92	8.04	1.5	0.45	1.78	1.09		
PLACE1010074	5.25	11.67	11.8	12.32	9.51	11.22		
PLACE1010076	12.75	11.95	29.01	19.58	15.88	16.82		
PLACE1010078	2.96	2.42	4.36	4.64	4.39	3.85		
PLACE1010081	2.74	4.1	3.7	6.85	7.81	4.59	*	+
PLACE1010083	0.69	2.53	1.51	1.22	1.86	2.26		
PLACE1010089	1.86	4.89	3.35	3.45	3.47	3.48		
PLACE1010096	2.17	7.73	2.91	3.43	4.19	3.2		
PLACE1010102	3.89	10.9	5.33	7.1	9.64	7.57		
PLACE1010105	2.98	7.46	4.93	7.31	9.04	9.82		
PLACE1010106	2.46	2.95	4.48	5.47	4.88	5.8	*	+
PLACE1010130	0.53	1.79	1.17	2.27	2.55	1.23		
PLACE1010132	2.49	4.65	5.3	5.07	4.39	4.19		
PLACE1010134	0.8	3.32	1.15	1.97	2.31	1.67		
PLACE1010139	6.67	10.51	12.98	14.99	16.1	14.58		
PLACE1010148	0.96	5.07	1.62	1.48	1.9	1.97		
PLACE1010152	3.11	5.68	5.16	6.33	6.64	5.76		
PLACE1010155	3.8	6.17	6.52	16.85	20.56	20.32	**	+
PLACE1010156	13.71	15.43	32.21	132.45	85.59	134.99	**	+
PLACE1010161	1.9	2.81	5.05	3.29	2.92	1.97		
PLACE1010181	0.73	2.22	1.51	2.58	1.99	2.53		
PLACE1010194	0.64	3.35	1.03	2.26	2.14	1.64		
PLACE1010202	0.4	4.14	1.2	2.91	1.65	2.16		
PLACE1010231	1.1	3.78	2.39	1.31	2.99	2.73		
PLACE1010235	1.26	4.24	1.94	2.68	2.42	3.16		
PLACE1010237	1.01	3.4	2.1	1.14	1.97	0.87		
PLACE1010251	0.59	0.98	1.95	2.57	3.18	1.62		

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PLACE1010261	0.97	2.63	2.07	2.69	1.69	1.55		
PLACE1010270	0.76	2.7	1.3	1.39	2.33	1.42		
PLACE1010273	0.97	3.27	0.46	1.48	2.25	1.5		
PLACE1010274	6.28	9.23	9.66	10.49	12.18	14.28		
PLACE1010277	6.03	10.14	12.68	14.6	16.06	15.84	*	+
PLACE1010293	1.8	5.68	3.55	3.65	3.37	3.96		
PLACE1010297	5.17	11.37	21	24.84	32.59	22.06		
PLACE1010300	4.18	4.78	8.22	8	9.95	6.87		
PLACE1010310	16.52	14.75	49.45	70.74	71	77.01	*	+
PLACE1010321	2.03	4.92	2.46	3.37	4.99	2.73		
PLACE1010324	0.88	3.49	1.56	1.12	1.54	1.2		
PLACE1010329	0.73	4.64	1.95	2.56	3.37	1.96		
PLACE1010330	3.78	9.09	7.29	2.42	10.45	7.67		
PLACE1010335	6.43	11.15	7.43	13.15	17.89	19.1	*	+
PLACE1010341	0.19	4.81	1.24	1.07	3.13	1.54		
PLACE1010342	0.77	0.9	0.75	0.48	2.12	0.8		
PLACE1010346	1.47	1.73	3.61	2.96	4.47	1.71		
PLACE1010362	1.31	2.69	2.22	2.18	3.49	3.31		
PLACE1010364	0.78	2.56	1.65	1.19	2.32	1.49		
PLACE1010368	1.66	5.44	3.51	3.41	3.87	4.48		
PLACE1010373	9.05	10.48	16.82	12.13	15.45	12.28		
PLACE1010383	1.91	5.52	5.13	5.58	6.39	4.9		
PLACE1010385	0.3	3.01	1.07	0.04	0.6	0.9		
PLACE1010389	6.28	7.98	13.24	22.3	13.64	22.94	*	+
PLACE1010401	0.73	2.72	1.32	1.99	2.87	2.21		
PLACE1010410	3.15	4.83	6.71	4.78	7.55	7.32		
PLACE1010418	1.88	4.73	4.2	4.71	5.14	4.66		
PLACE1010425	0.93	4.78	1.43	1.78	1.96	2.15		
PLACE1010443	6.98	13.83	51.39	36.22	63.67	48.93		

PLACE1010445	0.95	5.02	0.68	2.69	3.81	2.44		
PLACE1010481	1.19	2.06	2.46	1.75	2	1.85		
PLACE1010482	28.99	29.39	53.06	31.75	19.63	40.44		
PLACE1010491	3.36	6.4	5.38	4.96	5.98	3.26		
PLACE1010492	4	4.75	5.95	5.57	8.15	7.77		
PLACE1010509	0.8	4.32	3.15	3.09	3.01	2.99		
PLACE1010518	3.33	6.72	6.58	7.3	8.25	8.24		
PLACE1010522	2.3	5.96	4.35	1.87	3.52	2.64		
PLACE1010529	1.8	6.5	3.84	5.43	8.44	7.2		
PLACE1010547	0.79	1.57	1.76	1.51	1.93	2.45		
PLACE1010560	0.63	2.51	2.06	3.31	2.2	2.51		
PLACE1010562	0.74	2.68	1.65	1.64	2.1	1.63		
PLACE1010579	1.11	7.13	2.63	3.45	4.67	3.26		
PLACE1010580	1.35	9.12	3.79	3.27	2.49	4.52		
PLACE1010599	3.56	6.07	7.94	8.32	9.26	8.13		
PLACE1010606	1.17	4.42	1.64	3.39	4.17	3.51		
PLACE1010616	1.84	3.72	5.49	4.09	8.09	6.81		
PLACE1010622	2.1	3.43	3.91	5.07	4.74	4.69	*	+
PLACE1010624	1.43	3.35	3.98	4.21	6.17	5.22		
PLACE1010628	1.37	3.97	2.83	2.14	3.63	4.22		
PLACE1010629	1.08	4.64	2.24	3.01	3.3	3.5		
PLACE1010630	1.64	4.77	3.69	4.22	4.78	5.29		
PLACE1010631	0.5	5.35	2.64	1.55	1.66	2.67		
PLACE1010651	14.24	15.75	24.44	37.62	40.09	52.12	*	+
PLACE1010661	1.62	4.09	2.28	3.56	6.43	3.22		
PLACE1010662	1.32	2.48	1.6	2.98	2.3	1.61		
PLACE1010668	12.87	15.91	27.82	37.63	30.53	28.75		
PLACE1010702	1.46	2.34	4.24	3.59	3.6	3.2		
PLACE1010709	79.16	78.33	115.91	107.07	96.3	133.25		

PLACE1010713	7	10.81	14.7	9.14	8.16	15.14
PLACE1010714	0.82	7.41	1.58	1.75	2.04	1.47
PLACE1010716	0.71	6.19	4.31	2.08	2.3	1.93
PLACE1010717	0.9	6.49	2.13	2.17	3.9	2.61
PLACE1010720	14.03	17.05	53.79	46.72	50.7	41.49
PLACE1010739	0.9	1.2	1.11	1.73	1.21	1.93
PLACE1010743	1.09	2.3	1.99	2.63	2.05	2.21
PLACE1010752	0.87	2.92	1.85	1.76	2.05	1.53
PLACE1010761	3.6	8.83	13.51	12.07	16.4	17.08
PLACE1010771	1.41	6.89	5.03	6.13	10.3	5.42
PLACE1010784	0.9	9.66	1.97	2.07	1.72	1.34
PLACE1010786	1.21	8.77	2.83	2.91	3.68	2.21
PLACE1010789	0.6	1.16	1.52	1.8	1.89	1.17
PLACE1010800	2.18	2.86	3.25	3.95	3.24	2.93
PLACE1010802	2.97	4.63	5.31	5.72	4.27	3.3
PLACE1010811	0.89	2.19	1.96	1.83	1.75	2.18
PLACE1010813	8.89	13.3	55.85	48.82	72.26	46.7
PLACE1010827	1.54	6.43	3.94	4.3	5.52	4.81
PLACE1010833	0.93	8.13	2.63	2.68	3.64	2.09
PLACE1010839	1.57	6.22	3.21	4.22	6.72	4.13
PLACE1010856	7.58	8.94	12.34	8.02	6.53	8.59
PLACE1010857	3.41	3.81	7.63	8.24	5.98	4.56
PLACE1010870	1.3	2.24	2.05	1.62	2.38	1.94
PLACE1010877	1.67	4.66	2.69	2.77	3.92	2.62
PLACE1010882	0.49	4.8	0.99	1.74	1.27	0.51
PLACE1010891	1.1	7.73	1.12	1.85	1.73	0.95
PLACE1010896	1.19	5.29	3.18	3.98	3.05	3.47
PLACE1010900	7.41	13.29	27.9	23.88	20.99	18.85
PLACE1010916	1.55	1.18	2.06	1.89	1.9	2.2

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PLACE1010917	-0.04	0.82	0.36	1.05	2.25	0.56		
PLACE1010924	1.15	2.31	1.55	1.11	1.88	0.92		
PLACE1010925	2.76	5.36	2.17	4.92	6.32	4.16		
PLACE1010926	1.8	5.73	4.31	5.37	4.35	4.45		
PLACE1010942	1.7	6.25	5.63	5.53	7.88	7.69		
PLACE1010943	7.38	10.43	17.12	24.62	29.5	31.96	**	+
PLACE1010944	4.33	7.39	9.3	13.11	11.44	15.58	*	+
PLACE1010947	1.43	0.9	2.41	2.57	2.8	2.25		
PLACE1010954	3.56	2.92	7.4	7.92	8.55	7.64		
PLACE1010960	2.06	3.44	6.07	4.23	7.89	2.6		
PLACE1010965	2.33	3.81	3.54	6.09	4.92	5.03	*	+
PLACE1010968	1.55	4.69	1.38	4.95	6.51	3.68		
PLACE1010978	3.63	6.12	7.05	9	8.94	6.45		
PLACE1010982	2.23	5.77	5.6	4.74	5.66	4.88		
PLACE1010990	0.88	5.4	2.04	3.11	3.03	2.19		
PLACE1011017	5.6	3.78	22.57	25.64	35.47	20.97		
PLACE1011019	1.1	1.5	2.48	3.78	4.42	0.88		
PLACE1011026	4.17	4.93	6.23	6	5.19	2.74		
PLACE1011032	0.89	3.95	2.03	1.44	1.58	0.56		
PLACE1011041	1.07	4.13	1.03	1.69	1.22	1.43		
PLACE1011045	1.49	5.62	2.36	3.26	3.67	4.45		
PLACE1011046	0.83	5.25	1.79	2.57	3.17	1.87		
PLACE1011054	2.33	5.33	6.64	5.26	7.29	5.05		
PLACE1011056	5.78	5.43	16.22	14.56	19.78	15.67		
PLACE1011057	2	2.18	3.5	3.29	5.68	3.9		
PLACE1011059	0.93	1.37	1.56	1.74	2.96	1.79		
PLACE1011066	4.49	5.74	6.76	5.38	7.72	5.49		
PLACE1011087	7.6	7.04	16.48	12.43	17.42	9.79		
PLACE1011090	2.98	6.14	6.74	3.36	4.13	3.26		

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PLACE1011109	1.99	7.29	4.29	4.08	7.96	3.83		
PLACE1011114	1.62	4.4	3.13	3.33	4.68	3.29		
PLACE1011116	4.89	5.94	6.66	7.43	6.81	8.98		
PLACE1011122	0.93	2.52	1.84	2.1	1.61	1.64		
PLACE1011133	0.83	2.22	3.03	3.48	3.52	2.77		
PLACE1011134	12.47	15.29	66.86	44.95	68.68	51.65		
PLACE1011143	0.68	4.53	1.48	1.84	2.62	1.41		
PLACE1011146	0.91	5.93	1.74	1.97	3.23	2.36		
PLACE1011160	1.67	7.36	3.81	3.42	4.53	4.24		
PLACE1011165	1.77	2.34	3.39	2.15	3.39	3.8		
PLACE1011181	5.25	8.31	37.21	29.38	38.44	30.55		
PLACE1011185	2.47	4	3.57	4.66	5.15	4.8	*	+
PLACE1011186	13.16	12.8	16.45	21.18	25.69	28.83	*	+
PLACE1011203	1.08	4.64	2.19	1.75	2.94	1.96		
PLACE1011214	9.02	16.55	59.24	46.39	62.58	47.89		
PLACE1011219	1.41	4.91	3.6	3.26	4.96	2.9		
PLACE1011221	2.68	5.47	6.15	6.23	8.57	7.51		
PLACE1011229	1.38	4.2	2.69	2.43	2.43	3.09		
PLACE1011231	0.53	1.5	1.62	1.84	2.59	2.4		
PLACE1011236	5.69	7.9	43.53	33.48	56.77	44.25		
PLACE1011247	8.36	10.08	19.16	24.17	26.33	29.74	*	+
PLACE1011263	0.57	6.43	4.23	2.62	4.11	5.09		
PLACE1011273	0.72	3.62	1.17	2.01	1.64	1.72		
PLACE1011278	2.42	5	6.12	3.98	4.84	4.31		
PLACE1011289	2.73	5.84	7.57	6.34	6.13	6.08		
PLACE1011291	3.2	5.19	8.31	7.32	8.04	7.95		
PLACE1011296	0.93	2.45	1.94	1.76	2.63	2.05		
PLACE1011310	1.72	2.64	3.36	4.51	2.77	4.48		
PLACE1011311	1.8	3.97	6.33	7.8	9.34	6.73		

PLACE1011321	1.29	4.77	3.5	3.3	2.63	3.33		
PLACE1011325	0.63	4.2	1.84	2	2.74	1.59		
PLACE1011332	5.65	10.55	9.4	14.8	14.57	15.04	*	+
PLACE1011340	0.86	4.88	3.38	3.81	4.71	3.47		
PLACE1011353	5.39	5.53	8.39	10.06	8.58	4.43		
PLACE1011360	1.09	3.29	2.18	2.11	3.06	2.41		
PLACE1011364	4.88	5.69	7.92	6.34	4.57	4.57		
PLACE1011365	0.92	3.36	2.95	3.01	3.6	2.06		
PLACE1011371	9.37	10.69	63.06	56.51	87.51	64.33		
PLACE1011375	1.62	9.37	3.35	2.61	2.74	1.62		
PLACE1011386	3.91	12.96	4.18	6.88	5.51	5.93		
PLACE1011399	1.52	10.14	4.27	2.12	4.22	3.77		
PLACE1011406	1.25	2.05	1.81	5.03	3.26	2.38		
PLACE1011407	0.64	2.05	2.58	2.08	2.19	2.02		
PLACE1011419	2.83	3.2	6.02	6.23	4.18	3.72		
PLACE1011433	3.09	4.43	6.13	3.41	4.74	4.99		
PLACE1011440	0.77	5.81	2.48	2.1	2.24	2.27		
PLACE1011452	1.06	8.86	2.43	2.87	2.71	2.68		
PLACE1011465	0.09	8.53	1.96	1.04	1.68	0.85		
PLACE1011472	1.52	7.67	3.98	0.97	2.87	1.59		
PLACE1011477	11.18	12.29	54.35	31.86	55.86	45.67		
PLACE1011478	1.24	1.64	3.11	5.03	3.02	3.01		
PLACE1011492	2.24	3.54	5.01	5.45	6.74	5.27		
PLACE1011498	0.57	2.77	0.98	1.18	1.69	1.15		
PLACE1011501	0.49	4.67	1.8	4.87	5.63	7.5		
PLACE1011503	0.44	5.37	0.79	0.5	0.82	0.35		
PLACE1011509	1.1	7.8	3.38	4.62	5.08	5.74		
PLACE1011514	5.86	11.61	11.98	13	17.7	13.17		
PLACE1011516	10.37	13.29	18.32	18.32	8.08	3.63		

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PLACE1011520	0.34	0.95	1.34	1.3	1.73	1.01		
PLACE1011538	52.87	99.27	185.04	129.45	86.87	63.9		
PLACE1011555	0.87	2.88	2.83	1.55	2.03	1.48		
PLACE1011561	3.2	4.53	1.98	6.81	5.31	3.08		
PLACE1011563	1.35	4.74	3.49	2.52	2.64	2.87		
PLACE1011567	1.04	4.94	3.36	2.75	4.19	2.77		
PLACE1011569	0.32	4.35	2.77	2.38	2.46	2.28		
PLACE1011576	3.25	1.88	7.94	7.85	9.1	8.03		
PLACE1011586	3.24	2.5	6.22	4.43	4.35	2.94		
PLACE1011635	1.85	2.56	4.53	9.96	12.43	8.71	**	+
PLACE1011641	0.43	2.9	0.9	1.71	1.18	1.19		
PLACE1011642	5.05	6.96	10.37	12.13	10.86	10.09		
PLACE1011643	1.29	3.69	1.14	2.38	2.28	2.14		
PLACE1011646	8.68	12.8	30.53	39.05	54.16	37.76	*	+
PLACE1011649	1.35	5.7	3.88	4.5	4.61	5.46		
PLACE1011650	1.15	1.45	2.54	2.47	3.24	3.75		
PLACE1011661	1.02	2.26	2.8	3.95	5.92	3.46		
PLACE1011664	2.21	3.18	3.99	5.31	3.93	1.73		
PLACE1011672	0.88	4.14	0.72	2.69	3.57	2.04		
PLACE1011675	0.51	2.31	1.32	1.66	0.99	0.83		
PLACE1011682	2.04	4.56	2.23	2.22	4.03	2.12		
PLACE1011708	1.1	5.89	3.8	5.5	8.12	4.66		
PLACE1011719	1.07	4.58	1.66	3.55	3.88	3.03		
PLACE1011725	1.23	1.19	2.72	3.73	5.19	4.3	*	+
PLACE1011729	0.86	1.03	1.8	2.38	3.26	1.22		
PLACE1011741	2.36	3.67	3.64	4.16	2.52	4.23		
PLACE1011749	1.58	3.89	4.09	3.49	4.85	3.27		
PLACE1011757	20.92	30.53	55.88	56.6	55.88	49.59		
PLACE1011762	0.4	4.34	2.69	3.91	2.14	2.3		

PLACE1011778	0.51	4.39	1.99	1.34	2.02	1.34		
PLACE1011783	2.59	4.63	5.46	4.8	8.41	5.55		
PLACE1011795	0.74	1.28	2.24	1.47	1.8	1.22		
PLACE1011810	9.28	10.82	19.51	13.32	17.73	15.47		
PLACE1011824	5.38	8.17	38.05	25.52	42.89	16.75		
PLACE1011825	10.61	16.39	22.6	17.63	18.92	16.07		
PLACE1011835	24.64	32.67	47.67	32.09	26.75	37.23		
PLACE1011836	18.11	18.97	31.43	33.14	47.23	13.95		
PLACE1011847	2.67	6.74	6.42	5.34	7.18	5.84		
PLACE1011855	0.9	6.06	3.53	3.23	4.47	3.49		
PLACE1011858	5.83	7.44	9.37	6.88	6.25	8.35		
PLACE1011874	1.35	3.14	3.55	4.18	5.28	4.65		
PLACE1011875	0.57	2.29	1.11	2.66	2.48	2.64		
PLACE1011877	3.8	5.03	4.4	7.67	6.8	9.97	*	+
PLACE1011891	0.17	3.81	1.31	1.13	1.34	1.26		
PLACE1011896	-0.1	5.22	1.45	-0.19	1.07	0.32		
PLACE1011920	0.21	5.87	1.04	1.1	1.92	1.76		
PLACE1011922	2.4	4.18	4.72	3.72	2.88	3.98		
PLACE1011923	3.42	4.82	7.51	8.09	5.38	12.28		
PLACE1011937	3.16	2.24	3.76	3.81	5.58	4.64		
PLACE1011939	14.93	17.81	26.01	41.75	45.05	47.88	**	+
PLACE1011940	6.13	7.58	12.68	5.73	7	7.23		
PLACE1011962	3.28	7.83	7.35	6.39	8.38	8.01		
PLACE1011964	0.39	5.05	1.66	1.04	1.95	1.46		
PLACE1011978	1.55	4.65	3.35	4.48	5.91	5.14		
PLACE1011980	2.1	4.62	6.07	3.95	4.91	5.35		
PLACE1011981	5.77	7.28	38.2	27.22	35.24	34.99		
PLACE1011982	0.83	3.1	2.23	1.82	2.59	1.57		
PLACE1011995	0.81	3.4	3.73	2.51	3.59	2.86		

PLACE1012023	1.38	5.37	1.87	2.09	2.46	1.91		
PLACE1012026	1.95	5.72	4.23	6.08	9.51	9.8		
PLACE1012031	2.49	5.81	4.54	4.34	6.35	4.03		
PLACE2000003	1.18	3.64	6.86	7.38	8.12	8.92		
PLACE2000005	1.16	2.41	2.16	2.76	2.03	1.89		
PLACE2000006	2.52	4.13	15.6	11.34	16.58	13.4		
PLACE2000007	0.96	4.85	4.24	3.94	5.13	3.33		
PLACE2000011	1.72	3.27	3.34	4.3	5.06	3.62		
PLACE2000014	4.04	5.93	23.94	27.19	30.87	30.97	*	+
PLACE2000015	1.27	4.79	3.52	2.77	3.31	2.69		
PLACE2000017	0.48	4.78	2.15	2.65	2.56	2.45		
PLACE2000021	1.99	5.06	4.09	3.72	6.24	5.61		
PLACE2000022	1.8	2.8	4.31	3.35	4.64	2.71		
PLACE2000030	9.37	11.08	71.38	55.43	60.32	35.97		
PLACE2000032	1.23	2.89	3.51	3.53	3.24	2.32		
PLACE2000033	3.29	6.3	12.11	12.49	14.25	9.37		
PLACE2000034	0.6	4.3	1.92	1.79	2.19	2.44		
PLACE2000039	2.75	8.06	3.92	6.27	8.01	4.81		
PLACE2000043	7	11.08	22.94	19.27	26.58	17.38		
PLACE2000044	0.63	6.92	1.12	1.8	1.71	1.29		
PLACE2000047	0.84	5.25	5.15	5.4	6.46	7.32		
PLACE2000050	1.48	2.68	4.78	2.92	2.98	1.2		
PLACE2000061	0.47	2.07	1.17	0.95	1.34	0.25		
PLACE2000062	1.99	2.83	4.12	4.89	4.4	3.09		
PLACE2000072	0.78	2.45	1.57	1.85	1.62	1.69		
PLACE2000073	0.89	5.86	2.86	2.8	2.61	3.07		
PLACE2000097	8.54	19.93	23.93	27.69	35.36	26.36		
PLACE2000100	1.87	7.79	3.53	4.23	6.29	4.22		
PLACE2000103	1.03	7.44	2.25	3.51	5.17	4.38		

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PLACE2000106	1.53	2.42	4.19	5.71	3.29	4.01		
PLACE2000111	2.05	3.17	4.37	4.07	6.6	4.75		
PLACE2000115	0.3	2.06	0.75	0.31	1.29	0.97		
PLACE2000118	10.15	17.04	21.09	13.73	15.21	22.01		
PLACE2000124	10.14	17.83	62.13	53.2	98.37	62.96		
PLACE2000132	0.06	6.26	1.48	0.99	1.5	1.56		
PLACE2000136	0.55	7.94	0.91	1.47	1.37	1.02		
PLACE2000137	0.96	4.46	2.4	2.65	4.12	3.14		
PLACE2000140	2.91	5.24	14.34	13.2	12.08	9.43		
PLACE2000147	1.49	1.52	2.83	1.06	0.97	1.12		
PLACE2000153	0.3	3.44	2.15	1.69	2.45	1.95		
PLACE2000164	0.66	2.78	1.13	2.66	1.62	1.62		
PLACE2000170	1.54	6.18	4.69	5.26	9.09	6.24		
PLACE2000172	0.33	4.34	2.15	1.25	1.93	2.43		
PLACE2000173	0.92	4.97	3.37	3.33	3.71	2.74		
PLACE2000174	1.17	4.68	2.43	1.85	2.89	2.05		
PLACE2000176	1.22	1.57	2.58	3.28	2.27	1.42		
PLACE2000187	1.01	2.08	2.55	3.45	3.66	2.19		
PLACE2000216	7.03	9.28	11.47	14.09	9.13	3.68		
PLACE2000219	0.69	4.02	2.72	3.55	3.58	2.3		
PLACE2000221	2.49	6.81	6.53	7.22	9.33	8.56		
PLACE2000223	0.72	3.2	1.71	1.16	1.05	0.48		
PLACE2000231	1.02	3.97	3.11	3.43	2.61	2.47		
PLACE2000235	1.82	5.27	6.17	6.02	7.45	6.97		
PLACE2000246	1.93	2	6.06	4.58	5.09	3.93		
PLACE2000264	0.67	1.39	1.85	2.45	3.74	3	*	+
PLACE2000274	0.65	2.4	2.12	3.09	4.11	2.1		
PLACE2000287	0.81	4.44	1.49	2	2.59	1.34		
PLACE2000296	1.01	4.56	1.55	2.5	3.16	1.69		

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PLACE2000302	1.34	4.67	2.86	3.52	3.35	3.45		
PLACE2000305	3.09	6.65	5.42	6.3	7.15	5.02		
PLACE2000317	0.92	6.34	2.26	3.15	2.95	2.4		
PLACE2000324	1.19	1.25	3.09	4.2	5.84	3.3		
PLACE2000334	3.52	5	6.6	7.33	8.12	5.88		
PLACE2000335	1.47	4.35	4.24	5.68	6.25	4.76		
PLACE2000340	0.64	3.47	1.63	1.58	1.52	1.65		
PLACE2000341	4.21	7.87	28.81	18.94	32.45	19.16		
PLACE2000342	2.07	5.11	4.32	4.84	5.82	4.49		
PLACE2000347	1.24	5.26	5.58	7.83	6.22	7.55		
PLACE2000357	8.49	13.56	15.35	17.83	18.98	21.24	*	+
PLACE2000358	2.87	3.65	8.67	4.88	7.63	4.37		
PLACE2000359	1.27	1.79	4.45	3.28	6.65	3.61		
PLACE2000366	1.93	3.14	3.22	3.99	5.6	4.17		
PLACE2000371	4.29	5.2	6.08	5.95	9.06	7.32		
PLACE2000373	1.91	4.8	5.98	5.69	6.29	4.19		
PLACE2000374	1.86	5.17	2.78	1.62	2.79	1.49		
PLACE2000379	0.34	4.85	1.32	1.28	0.92	0.04		
PLACE2000386	39.29	43.92	84.66	87.53	104.55	76.56		
PLACE2000388	1.96	3.35	3.89	2.78	3.48	3.49		
PLACE2000392	33.29	39.2	59.56	42.5	52.12	58.24		
PLACE2000394	1.26	3.27	3.01	5.69	4.35	4.34	*	+
PLACE2000398	0.73	3.88	2.36	2.03	3.59	1.35		
PLACE2000399	3.7	6.82	7.01	7.15	7	6.79		
PLACE2000402	2.15	6.88	3.84	2.86	3.68	3.9		
PLACE2000404	5.2	9.96	10.67	10.03	11.04	6.47		
PLACE2000411	3.21	7.2	5.21	5.27	5.73	6.68		
PLACE2000418	0.73	2.28	2.41	2.22	3.07	2.37		
PLACE2000419	0.99	2.32	2.54	4.95	4.55	3.29	*	+

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PLACE2000425	1.26	3.98	3.11	4.28	4.81	5.2		
PLACE2000427	0.7	5.13	3.27	2.54	3.04	2.47		
PLACE2000433	0.77	7.05	2.6	2.33	3.09	2.46		
PLACE2000435	0.48	5.19	1.49	1.69	1.63	1.5		
PLACE2000438	1.61	4.74	3.66	2.33	2.81	3.15		
PLACE2000450	3.01	4.38	5.67	6.51	7.39	5.63		
PLACE2000455	0.24	2.62	1.24	1.65	2	1.82		
PLACE2000458	0.38	3.3	1.81	1.06	2.7	1.24		
PLACE2000464	2.15	4.91	5.3	7.43	9.68	8.83	*	+
PLACE2000465	1.43	6.72	6	6.51	8.27	6.31		
PLACE2000473	120.94	179.35	328.3	214.7	297.75	279.74		
PLACE2000477	0.43	3.87	1.34	1.13	2.22	0.97		
PLACE3000004	2.22	4.63	6.39	5.27	7.51	5.2		
PLACE3000009	19.91	19.71	105.63	77.3	140.99	92.95		
PLACE3000020	10.03	9.03	49.6	36.74	46.52	23.82		
PLACE3000029	6.59	9.63	24.88	14.88	18.47	20.04		
PLACE3000038	0.52	2.37	2.47	1.44	2.4	2.05		
PLACE3000052	5.13	7.95	23.92	25.01	29.61	24.94		
PLACE3000059	0.57	5	2.42	0.75	2.8	1.27		
PLACE3000067	2.51	5.79	7.44	5.66	8.53	7.75		
PLACE3000069	1.95	5.61	3.58	5.24	3.79	4.55		
PLACE3000070	2.57	5.57	9.04	9.5	10.42	10.57		
PLACE3000103	3.85	7.84	11.87	6.6	8.32	4.37		
PLACE3000119	1.59	2.74	3.15	3.24	3.67	2.95		
PLACE3000121	7.58	8.44	38.1	30.63	42.28	32.64		
PLACE3000124	1.53	4.54	5.95	6.35	7.75	7.18		
PLACE3000135	0.69	5.46	1.1	0.76	0.9	0.59		
PLACE3000136	0.77	10.46	4.46	2.12	2.77	2.01		
PLACE3000142	0.7	9.94	1.75	1.53	2.76	1.13		

PLACE3000145	8.69	17.55	55.33	42.85	49.12	39.96		
PLACE3000147	15.7	12.92	39.97	64.96	54.76	30.34		
PLACE3000148	0.7	2.08	1.48	0.82	1.4	1.38		
PLACE3000154	0.48	1.86	0.67	1.5	0.87	0.44		
PLACE3000155	1.28	4.26	2.53	3.97	4.76	3.04		
PLACE3000156	1.11	7.96	2.07	1.96	3.4	2.81		
PLACE3000157	0.92	8.37	1.75	2.06	3.02	2.72		
PLACE3000158	1.73	8.82	5.05	3.81	5.63	4.77		
PLACE3000160	8.11	15.22	19.5	33.66	34.71	33.78	**	+
PLACE3000169	2.15	2.65	6.87	4.3	5.11	5.12		
PLACE3000181	1.06	2.14	3.94	3.22	2.62	3		
PLACE3000194	0.31	2.83	1.77	1.89	2.58	2.42		
PLACE3000197	1.18	2.66	2.09	2.42	2.46	2.21		
PLACE3000199	0.22	4.8	1.63	0.55	0.86	0.43		
PLACE3000205	11.79	17.95	57.49	51.4	63.83	42.63		
PLACE3000207	3.37	6.91	7.13	6.7	8.92	6.23		
PLACE3000208	2.26	4.96	2.66	5.28	5.97	5.84		
PLACE3000213	4.79	5.55	10.8	5.12	5.16	5.05		
PLACE3000215	1.88	5.02	5.71	4.74	5	3.03		
PLACE3000218	0	1.63	1.18	0.97	0.62	0.31		
PLACE3000220	1.96	3.55	4.58	6.74	7.52	6.69	*	+
PLACE3000221	14.42	25.34	40.15	43.8	51.16	36.99		
PLACE3000225	1.15	4.68	3.11	2.11	2.67	1.28		
PLACE3000226	1.37	5.65	5.16	3.78	7.42	3.68		
PLACE3000230	0.83	3.46	1.36	2	2.8	1.73		
PLACE3000231	1.31	1.97	2.37	4.86	3.95	4.12	**	+
PLACE3000235	1.12	1.75	3.89	3.95	4.21	3.39		
PLACE3000242	2.6	5.11	9.24	9.46	10.97	8.29		
PLACE3000244	1.05	3.2	1.81	1.85	1.81	0.64		

PLACE3000253	0.7	3.75	1.64	2.67	2.11	1.27		
PLACE3000254	2.5	4.75	4.04	6.19	6.09	5.75	*	+
PLACE3000271	2.67	6.06	6.81	10.96	10.99	9.5	*	+
PLACE3000276	1.1	5.78	2.27	1.48	1.9	1.78		
PLACE3000304	5.55	4.69	10.81	11.19	11.49	10.5		
PLACE3000309	0.43	1.67	1.87	2.43	2.94	2.78	*	+
PLACE3000310	2.19	2.19	3.73	4.84	4.81	3.4		
PLACE3000320	1.02	3.65	1.8	2.54	2.37	2.32		
PLACE3000322	1.31	4.23	6.63	7.5	7.8	6.09		
PLACE3000330	24.05	24.44	41.08	31.87	35.83	29.17		
PLACE3000331	1.21	5.86	4.14	4.34	5.7	4.31		
PLACE3000336	2.61	6.99	4.42	4.24	5.72	5.11		
PLACE3000339	7.36	5.1	11.41	16.25	18.28	17.37	**	+
PLACE3000341	1.65	1.32	2.41	4.08	4.35	3.65	**	+
PLACE3000350	5.88	6.4	12.86	15.45	18.5	15.41	*	+
PLACE3000352	1.54	3.88	2.13	2.37	2.25	1.71		
PLACE3000353	5.38	9.72	11.8	19.12	22.98	15.5	*	+
PLACE3000362	0.62	4.92	4.72	3.61	5.33	3.39		
PLACE3000363	2.19	5.13	2.32	1.89	3.28	2.07		
PLACE3000365	1.34	6.11	3.37	3.34	4.05	2.12		
PLACE3000373	0.89	1.52	3.66	2.93	6.08	2.3		
PLACE3000374	1.07	1.85	2.91	2.72	2.99	2.15		
PLACE3000387	0.31	3.32	1.04	1.24	1.65	1.29		
PLACE3000388	1.18	3.22	1.94	2.76	3.49	2.22		
PLACE3000399	2.12	4.66	6.28	7.42	9.84	6.05		
PLACE3000400	3.08	5.44	11.87	7.97	10.77	7.82		
PLACE3000401	7.52	11.42	18.59	22.61	29.55	23.4	*	+
PLACE3000402	1.79	3.21	3.4	2.19	1.74	1.79		
PLACE3000405	3.37	3.74	5.82	5.54	7.22	6.01		

PLACE3000406	2.1	2.91	3.11	3.48	3.68	2.42
PLACE3000413	1.18	2.72	2.69	1.71	2.06	1.52
PLACE3000416	1.05	4.03	4.04	3.43	2.67	2.72
PLACE3000425	1.21	6.27	4.33	3.98	6.36	3.92
PLACE3000437	4.79	10.85	29.89	16.69	25.26	19.14
PLACE3000455	2.97	8.07	10.62	8.97	10.39	7.91
PLACE3000475	16.52	19.2	47.35	40.22	39.77	34.21
PLACE3000477	5.44	4.79	5.56	8.05	5.52	8.42
PLACE4000003	0.38	2.97	1.61	3.14	2.33	2.31
PLACE4000008	15.19	11.38	16.76	13.05	14.26	8.84
PLACE4000009	1.17	6.19	3.39	3.93	3.37	1.82
PLACE4000014	1.31	5.12	1.77	2.16	3.03	2.19
PLACE4000029	6.33	8.48	35.37	23.93	32.21	24.25
PLACE4000034	2.27	6.24	5.22	6.46	6.52	4.91
PLACE4000049	3.39	3.35	5.21	3.85	5.82	4.86
PLACE4000052	1.41	3.36	2.2	2.62	2.64	2.02
PLACE4000062	1.6	4.94	5.06	4.25	5.06	3.71
PLACE4000063	2.59	6.87	5.19	4.86	4.81	3.73
PLACE4000089	1.52	6.31	3.35	2.81	3.91	2.84
PLACE4000093	0.44	5.6	1.61	1.28	1.65	1.98
PLACE4000100	2.72	6.13	4.75	4.33	3.62	3.94
PLACE4000103	0.63	4.48	5.64	4.4	5.67	2.9
PLACE4000106	3.2	5.33	6.63	7.1	5.13	7.21
PLACE4000128	1.93	3.97	4.88	4.15	4.96	4.4
PLACE4000129	0.74	3.26	1.64	1.57	2.11	1.78
PLACE4000131	7.14	10.85	41.43	32.45	41.08	31.22
PLACE4000147	0.34	3.65	0.54	0.45	0.93	0.61
PLACE4000156	2.47	6.08	8.06	7.83	13.47	9.07
PLACE4000175	0.72	4.08	1.48	0.98	0.91	0.84

PLACE4000190	14.55	18.47	70.34	49.15	74.82	60.76		
PLACE4000192	1.3	2.27	3.6	2.36	2	1.25		
PLACE4000206	5.35	6.65	12.44	7.13	7.1	6.02		
PLACE4000211	3.34	4.64	22.23	11.68	12.35	13.44		
PLACE4000214	0.86	3.61	2.68	2.08	2.53	1.69		
PLACE4000222	0.93	5.28	4.36	4.13	4.75	3.5		
PLACE4000223	0.46	4.51	1.79	1.37	1.22	0.38		
PLACE4000229	1.9	5.79	2.11	2.81	3.36	3.48		
PLACE4000230	1.11	5.89	6.51	3.61	6.81	5.15		
PLACE4000233	1.26	3.02	5.66	2.92	2.98	3.51		
PLACE4000239	2.35	3.68	4.17	4.19	3.97	3.35		
PLACE4000247	0.52	2.37	3.38	2.64	3.1	2.35		
PLACE4000250	1.18	3.24	2.35	3.33	3.68	2.8		
PLACE4000252	1.06	4.99	2.25	1.92	1.75	1.64		
PLACE4000259	4.42	11.95	18.1	14.47	22.09	14.02		
PLACE4000261	0.87	10.29	1.07	2.03	1.9	1.12		
PLACE4000264	15.86	24.96	36.9	11.96	21.82	22.51		
PLACE4000269	3.48	3.71	7.95	4.62	4.55	2.85		
PLACE4000270	0.43	1.42	1.87	1.75	1.83	0.59		
PLACE4000281	17.84	20.97	44.05	32.93	28.37	28.87		
PLACE4000300	0.67	2.06	2.04	3.21	2.88	3.58	*	+
PLACE4000320	1.33	5.86	3.1	2.84	5.32	3.21		
PLACE4000323	1.63	7.43	5.13	4.03	4.65	4.82		
PLACE4000326	1.8	10.98	5.67	5.72	8.73	5.59		
PLACE4000344	0.22	5.75	2.62	1.66	1.6	1.18		
PLACE4000347	4.7	3.82	13.93	16.83	16.75	17.36	*	+
PLACE4000354	3.18	6.29	10.68	5.17	2.81	2.79		
PLACE4000367	0.79	2.97	1.71	0.87	1.3	1.38		
PLACE4000369	1.35	3.97	2.36	1.99	1.96	0.82		

PLACE4000379	2.44	6.66	5.44	5.94	7.55	5.07
PLACE4000387	0.88	5.86	2.11	1.28	0.84	1.12
PLACE4000392	0.42	5.58	1.32	1.81	1.02	1.63
PLACE4000399	10.99	17.08	75.17	59.11	80.22	58
PLACE4000401	0.72	0.7	1.53	1.17	0.83	1.4
PLACE4000403	3.15	4.13	8.51	5.29	6.38	5.87
PLACE4000411	2.22	2.28	4	2.27	2.6	1.82
PLACE4000415	0.7	3.55	2.8	1.16	1.86	0.78
PLACE4000416	25.49	29.13	33.54	23.65	21.92	24.83
PLACE4000424	1.61	5.59	3.33	3.27	3.92	2.51
PLACE4000431	3.89	7.39	21.01	17.68	28.21	16.79
PLACE4000443	0.07	4.33	2.15	1.52	2.83	1.14
PLACE4000445	3.94	5.43	9.98	7.62	6.99	6.27
PLACE4000450	2.99	3.65	23.28	15.51	24.53	16.04
PLACE4000455	5.18	7.39	9.55	8	7.21	4.63
PLACE4000465	1.39	4.34	3.26	4.15	6.07	4.34
PLACE4000466	120.96	98.04	201.25	113.83	170.96	145.31
PLACE4000472	3.12	9.6	10.17	10.92	13.21	9.22
PLACE4000487	3.18	7.83	16.5	14.66	16.62	15.05
PLACE4000489	0.93	4.69	3.41	1.95	3.88	1.69
PLACE4000494	1.15	1.6	4.07	2.74	3.1	2.08
PLACE4000502	6.3	5.39	10.92	11.65	15.08	6.37
PLACE4000521	2.5	3.44	16.06	12.78	20.63	11.2
PLACE4000522	5.07	6.17	9.07	12.43	8.68	14.11
PLACE4000537	0.98	4.28	1.27	1.67	1.61	1.22
PLACE4000548	1.99	5.69	2.46	3.04	3.68	2.32
PLACE4000558	0.87	6.72	1.97	3.15	2.41	2.15
PLACE4000581	2.1	7.22	7.04	3.9	5.96	5.44
PLACE4000590	0.4	0.61	0.15	0.4	0.81	-0.25

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PLACE4000593	2.94	2.98	5.22	4.44	5.82	3.83		
PLACE4000612	0.68	3.33	3.33	1.5	3.02	2.74		
PLACE4000638	1.25	4.24	0.84	1.2	1.44	1.58		
PLACE4000650	0.82	4.67	1.02	1.43	1.11	1.16		
PLACE4000651	2.42	6.4	7.48	5	7.01	6.07		
PLACE4000654	0.98	5.7	2.47	1.35	2.48	1.47		
PLACE4000670	0.5	4.06	2.92	0.76	1.29	0.67		
PLACE4000685	6.35	8.68	13.83	13.46	14.26	13.77		
PLACE4000687	0.37	3.02	1.11	2.2	1.4	1.12		
PLACE5000003	1.1	2.74	3.31	3.21	3.55	3.07		
PLACE5000005	12.43	16.53	27.36	24.54	24.57	24.76		
PLACE5000019	0.4	4.15	1.13	0.59	1.89	0.79		
PLACE5000021	0.74	4.59	1.61	0.39	0.93	0.32		
PLACE5000022	1.2	6.11	2.25	3.17	2.76	2.09		
PLACE5000024	1.77	2.58	2.27	2.92	3.39	3.84	*	+
PLACE5000036	1.81	3.24	3.11	2.41	3.19	2.84		
PLACE5000059	14.41	17.79	26.55	25.98	30.03	34.87		
PLACE5000076	1.41	3.61	2.22	4.04	3.96	2.54		
PLACE5000117	7.44	12.48	15.66	16.87	18.78	20.64		
PLACE5000143	0.85	6.45	2.11	1.67	2.85	2.73		
PLACE5000152	0.42	4.49	1.23	1.61	1.95	1.57		
PLACE5000154	18.23	23.5	45.06	21.81	25.65	31.8		
PLACE5000155	3.35	2.81	5.51	3.94	2.78	4.87		
PLACE5000165	3.78	4.4	6.67	4.51	5.99	5.82		
SKNMC1000004	9.7	11.62	16.77	10.19	12.16	13.96		
SKNMC1000011	1.82	8.58	4.12	5.89	3.95	6.77		
SKNMC1000013	0.51	6.69	1.13	1.21	2.14	1.44		
SKNMC1000014	1.28	4.18	3.22	3.77	6.37	3.96		
SKNMC1000018	3.42	5.19	5.25	5.51	5.68	3.44		

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SKNMC1000020	0.95	4.03	3.46	3.6	4.68	4.56		
SKNMC1000046	2	3.17	3.48	3.95	3.26	2.55		
SKNMC1000050	4.99	8.04	10.32	5.4	6.28	6.12		
SKNMC1000062	9.79	12.6	20.18	19.2	15.42	18.73		
SKNMC1000075	1.45	4.3	2.01	1.98	1.89	2.92		
SKNMC1000082	1.12	4.39	2.13	1.85	1.78	2.39		
SKNMC1000091	4.54	7.52	7.95	11.74	12.86	12.77	**	+
SKNMC1000099	0.33	4.29	1.98	1.32	0.65	1.18		
SKNMC1000104	1.13	4.24	3.45	1.47	3.14	2.43		
SKNMC1000113	0.97	1.83	1.2	1.74	2.63	0.89		
SKNMC1000119	1.73	2.64	5.07	4.48	5.34	4.67		
SKNMC1000142	0.04	2.87	0.99	1.27	0.75	1		
SKNMC1000170	0.91	4.75	2.34	1.71	1.49	1.11		
SKNMC1000178	3.02	8.39	7.08	5.77	9.65	9.02		
SKNMC1000194	0.63	9.82	1.51	0.61	1.73	1.3		
SKNMC1000198	1.35	11.01	3.33	2.65	2.1	2.88		
SKNMC1000225	1.35	6.44	2.97	2.39	3.4	3.26		
SKNMC1000249	0.49	2.14	0.75	0.57	0.51	0.52		
SPLEN1000007	0.74	2.15	2.11	1.7	2.26	1.99		
SPLEN1000012	0.39	1.9	1.72	1.19	0.8	0.84		
SPLEN1000014	1.78	4.4	4.9	5.75	4.33	3.99		
SPLEN1000036	4.95	11.64	24.32	20.56	27.73	21.68		
SPLEN1000059	0.04	6.69	1.06	0.91	1.79	1.47		
SPLEN1000068	1.68	10.81	5.71	5.79	5.17	5.64		
SPLEN1000072	1	8.5	4.7	2.82	3	2.21		
SPLEN1000101	20.01	18.4	45.64	29.93	25.24	12.63		
SPLEN1000108	0.56	1.54	0.98	0.75	1.11	0.76		
SPLEN1000113	1.33	2.27	3.04	2.72	4.13	3.04		
SPLEN1000114	2.97	4.19	6.03	3.59	4.76	6.32		

SPLEN1000132	0.85	4	1.72	2.25	2.67	1.99		
SPLEN1000135	3.13	8.76	14.93	11.12	15.28	10.52		
SPLEN1000136	12.41	21.47	15.14	20.24	27.48	21.8		
SPLEN1000141	2.26	7.07	10.79	4.03	5.41	4.51		
SPLEN1000164	2.49	3.79	8.58	3.98	5.88	7.61		
SPLEN1000166	0.4	2.9	2.96	1.67	1.19	1.68		
SPLEN1000175	2.16	4.48	6.1	5.65	4.12	4.15		
SPLEN1000182	0.98	2.66	0.23	0.83	0.6	0.67		
SPLEN1000185	3.41	8.49	8.54	11.38	10.43	11.95		
THYMU1000004	10.22	14.07	20.43	22.34	22.76	23.6		
THYMU1000009	9.48	10.13	14.9	13.48	23.86	22.1		
THYMU1000015	8.87	10.42	16.18	19.25	22.21	20.8	*	+
THYMU1000016	6.24	5.96	13.03	10.3	8.45	9.38		
THYMU1000023	0.77	1.86	3.6	5.22	3.68	3.6		
THYMU1000034	0.16	1.77	1.8	0.79	0.88	0.14		
THYMU1000035	0.62	2.8	0.97	1.17	0.95	1.31		
THYMU1000037	1.53	4.15	2.11	2.06	2.81	1.45		
THYMU1000042	5.97	10.24	12.23	12.03	13.98	13.28		
THYMU1000047	2.72	6.03	6.72	6.04	7.77	7.23		
THYMU1000080	0.56	4.31	2.6	3.26	1.85	2.11		
THYMU1000094	2.77	3.47	7.91	9.17	8.35	4.55		
THYMU1000109	17.28	14.34	111.37	98.05	142.29	93.04		
THYMU1000127	2.75	5.95	10.76	8.18	9.98	6.74		
THYMU1000130	2.5	4.4	4.55	6.69	6.07	4.94		
THYMU1000137	3.53	7.18	10.26	12.67	18.55	13.05	*	+
THYMU1000146	4.37	8.38	6.52	8.29	7.46	7.74		
THYMU1000159	5.43	9.51	16.37	12.4	15.15	13.27		
THYMU1000163	5.85	12.26	37.58	45.53	58.37	36.93		
THYMU1000167	2.39	3.02	4.73	4.89	6.79	3.97		

THYMU1000186	0.69	1.05	1.45	1.31	2.45	0.66
THYRO1000017	0.94	3.45	2.54	2.02	3.54	2.11
THYRO1000026	1.56	5.63	4.02	3.96	4.82	3.36
THYRO1000034	0.49	4.16	1.59	1.99	2	1.82
THYRO1000035	0.86	4.84	1.34	2.29	2.48	2.11
THYRO1000036	0.93	8.32	4	3.08	4.36	5.59
THYRO1000040	2.58	7.02	4.76	4.66	4.83	4.93
THYRO1000061	2.01	1.91	3.07	3.53	3.8	2.61
THYRO1000067	1.98	2.8	5.12	3.37	4.14	3.3
THYRO1000070	1.26	2.09	3.59	2.65	3.85	3.45
THYRO1000072	1.33	3.37	4.22	2.54	4.08	2.06
THYRO1000084	8.07	12.69	22.39	2.99	5.61	4.42
THYRO1000085	1.44	5.66	3.99	2.42	3.86	2.85
THYRO1000086	-0.05	5.46	1.74	0.89	1.18	1.15
THYRO1000087	0.72	3.86	1.01	0	0.58	0.17
THYRO1000092	2.32	5.1	4.66	3.75	4.43	4.5
THYRO1000093	0.35	3.24	0.83	1.54	1.27	0.95
THYRO1000099	0.45	2.53	2.73	2.8	1.67	2.39
THYRO1000107	0.5	2.95	2.7	2.86	3.22	2
THYRO1000111	0.85	4.58	1.78	1.4	2.06	2.36
THYRO1000121	1.33	5.72	2.52	1.94	2.4	2.95
THYRO1000124	0.27	5.55	0.64	0.86	0.89	0.64
THYRO1000129	0.36	2.1	0.11	0.94	1.11	0.92
THYRO1000130	1.82	3.11	3.13	3.85	3.01	2.39
THYRO1000132	2.4	3.62	9.43	11.14	6.99	6.26
THYRO1000134	1.5	4.07	3.22	4.06	3.65	3.73
THYRO1000144	1.72	4.78	3.15	7.87	7.09	2.33
THYRO1000155	1.6	4.1	1.45	1.77	1.9	2.23
THYRO1000156	1.13	6.53	3.62	2.45	4.29	2.58

THYRO1000163	3.62	8.42	5.28	4.76	6.63	2.24		
THYRO1000173	1.19	4.45	2.26	3.33	1.36	2.75		
THYRO1000186	1.98	3.24	7.86	6.91	6.84	6.35		
THYRO1000187	2.7	3.58	5.3	4.92	6.24	5.22		
THYRO1000190	1.12	3.32	2.94	3.73	4.55	2.71		
THYRO1000196	0.3	5.28	0.81	0.66	1.21	0.52		
THYRO1000197	2.05	7.28	4.69	4.08	6.24	3.89		
THYRO1000199	0.76	6.28	4.13	1.93	2.08	1.98		
THYRO1000206	8.47	6.92	9.25	8.44	11.6	7.5		
THYRO1000221	1.9	3.17	4.42	4.02	5.87	4.54		
THYRO1000222	3.65	4.26	4.23	4.68	4.96	4.93	*	+
THYRO1000228	0.81	3.67	2.85	2.24	3.04	2.94		
THYRO1000241	1.76	3.7	6.29	4.62	5.54	4.01		
THYRO1000242	0.63	4.16	4.46	2.49	2.56	2.62		
THYRO1000246	1.61	5.5	3.9	3.43	4.7	3.91		
THYRO1000253	1.07	4.05	1.73	1.99	3.35	2.31		
THYRO1000270	1.15	5.12	1.39	1.22	2.5	1.26		
THYRO1000279	0.42	2.84	0.25	0.65	1.01	0.58		
THYRO1000285	2.75	4.65	7.31	7.03	7.75	4.88		
THYRO1000288	7.76	7.59	11.77	5.68	5.07	7.22		
THYRO1000296	4.18	6.04	6.22	7.4	11.24	8.96	*	+
THYRO1000320	1.54	5.83	4.97	3.65	4.45	3.34		
THYRO1000322	1.1	5.48	2.48	1.76	3.93	1.76		
THYRO1000327	1.75	7.69	4.77	6.21	5.23	4.41		
THYRO1000343	2.5	6.12	5.35	5.06	5.04	6.13		
THYRO1000345	1.36	7.34	11.92	7.82	5.84	9.49		
THYRO1000358	1.82	3.39	3.08	1.92	2.32	1.54		
THYRO1000368	0.76	2.39	2.73	1.43	2.82	0.58		
THYRO1000375	3.2	7.03	4.79	7.38	6.09	9.77		

THYRO1000381	0.92	2.88	2.19	3.87	3.11	2.74		
THYRO1000387	0.98	6.66	3.22	2.53	3.56	2.51		
THYRO1000394	1.31	9.88	4.59	4.29	5.19	2.61		
THYRO1000395	0.8	10.44	2.26	1.97	2.07	2.02		
THYRO1000400	0.57	8.1	2.82	2.35	2.96	2.52		
THYRO1000401	0.86	1.94	2.5	1.87	1.16	1.57		
THYRO1000407	1.97	2.3	1.36	1.37	1.58	0.55		
THYRO1000420	1.8	2.67	4.46	3.52	3.53	3.39		
THYRO1000438	1.78	4.37	3.26	2.94	3.33	3.15		
THYRO1000452	2.62	7.99	6.45	3.71	5.75	4.38		
THYRO1000455	0.32	6.67	2.31	0.25	0.97	0.87		
THYRO1000471	0.99	8.03	2.05	1.11	2.08	1.02		
THYRO1000481	1.33	6.23	4.68	3.79	3.45	4.55		
THYRO1000484	1.2	1.42	2.41	2.35	3	2.21		
THYRO1000488	1.18	2.64	2.44	1.49	2.02	1.7		
THYRO1000501	1.12	4.01	2.78	3	1.92	1.82		
THYRO1000502	0.34	3.7	1.69	1.79	1.44	1.2		
THYRO1000505	0.13	4.64	1.19	1.14	1.02	0.6		
THYRO1000535	11.1	20.54	39.24	54.13	69.59	62.96	*	+
THYRO1000556	1.89	6.36	4.13	3.77	5.17	3.69		
THYRO1000558	0.25	2.82	1.12	1.16	0.81	0.61		
THYRO1000569	2.88	4.12	6.05	5.78	4.46	4.88		
THYRO1000570	2.31	3.28	8.46	8.53	6.04	3.49		
THYRO1000572	0.43	2.04	1.11	0.17	0.97	-0.42		
THYRO1000573	0.69	4.02	1.73	2.02	2.2	1.78		
THYRO1000577	1.06	5	1.34	0.96	1.22	0.71		
THYRO1000580	0.79	3.72	3.01	2.82	2.2	1.79		
THYRO1000584	2.18	6.88	8.8	7.57	6.61	7.58		
THYRO1000585	4.83	9.37	9.83	5.76	6.27	9.52		

THYRO1000596	0.22	0.93	1.19	0.44	1.36	0.21
THYRO1000602	2.08	2.95	4.01	4.05	4.65	4.97
THYRO1000605	0.37	3.01	0.98	2.13	2.14	1.56
THYRO1000615	1.02	3.62	1.24	1.55	1.36	1.29
THYRO1000625	0.71	5.48	2.28	2.46	2.9	1.78
THYRO1000636	3.67	5.65	6.9	6.53	7.84	6.67
THYRO1000637	0.91	3.96	1.71	1.18	2.03	1.54
THYRO1000641	0.38	4.19	2.49	1.36	1.67	1.64
THYRO1000657	2.99	3.69	5.42	7.67	12.28	3.86
THYRO1000658	2.68	3.62	5.39	5.4	5.55	6.09
THYRO1000662	1.1	3.19	2.09	2.42	2.69	1.66
THYRO1000666	0.57	3.19	2.28	1.63	1.48	1.43
THYRO1000676	1.37	4.53	2.01	1.75	1.83	1.56
THYRO1000678	0.52	5.86	0.99	1.29	1.4	0.53
THYRO1000684	0.95	4.98	2.94	1.92	2.65	1.47
THYRO1000694	2.08	6.64	4.65	2.8	2.48	3.59
THYRO1000699	2.98	2.14	5.55	4.86	7.08	7.12
THYRO1000712	1.88	4.25	5.9	6.25	6.75	7.78
THYRO1000715	5.74	5.67	27.37	21.74	28.63	16.99
THYRO1000716	0.92	3.26	3.2	1.88	1.78	1.35
THYRO1000717	1.58	5	4.36	2.98	4.63	1.91
THYRO1000723	0.6	4.54	1.6	0.55	1.06	0.85
THYRO1000734	-0.01	4.81	1.89	1.49	1.73	1.07
THYRO1000748	0.98	5.51	5.23	2.35	3.85	3.18
THYRO1000755	1.74	3.26	4.32	4.33	3.47	4.38
THYRO1000756	2.79	4.24	3.24	3.46	4.2	3.41
THYRO1000776	0.48	2.17	3.02	3.36	3.99	3.34
THYRO1000777	1.81	3.39	4.54	4.99	2.05	2.37
THYRO1000779	1.45	3.55	0.88	0.18	1.01	-0.26

THYRO1000782	3.92	10.13	12.52	10.76	15.05	14.05		
THYRO1000783	0.12	5.51	1.2	1.11	1.41	0.92		
THYRO1000786	6.65	9.54	19.71	15.74	7.92	13.7		
THYRO1000787	0.23	1.88	1.67	1.31	1.54	0.78		
THYRO1000792	1.51	3.13	2.29	3.09	3.13	2.11		
THYRO1000793	0.11	3.13	0.84	1.51	1.86	1.16		
THYRO1000795	1.23	6.03	3.54	2.76	3.1	3.05		
THYRO1000796	0.6	7.73	2.44	2.26	2.95	1.66		
THYRO1000798	1.89	5.82	2.51	2.59	3.57	3.53		
THYRO1000800	9.26	17.2	24.74	17.74	20.68	21.06		
THYRO1000805	0.49	3.04	1.08	0.72	2.66	1.38		
THYRO1000815	2.54	3.49	9.48	7.61	5.47	7.87		
THYRO1000829	5.55	7.83	10.57	3.78	8.32	10.01		
THYRO1000835	0.96	3.2	1.93	1.07	2.36	1.8		
THYRO1000843	1.09	11.48	3.56	3.69	4.41	3.62		
THYRO1000846	0.76	5.71	1.32	2.67	1.62	1.26		
THYRO1000852	1.59	6.02	5.63	2.8	4.7	3.32		
THYRO1000855	3.14	5.02	6.63	9.03	15.1	10.07	*	+
THYRO1000865	1.86	4.3	11.97	10.01	11.47	8.95		
THYRO1000866	7.47	6.29	12.66	4.49	7.87	6.01		
THYRO1000881	5.62	7.3	10.93	15.65	26.64	29.58	*	+
THYRO1000894	0.33	3.95	1.36	1.75	1.48	1		
THYRO1000895	0.58	4.43	1.42	1.62	1.46	0.82		
THYRO1000916	1.22	5.49	3.43	2.43	3.13	2.29		
THYRO1000917	16.19	25.26	34.11	30.37	37.42	35.89		
THYRO1000926	0.78	3.13	1.27	1.76	1.57	0.82		
THYRO1000934	0.08	3.1	1.34	0.43	1.38	1.46		
THYRO1000951	0.52	2.46	1.26	2.33	2.11	1.9		
THYRO1000952	2.25	3.81	6.01	2.38	2.53	2.24		

THYRO1000956	0.06	2.55	1.81	1.16	1.5	0.87
THYRO1000960	0.5	6.72	2.89	1.85	2.79	1.48
THYRO1000961	1.67	7.77	3.56	4.73	5.26	4.64
THYRO1000964	0.42	11.59	0.76	1	1.27	1.06
THYRO1000971	1.82	9.9	3.56	3.29	3.33	2.19
THYRO1000974	2.87	8.83	7.53	9.87	11.79	8.71
THYRO1000975	1.5	2.19	3.8	4.02	3.68	3.68
THYRO1000983	6.42	8.31	11.63	12.67	8.49	7.12
THYRO1000984	2.4	2.83	3.03	3.29	2.98	3.26
THYRO1000988	1.36	4.14	3.23	3.48	3.68	2.67
THYRO1000991	1.22	4.71	2.05	1.76	2.22	3.2
THYRO1000999	0.87	9.64	3.26	1.96	3.14	2.26
THYRO1001003	2.97	8.43	4.42	3.1	4.52	3.56
THYRO1001015	0.6	6.29	2.04	2.22	1.79	1.66
THYRO1001016	1.73	2.26	3.34	2.06	1.85	1.24
THYRO1001022	0.9	1.86	0.86	1.68	1.25	1.41
THYRO1001031	4.65	3.97	4.55	5.03	7.03	6.16
THYRO1001033	1.18	3.34	2.46	2.86	3.45	2.02
THYRO1001062	1.21	5.4	4.14	2.9	4.31	2.62
THYRO1001063	0.5	8.74	2.38	2.37	2.09	2.84
THYRO1001071	0.12	7.45	0.88	1.33	0.68	0.76
THYRO1001080	2.56	6.75	5.11	4.96	4.31	4.78
THYRO1001093	0.77	1.63	3.24	5.11	1.74	1.5
THYRO1001100	0.52	1.89	2.05	1.89	1.21	0.78
THYRO1001102	2.61	3.6	5.7	4.4	4.95	6.93
THYRO1001104	3.67	6.54	6.55	8.77	8.01	11.18
THYRO1001109	1.81	6.02	2.68	3.06	2.58	1.99
THYRO1001113	11.41	17.42	32	21.81	26.65	18.72
THYRO1001120	1.65	6.22	5.27	4.78	5.8	3.72

THYRO1001121	1.57	4.28	4.19	3.92	2.72	3		
THYRO1001128	1.64	2.77	5.86	3.52	3.19	5.09		
THYRO1001133	1.14	3.02	7.23	6.54	4.54	4.12		
THYRO1001134	2.97	4.78	1.63	3.14	2.83	1.38		
THYRO1001142	0.3	2.69	0.63	1.3	1.71	0.22		
THYRO1001173	8.37	12.87	7.72	11.14	9.92	10.62		
THYRO1001175	3.26	6.63	5.51	3.46	4.62	3.52		
THYRO1001177	1.36	5.85	5.93	4.66	7.27	7.97		
THYRO1001189	2.74	6.93	11.42	7.84	7.27	9.94		
THYRO1001194	1.05	2.62	4.96	4.89	4.57	2.31		
THYRO1001204	2.17	3.58	4.27	4.03	4.74	4		
THYRO1001205	5.76	10.65	20.23	18.54	19.57	20.9		
THYRO1001213	1.21	4.69	4.44	3.12	3.21	2.33		
THYRO1001224	3.59	8.25	6.37	9.92	12.69	10.55	*	+
THYRO1001237	2.82	6.25	4.99	3.61	4.53	4.46		
THYRO1001242	9.74	11.65	19.04	20.02	19.98	20.46		
THYRO1001258	2.08	5.45	3.58	3.33	2.05	2.66		
THYRO1001262	0.86	2.64	3.38	2.36	3.61	2.69		
THYRO1001266	0.15	2.39	1.02	0.97	1.64	0.66		
THYRO1001271	1.85	4.12	4.12	2.46	2.77	2.97		
THYRO1001287	7.3	8.3	39.26	30.14	43.68	26.2		
THYRO1001290	0.38	3.25	1.14	1.15	1.35	0.36		
THYRO1001291	0.96	7.17	4.38	4.31	4.97	3.5		
THYRO1001297	3.05	8.04	6.14	6.85	7.47	9.18		
THYRO1001302	1.72	5.59	5.17	3.8	3.71	3.5		
THYRO1001313	1.61	2.33	2.91	2.91	2.62	1.48		
THYRO1001320	1.76	2.52	5.31	5.07	5.74	4.83		
THYRO1001321	2.25	2.65	4.3	2.48	4.23	4.23		
THYRO1001322	1.34	3.93	3.34	1.75	2.67	2.01		

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THYRO1001327	1.29	6.01	4.18	1.4	3.89	2.49
THYRO1001336	1.89	6.84	6.72	4.62	4.43	4.18
THYRO1001347	0.43	4.12	3.35	1.85	2.81	0.65
THYRO1001358	2.57	5.74	4.52	4.3	5.75	5.1
THYRO1001363	0.8	2.15	1.52	2.09	2.24	2.28
THYRO1001365	0.86	3	1.6	2.19	2.6	1.96
THYRO1001374	1.85	4.45	12.86	9.4	13.01	6.21
THYRO1001401	1.76	5.33	4.89	5.39	7.86	6.29
THYRO1001403	1.26	5.15	3.22	3.22	4.42	3.94
THYRO1001405	6.99	12.5	10.86	6.69	8.56	10.63
THYRO1001406	15.73	14.87	27.69	21.36	22.77	21.36
THYRO1001411	4.49	5.46	10.08	8.93	12.44	8.12
THYRO1001420	11.55	15.25	47.52	42.01	44.49	49.87
THYRO1001426	3.42	5.56	8.83	9.32	12.77	11.18
THYRO1001430	6.97	6.54	10.84	11.13	11.7	13.81
THYRO1001434	0.68	5.19	2.11	2.08	4.23	1.73
THYRO1001456	1.74	6.05	2.63	2.89	2.66	2.4
THYRO1001457	1.71	4.72	2.04	2.95	4.7	2.67
THYRO1001458	0.95	5.44	6.11	6.13	9.17	7.23
THYRO1001459	4.54	5.07	9.42	7.18	9.87	14.21
THYRO1001471	0.91	2.07	1.93	2.36	2.91	1.64
THYRO1001478	0.58	3.09	1.34	0.95	2.61	2.75
THYRO1001480	5.4	10.53	13.62	14.79	15.94	15.57
THYRO1001481	2.95	8.64	7.24	4.91	7.76	7.13
THYRO1001487	1.36	5.51	3.52	4.1	2.67	3.48
THYRO1001495	2.06	5.57	5.43	5.06	9.4	7.55
THYRO1001498	5.39	8.08	13.42	11.59	16.38	19.6
THYRO1001510	1.67	2.88	1.59	1.65	2.57	3.35
THYRO1001512	26.7	26.97	110.28	56.03	90.95	68.54

THYR01001519	5.92	7.77	11.05	8.91	5.75	10.38		
THYR01001522	2.02	4.7	5.79	4.15	4.69	5.51		
THYR01001523	1.83	4.92	3.73	4.38	4.07	4.26		
THYR01001526	26.21	28.22	44.73	34.28	47.64	46.52		
THYR01001529	1.64	5.27	2.8	2.32	2.42	2.98		
THYR01001534	1.41	4.01	4.96	5.1	5.9	4.54		
THYR01001537	7.4	5.17	12.33	5.97	7.42	7.23		
THYR01001541	2.14	3.88	8.27	7.76	8.7	6.73		
THYR01001545	1.26	3.84	2.9	4.95	3.57	3.16		
THYR01001559	4.52	6.34	8.04	9.06	10.5	10.54	*	+
THYR01001563	9.49	14.06	15.89	10	15.49	22.09		
THYR01001570	2.01	8.2	3.85	4.25	5.17	3.41		
THYR01001573	1.15	5.77	2.22	1.47	2.87	2.67		
THYR01001584	2.47	8.54	8.38	5.14	7.81	7.29		
THYR01001593	4.27	5.67	11.17	9.5	10.93	9.52		
THYR01001595	3.14	4.53	7.06	5.97	6.35	7.29		
THYR01001596	4.71	5.48	7.44	6.45	5.86	2.51		
THYR01001602	1.49	3.26	3.52	4.95	5.22	3.41		
THYR01001605	1.58	4.48	3.22	3.2	3.43	2.42		
THYR01001608	1.87	9.45	5.1	5.04	8.23	4.7		
THYR01001617	6.06	13.68	11.47	9.75	10.87	9.61		
THYR01001634	1.87	9.08	3.46	2.93	5.59	2.05		
THYR01001637	3.51	3.13	9.65	8.72	7.94	9.07		
THYR01001641	2.57	3.73	5.09	4.03	3.08	2.94		
THYR01001656	1.59	2.94	4.16	2.82	5.36	2.33		
THYR01001658	22.34	29.19	40.11	34.98	33.16	42.01		
THYR01001661	1.4	5.83	2.31	2.93	3.31	2.05		
THYR01001671	0.67	7.36	2.68	1.89	1.34	1.8		
THYR01001672	1.1	9.24	2.1	1.14	1.52	1.66		

THYRO1001673	1.59	7.6	3.49	2.86	4.74	2.16		
THYRO1001677	1.6	2.27	3.87	3.03	3.54	3.36		
THYRO1001683	12.71	17.66	29.06	24.4	15.4	16.72		
THYRO1001700	1.39	2.52	2.67	2.09	1.58	1.37		
THYRO1001702	11.83	15.98	16.19	15.63	14.35	14.29		
THYRO1001703	1.63	6.74	4.25	4.72	3.27	4.21		
THYRO1001706	1.7	6.47	3.01	2.96	5.6	3.53		
THYRO1001721	1.84	5.66	3.2	2.73	6.37	2.77		
THYRO1001725	5.3	6.55	9.69	8.97	8.65	8.29		
THYRO1001730	17.72	20.4	40.1	30.61	26.56	34.8		
THYRO1001738	1.35	3.18	4.65	3.52	2.82	1.78		
THYRO1001743	0.19	2.13	1.85	1.8	1.64	1.06		
THYRO1001745	0.47	2.88	1.55	1.05	1.2	1.27		
THYRO1001746	1.9	6.25	4.04	6.12	4.01	3.88		
THYRO1001770	15.49	20.38	35.39	41.65	44.42	40.17	*	+
THYRO1001772	1.12	4.88	3.64	4.78	4.24	3.06		
THYRO1001778	3.89	6.68	9.89	14.67	13.47	14.25	*	+
THYRO1001793	3.85	3.77	9.43	10.3	10.42	4.92		
THYRO1001796	1.35	2.28	2.28	3.45	4.22	3.24	*	+
THYRO1001800	1.82	2.99	2.75	4.17	5.12	2.09		
THYRO1001803	3.42	6.03	5.21	4.31	4.14	3.42		
THYRO1001809	1.6	4.26	3.4	5.9	4.23	3.39		
THYRO1001817	8.69	18.33	24.88	22.11	22.77	25.27		
THYRO1001819	4.68	8.46	9.01	7.84	10.46	6.77		
THYRO1001828	21.89	24.53	104.32	106.68	121.95	68.55		
THYRO1001854	6.67	6.12	12.45	13.43	15.86	13.31		
THYRO1001895	0.85	1.31	2.52	3.54	4.31	1.28		
THYRO1001907	2.16	3.08	3.37	3.9	4.53	2.74		
TRACH1000006	2.51	5.87	6.63	4.34	3.46	3.22		

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TRACH1000013	1.53	4.65	3.68	2.55	3.33	2.65		
TRACH1000074	2.65	6.75	6.09	7.5	7.26	4.77		
TRACH1000095	0.28	5.66	2.23	2.46	1.48	1.11		
TRACH1000102	2.42	6.66	4.09	5.79	5.04	3.65		
TRACH1000108	1.1	1.01	2.05	1.75	2.49	1.09		
TRACH1000126	0.96	1.75	2.71	1.82	3.79	2.54		
TRACH1000146	1.3	2.67	2.31	3.02	5.18	3.75		
TRACH1000160	0.61	4.06	1.5	1.47	1.76	0.72		
TRACH1000184	4.45	7.16	10.16	7.47	8.73	5.69		
VESEN1000004	0.69	5.55	3.19	2.56	2.95	2.02		
VESEN1000007	0.93	5.32	2.94	2.38	3.45	2.94		
VESEN1000013	5.96	10.11	16.78	10.76	11.25	13.88		
VESEN1000028	5.2	7.5	9.88	13.18	11.71	14.08	*	+
VESEN1000059	1.55	2.88	2.1	3.38	2.82	2.27		
VESEN1000100	1.96	3.22	3.35	3.49	4.58	3.59		
VESEN1000107	0.88	4.84	2.88	3.12	2.9	2.48		
VESEN1000117	1.63	6.43	2.46	2.16	2.7	1.79		
VESEN1000122	1.52	5.34	1.24	4.79	4.51	4.5		
VESEN1000137	0.76	5.47	1.92	1.75	3.33	1.65		
VESEN1000195	7.79	7.93	11.67	8.42	7.51	10.27		
VESEN1000215	1.48	3.03	2.06	2.67	3.84	1.87		
VESEN1000279	8.71	11.32	18.49	22.93	23.38	34.68	*	+
VESEN1000363	3.52	6.07	9.99	7.2	9.06	4.59		
VESEN1000388	2.55	6.48	3.31	4.17	3.75	6.7		
VESEN1000394	0.44	7.11	2.33	2.37	2.55	2.36		
VESEN1000410	1.11	5	1.78	2.36	2.71	3.69		
VESEN1000411	2.37	4.95	5.08	6.76	7.55	9	*	+
VESEN1000415	1.54	2.64	4.03	5.57	3.92	5.29		
VESEN1000440	7	5.53	7.81	3.79	9.4	12.22		

VESEN1000452	1.22	3.65	2.33	2.91	3.97	4.11		
VESEN1000539	191.54	185.28	334.6	389.84	403.89	547.31	*	+
VESEN1000554	0.67	6.47	1.43	1.47	2.55	1.58		
VESEN1000557	4.22	7.94	7.73	6.55	9.07	10		
VESEN1000575	7.49	9.75	16.33	11.95	11.73	14.8		
VESEN1000585	1.69	4.49	3.37	2.53	2.93	3.08		
VESEN1000592	1.58	2.31	1.58	2.02	1.83	1.46		
VESEN1000658	1.96	3.56	4.45	5.86	3.91	4.91		
VESEN1000669	8.43	10.02	16.35	15.06	14.17	15.51		
VESEN1000743	0.97	3.3	2.52	1.99	3.37	3.21		
VESEN1000752	37.43	51.51	72.35	49.32	57.03	57.96		
VESEN1000761	13.48	18.17	19.37	24.6	33.21	31.28	*	+
VESEN2000039	10.45	15.98	15.56	13.56	18.3	20.1		
VESEN2000102	0.4	3.99	1.6	1.21	1.51	1.61		
VESEN2000164	2.45	3.52	4.8	5.55	4.36	3.66		
VESEN2000175	0.57	2.64	1.94	3.03	2.05	2.59		
VESEN2000186	3.77	5.53	6.53	6.68	3.87	2.47		
VESEN2000199	8.94	13.26	21.75	19.58	24.45	24.12		
VESEN2000200	0.5	4.97	2.78	3.03	3.1	1.6		
VESEN2000204	0.48	12.7	1.02	0.98	1.2	0.33		
VESEN2000218	6.66	20.26	19.48	21.37	20.75	18.86		
VESEN2000230	0.84	7.4	1.45	2.74	1.7	2.41		
VESEN2000272	2.29	4	8.92	7	8.31	5.88		
VESEN2000299	1.99	2.97	3.2	3.3	3.77	3.31		
VESEN2000323	4.51	8.12	8.37	8.91	9.5	9.36		
VESEN2000327	3.16	5.8	4.42	3.62	7.66	5.07		
VESEN2000328	5.44	8.02	11.88	8.73	15.35	14.36		
VESEN2000330	6.39	15.42	14.7	14.59	27.73	18.86		
VESEN2000336	0.82	8.97	2.54	3.46	3.83	2.88		

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VESEN2000354	1.56	8.24	2.48	1.53	2.71	2.1		
VESEN2000378	7.17	8.87	14.57	13.23	11.14	10.3		
VESEN2000379	19.87	23.02	44.55	49.13	42.81	32.61		
VESEN2000397	0.72	2.38	1.24	1.36	2.06	1.54		
VESEN2000416	2.83	3.88	4.41	5.74	5.31	5.71	*	+
VESEN2000420	1.08	3.58	1.94	0.95	1.21	1.13		
VESEN2000430	0.51	6.68	1.53	2.06	1.79	1.8		
VESEN2000448	0.51	6.87	1.73	2.12	2.69	1.5		
VESEN2000449	2.43	8.07	6.59	8.3	11.31	8.21		
VESEN2000456	0.74	0.87	2.11	1.54	1.22	0.87		
VESEN2000562	4.07	3.42	17.42	13.67	22.82	14.47		
VESEN2000573	0.18	1.75	1.75	1.04	1.21	1.13		
VESEN2000604	1.73	3.44	2.24	2.04	1.67	2.15		
VESEN2000614	4.16	9.02	14.64	13.54	16.27	12.27		
VESEN2000638	0.48	5.92	1.98	1.33	1.91	1.68		
VESEN2000641	0.83	3.69	1.34	1.95	2.21	1.43		
VESEN2000645	2.18	5.29	5.38	5.91	5.73	5.5		
Y79AA1000013	2.57	2.7	4.33	3.45	3.8	3.94		
Y79AA1000030	1.79	4.06	4.52	3.24	3.85	2.47		
Y79AA1000033	2.87	6	8.4	8.37	10.17	5.83		
Y79AA1000037	1.38	3.36	5.71	4.84	6.82	4.49		
Y79AA1000041	1.05	5.16	3.79	4.73	3.65	2.06		
Y79AA1000059	1.69	5	4.09	3.88	4.51	2.82		
Y79AA1000065	24.06	28.99	52.25	82.48	101.48	98.73	**	+
Y79AA1000081	39.47	49.78	73.62	113.19	114.49	98.22	**	+
Y79AA1000127	4.08	4.21	5.8	8.42	10.03	7.39	*	+
Y79AA1000130	2.24	2.48	5.76	6.61	8.1	8.03	*	+
Y79AA1000131	507.64	569.21	946.04	769.75	725.35	342.07		
Y79AA1000134	1.99	4.93	4.21	5.63	4.75	5.38		

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Y79AA1000143	3.58	8.79	4.83	9.98	10.98	11.04	*	+
Y79AA1000144	4.63	10.79	10.59	11.02	11.62	11		
Y79AA1000150	18.39	22.18	84.69	93.5	117.62	78.89		
Y79AA1000153	183.67	191.4	436.64	423.46	442.52	386.45		
Y79AA1000166	2.13	2.25	4.15	3.52	4.97	3.6		
Y79AA1000179	2.58	3.76	4.2	6.85	7.58	3.89		
Y79AA1000181	1.96	3.92	4.2	4.82	5.66	3.79		
Y79AA1000202	22.93	24.47	55.57	91.68	86.86	83.22	**	+
Y79AA1000207	5.22	7.51	9.82	14.95	16.24	12.62	*	+
Y79AA1000214	14.94	22.18	33.76	50.43	60.78	41.96	*	+
Y79AA1000222	11.8	14.89	21.69	49.21	58.01	68.86	**	+
Y79AA1000226	11.04	14.94	34.41	22.86	33.54	30.03		
Y79AA1000227	5.95	4.52	7.25	8.98	9.51	9.62	*	+
Y79AA1000230	1.09	1.49	2.02	2.07	2.88	2.59		
Y79AA1000231	5.99	9.04	15.81	14.63	23.77	17.1		
Y79AA1000239	15.47	20.55	25.65	18.95	24.01	22.11		
Y79AA1000258	2.64	5.17	6.72	5.87	4.95	5.84		
Y79AA1000268	2.65	5.48	5.09	4.33	5.76	4.01		
Y79AA1000269	4.32	7.88	7.86	8	6.86	8.24		
Y79AA1000270	5.28	8.35	11.58	13.17	17.58	16.23	*	+
Y79AA1000280	1.74	4.17	4.9	5.29	3.1	5.27		
Y79AA1000285	3.44	4.21	5.91	4.01	6.86	5.22		
Y79AA1000295	0.75	3.06	4.85	4.32	4.23	4.45		
Y79AA1000307	2.88	3.91	5.06	9.35	7.58	11.25	*	+
Y79AA1000313	3.11	9.02	9.85	10.61	12.84	13.36		
Y79AA1000314	4.23	10.74	9.19	6.93	6.53	7.51		
Y79AA1000328	4.65	10.05	2.64	7.73	9.28	8.68		
Y79AA1000334	1.43	4.22	3.55	2.68	2.81	3.46		
Y79AA1000342	10.65	10.05	26.47	23.7	19.13	28.35		

Y79AA1000346	7.61	8.17	7.9	20.1	22.06	20.18	**	+
Y79AA1000347	6.94	7.96	12.42	18.78	16.47	18.48	**	+
Y79AA1000349	6.93	9.63	12.67	12.31	11.96	14.75		
Y79AA1000355	3.17	8.28	8.94	8.84	13.55	8.77		
Y79AA1000368	5.24	8.39	24.43	22.48	35.67	22.55		
Y79AA1000388	22.9	32.66	62.37	94.17	128.35	109.08	**	+
Y79AA1000392	3.02	6.81	3.76	3.42	2.73	3.78		
Y79AA1000405	3.98	5.97	8.25	7.14	8.17	9.32		
Y79AA1000410	6.01	7.87	15.72	13.79	17.05	14.95		
Y79AA1000420	1.54	4.78	3.13	3.32	3.95	5.1		
Y79AA1000423	1.38	7.08	5.59	5.22	6.04	10.27		
Y79AA1000426	3.61	9.44	8.66	4.24	4.43	5.22		
Y79AA1000432	0.8	4.79	2.16	1.91	2.01	2.34		
Y79AA1000453	23.94	30.67	47.79	39.74	50.65	58.24		
Y79AA1000465	4.12	6.02	6.65	4.77	4.14	7.69		
Y79AA1000469	11.59	9.61	18.04	13.82	16.21	17.18		
Y79AA1000480	1.24	4.37	2.78	3.33	3.57	2.79		
Y79AA1000502	5.31	7.97	12.58	10.49	11.35	15.26		
Y79AA1000521	1.24	4.4	4.13	2.51	3.61	2.7		
Y79AA1000534	3.22	8.13	8.92	11.97	14.41	13.46	*	+
Y79AA1000538	3.58	6.95	8.79	9.52	12.12	8.41		
Y79AA1000539	12.76	14.96	53.11	42.61	68.56	50.97		
Y79AA1000540	1.32	3.59	1.61	2.54	2.97	3.21		
Y79AA1000560	160.46	140.99	339.33	380.8	313.21	220.43		
Y79AA1000574	1	2.92	1.65	1.98	2.04	1.59		
Y79AA1000584	2.07	4.55	4.97	4.62	5.39	4.04		
Y79AA1000589	10.74	13.67	81.43	59.09	95.35	68.5		
Y79AA1000598	1.43	7.64	2.17	1.85	3.88	3.18		
Y79AA1000600	2.7	10.02	7.93	13.64	15.64	12.84	*	+

Y79AA1000609	1.18	5.16	1.44	2.28	2.77	1.55		
Y79AA1000618	1.85	10.59	5.76	7.4	9.5	9.37		
Y79AA1000627	1.91	3.93	4.57	3.27	3.02	2.43		
Y79AA1000636	5.16	5.7	9.9	15.57	11.52	5.38		
Y79AA1000649	9.45	10.97	12.73	18.7	11.56	20.54		
Y79AA1000656	15.32	20.21	96.75	80.17	115.97	82.61		
Y79AA1000673	1.02	5.86	2.14	1.39	3.13	2.4		
Y79AA1000674	11.88	21.96	78.28	59.4	98.22	62.67		
Y79AA1000678	2.48	8.91	3.88	3.01	4.15	2.45		
Y79AA1000682	17.99	53.99	93.7	102.53	110.87	118.22		
Y79AA1000683	1.87	2.66	3.21	4.27	2.59	2.17		
Y79AA1000697	21.76	27.52	43.01	21.93	24.76	27.31		
Y79AA1000700	5.07	7.1	7.08	7.51	6.93	9.97		
Y79AA1000702	5.13	14.57	13.31	41.48	56.57	63.15	**	+
Y79AA1000704	1.34	5.24	1.14	1.5	2.1	1.18		
Y79AA1000705	1.86	9.7	6.24	6.06	7.98	6.45		
Y79AA1000717	6.18	12.39	9.42	9.73	11.1	8.7		
Y79AA1000722	5.61	8.6	8.65	26.26	34.81	34.31	**	+
Y79AA1000724	6.42	9.77	18.55	26.57	21.7	11.95		
Y79AA1000726	0.77	1.24	0.83	1.46	2.01	0.71		
Y79AA1000734	2.05	4.46	4.92	3.57	3.3	2.94		
Y79AA1000748	0.88	4.38	1.77	2.14	2.99	1.56		
Y79AA1000750	4.17	8.47	20.58	18.11	20.02	18.62		
Y79AA1000752	1.25	5.13	2.33	2.23	3.38	3.38		
Y79AA1000774	2.11	6.23	4.24	4.28	5.79	4.21		
Y79AA1000776	1.2	4.37	1.9	2.13	1.83	2.11		
Y79AA1000777	4.36	5.84	9.63	10.05	6.99	6.01		
Y79AA1000778	1.72	3.77	3.79	3.87	4.19	1.44		
Y79AA1000782	2.08	4.18	3.72	3.53	2.89	2.96		

Y79AA1000784	7.04	10.01	7.78	13.87	15.58	14.26	**	+
Y79AA1000794	0.61	5.21	1.88	2.92	1.69	1.23		
Y79AA1000800	1.59	5.44	3.82	3.38	2.97	3.39		
Y79AA1000802	0.64	4.18	1.15	2.52	1.77	2.1		
Y79AA1000805	2.29	4.03	2.63	2.43	2.11	2.6		
Y79AA1000814	2.73	3.9	4.14	4.98	7.09	6.76	*	+
Y79AA1000823	7.91	9.99	12.07	12.02	12.42	6.56		
Y79AA1000824	0.98	2.47	1.84	2.75	2.26	0.79		
Y79AA1000827	1.6	4.02	7.27	6.71	8.91	6.14		
Y79AA1000831	7.04	10.49	17.32	26.61	30.43	27.82	**	+
Y79AA1000833	62.14	67.46	191.76	270.42	308.16	248.21	*	+
Y79AA1000850	1.69	5.68	2.72	4.92	4.59	4.21		
Y79AA1000856	3.49	6.78	6.31	9.28	6.01	8.51		
Y79AA1000862	2.22	2.76	2.44	3.08	2.87	2.59		
Y79AA1000876	7.46	10.04	17.91	27.36	27.61	25.46	**	+
Y79AA1000888	4.59	5.07	28.1	24.51	38.78	22.48		
Y79AA1000902	4.65	5.74	8.44	12.18	12.32	7.68		
Y79AA1000935	3.53	5.99	6.69	8.28	10.07	9.18	*	+
Y79AA1000959	0.74	6.29	4.35	6.71	5.77	6.07		
Y79AA1000962	1.22	4.45	3.18	2.9	2.41	1.79		
Y79AA1000963	18.6	26.86	35.93	31.61	42.17	49.13		
Y79AA1000966	18.52	19.25	98.18	77.47	116.12	61.1		
Y79AA1000967	8.62	8.82	33.82	34.47	40.36	29.3		
Y79AA1000968	3.32	5.67	6.89	8.86	9.4	7.96	*	+
Y79AA1000969	0.91	3.18	3.04	2.66	2.91	1.41		
Y79AA1000976	1.43	4.72	3.02	2.55	3.51	1.43		
Y79AA1000978	1.99	5.6	7.26	6.9	10.54	5.56		
Y79AA1000985	9.39	12.84	40.49	38.26	44.3	27.89		
Y79AA1000989	21.59	22.49	46.19	51.84	58.65	55.19	*	+

Y79AA1000991	22.11	22.21	110.42	72.46	96.96	82.23		
Y79AA1001013	59.2	62.64	140.9	174.85	214.13	201.9	*	+
Y79AA1001014	2.27	4.16	4.1	4.8	5.2	6.55		
Y79AA1001019	3.37	5.89	7.74	9.24	9.02	9.43	*	+
Y79AA1001020	5.37	7.82	9.43	12.31	11.11	10.86	*	+
Y79AA1001023	0.83	6.11	2.29	1.22	1.95	1.54		
Y79AA1001030	4.23	8.79	10.87	11.14	10.72	12.43		
Y79AA1001035	0.19	2.88	0.03	14.44	8.19	17.16	*	+
Y79AA1001041	1.78	2.46	2.36	2.93	2.45	2.78		
Y79AA1001043	11.65	12.62	15.22	8.64	12.01	14.71		
Y79AA1001048	1.1	4.78	3.73	4.05	4.52	4.21		
Y79AA1001056	4.56	7.82	11.04	8.27	7.11	9.94		
Y79AA1001061	1.53	7.79	5.28	6.13	7.46	6.66		
Y79AA1001062	2.62	6.14	5.02	4.44	6.01	4.67		
Y79AA1001068	3.46	6.39	7.29	6.61	8.69	7.05		
Y79AA1001073	8.19	13.08	17.46	24.14	22.1	29.81	*	+
Y79AA1001077	7.1	7.08	17.15	14.69	14.74	17.08		
Y79AA1001078	3.11	8.34	11.07	5.01	12.15	12.92		
Y79AA1001081	3.59	5.61	4.94	9.62	9.98	10.5	**	+
Y79AA1001088	27.75	38.61	69.33	93.1	88.97	113.04	*	+
Y79AA1001089	4.64	7.8	11.92	22.67	22.6	27.73	**	+
Y79AA1001090	1.38	4.15	2.2	3.58	2.83	2.35		
Y79AA1001105	3.7	5.23	15.81	12.52	22.1	13.35		
Y79AA1001142	8.53	13.38	15.85	14.28	11.42	22.32		
Y79AA1001145	2.22	4.68	5.13	4.97	6.26	5.87		
Y79AA1001162	2.27	2.91	1.62	1.62	4.56	4		
Y79AA1001167	0.86	2.76	2.38	1.12	2.35	0.77		
Y79AA1001176	0.57	3.33	1.14	2.02	1.68	0.88		
Y79AA1001177	1.21	5.5	2.22	2.35	3.01	1.99		

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Y79AA1001179	6.81	8.66	16.73	22.82	22.64	20.07	*	+
Y79AA1001185	1.33	5.3	4.55	3.65	4.49	5.8		
Y79AA1001201	5.69	11.3	16.13	14.57	15.21	19.38		
Y79AA1001205	1.87	3.28	2.85	5.87	4.85	4.09	*	+
Y79AA1001211	1.64	4.75	6.93	4.83	4.36	4.15		
Y79AA1001212	3.55	6.93	15.91	13.74	15	11.65		
Y79AA1001216	52.59	51.46	93.73	76.52	97.53	109.55		
Y79AA1001228	6.1	11.21	9.34	8.99	12.19	10.24		
Y79AA1001233	0.68	11.46	2.39	0.92	1.66	1.09		
Y79AA1001236	4.46	12.86	9.25	11.4	10.66	13.08		
Y79AA1001239	4.62	13.93	9.94	11.53	12.15	12.94		
Y79AA1001240	8.74	8.6	13.75	9.13	6.68	3.01		
Y79AA1001255	10.37	12.22	22.61	12.47	7.51	6.57		
Y79AA1001264	3.63	5.15	4.49	7.73	8.59	8.75	**	+
Y79AA1001272	10.81	13.63	17.47	21.56	20.67	21.32	*	+
Y79AA1001281	0.45	4.95	1.89	1.42	1.81	0.95		
Y79AA1001299	2.49	11.34	9.06	9.9	9.26	9.81		
Y79AA1001312	2.49	10.36	5.17	2.15	4.77	4.14		
Y79AA1001319	3.34	11.88	5.27	7.23	6.05	7.15		
Y79AA1001323	1.22	1.16	2.09	1.11	1.55	0.89		
Y79AA1001328	2.04	3.18	3.62	4.66	4.48	4.05	*	+
Y79AA1001343	154.19	151.55	345.05	304.88	394.54	265.65		
Y79AA1001351	0.81	2.77	1.67	0.03	1.26	0.96		
Y79AA1001364	1.65	6.07	4.03	3.39	4.43	3.6		
Y79AA1001367	2.16	7.41	2.93	3.09	5.34	3.19		
Y79AA1001384	0.5	5.14	1.98	0.73	1.15	0.94		
Y79AA1001391	0.59	3.73	2.88	1.35	1.65	1.2		
Y79AA1001394	3.12	4.66	12.92	10.94	9.56	10.94		
Y79AA1001402	2.77	3.7	5.95	5.65	5.09	4.14		

Y79AA1001410	0.82	2.78	2.33	2.06	2.31	2.25		
Y79AA1001414	2.76	7.5	7.59	11.08	10.73	10.06	*	+
Y79AA1001426	0.61	4.36	2.61	1.5	1.43	1.82		
Y79AA1001427	14.22	13.44	86.36	59.92	88.36	63.53		
Y79AA1001430	11.28	16.98	20.98	29.04	34.03	34.38	**	+
Y79AA1001439	16.22	21.53	33.42	45.02	43.74	43.1	*	+
Y79AA1001485	1.65	2.51	4.38	4.85	3.88	3.57		
Y79AA1001493	1.29	2.3	3.43	2.43	2.35	2.46		
Y79AA1001511	4.79	8.57	11.05	9.39	9.11	6.47		
Y79AA1001523	2.64	6.57	5.08	8.74	7.37	6.1		
Y79AA1001530	7.46	11.69	22	41.43	36.37	36.07	**	+
Y79AA1001532	5.12	7.35	6.69	10.49	14.82	12.9	*	+
Y79AA1001533	1.84	4.89	2.53	4.15	4	4.19		
Y79AA1001541	2.82	5.89	7.54	7.23	5.08	7.34		
Y79AA1001548	4.25	4.84	9.82	10.46	7.37	7.1		
Y79AA1001555	2	2.55	3.65	4.7	5.28	4.25	*	+
Y79AA1001562	7.76	10.11	17.15	14.07	16.16	10.83		
Y79AA1001581	2	5.05	4.47	5.1	7.01	3.54		
Y79AA1001585	3.18	7.38	10.96	9.72	10.93	8.05		
Y79AA1001592	2.61	7.38	5.97	8.15	8	7.02		
Y79AA1001594	0.76	4.73	3.85	1.96	3.24	1.73		
Y79AA1001603	56.74	70.81	153.14	131.56	112.16	107.66		
Y79AA1001613	3.74	3.52	14.81	13.12	15.36	10.66		
Y79AA1001630	0.71	2.36	1.73	1.14	2.64	0.67		
Y79AA1001647	1.96	3.57	2.47	4.14	4.32	2.65		
Y79AA1001664	4.67	8.39	11.43	8.96	10.01	8.73		
Y79AA1001665	1.39	6.4	3.73	4.67	4.71	3.75		
Y79AA1001679	8.92	15.94	20.71	20.53	26.67	25.35		
Y79AA1001692	1.87	5.55	3.95	3.99	3.95	3.51		

Y79AA1001696	1.97	6.49	2.77	1.83	2.63	2.55		
Y79AA1001705	6.09	6.44	10.39	7.62	7.92	7.85		
Y79AA1001711	16.17	12.34	29.74	13.73	23.83	21		
Y79AA1001717	0.72	2.99	1.29	1.68	3.13	1.14		
Y79AA1001719	2.5	5.79	6.44	6.15	6.07	6.43		
Y79AA1001727	6.87	12.13	14.99	8.73	14.71	8.77		
Y79AA1001750	10.21	13.63	21.67	21.92	32.29	24.33		
Y79AA1001760	25.24	27.31	122.97	113.56	155.17	83.24		
Y79AA1001777	1.17	3.59	1.6	2.49	1.75	1.28		
Y79AA1001781	0.31	2.3	0.42	1.62	1.84	1.42		
Y79AA1001787	1	3.94	3.54	5.51	5.18	5.15		
Y79AA1001793	16.23	15.19	91.7	60.44	87.21	75.35		
Y79AA1001795	1.23	3.84	2.24	2.05	2.45	2.8		
Y79AA1001799	4.9	8.35	6.99	10.7	10.72	11.26	*	+
Y79AA1001800	2.25	8.3	10.1	8.49	10.51	9.9		
Y79AA1001801	1.77	6.44	4.87	7.67	5.91	7.33		
Y79AA1001803	0.74	2.15	1.72	1.85	1.68	1.17		
Y79AA1001805	6.05	6.88	12.15	10.21	8.32	11.15		
Y79AA1001807	3.37	6.33	12.56	11.76	17.8	16.79		
Y79AA1001827	1.7	4.41	3.12	3.43	3.6	2.52		
Y79AA1001846	1.82	6.52	5.51	6.52	5.09	5.07		
Y79AA1001848	0.86	5.57	2.75	5.98	4.78	5.14		
Y79AA1001853	1.38	6.16	2.76	3.24	4.56	3.63		
Y79AA1001863	0.86	5	2.53	2.93	3.83	3.85		
Y79AA1001866	2.29	3.2	5.81	3.53	3.98	3.46		
Y79AA1001874	0.12	2.18	-0.21	1.17	0.75	0.51		
Y79AA1001875	9.33	12.67	13.09	11.05	17.79	18.63		
Y79AA1001907	68.02	70.94	96.4	118.34	86.75	104.86		
Y79AA1001908	0.64	8.4	2.29	1.92	2.59	2.31		

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Y79AA1001923	1.61	6.64	3.03	3.86	3.76	3.35		
Y79AA1001927	19.1	22.05	36.94	42.46	45.29	48.81	*	+
Y79AA1001930	4.07	6.65	8.07	7.92	12.42	12.21		
Y79AA1001932	2.84	4.41	8.47	11.51	9.1	8.57		
Y79AA1001933	2.14	3.27	3.69	4.34	7.99	6.65	*	+
Y79AA1001942	1.58	3.45	2.69	2.94	2.13	2.41		
Y79AA1001963	9.6	9.37	46.06	38.48	49.64	47.27		
Y79AA1001968	18.61	27.73	37.44	42.93	44.16	55.23	*	+
Y79AA1001983	1.81	6.35	4.28	3.97	5.86	4.47		
Y79AA1002000	2.55	5.35	4.55	4.42	3.21	2.83		
Y79AA1002004	13.1	18.87	27.47	23.72	29.45	40.93		
Y79AA1002008	2.51	3.73	3.79	4.54	2.19	2.85		
Y79AA1002012	1.37	3.22	2.81	3.22	2.29	2.87		
Y79AA1002017	1.34	2.53	2.46	3.51	3.07	2.82		
Y79AA1002022	2.99	4.94	5.93	7.32	7.51	6.01		
Y79AA1002027	2.02	6.33	2.67	2.69	4.03	4.09		
Y79AA1002050	2.53	8.12	4.22	6.68	6.91	5.11		
Y79AA1002058	13.69	21.8	70.12	59.07	70.89	55.33		
Y79AA1002060	6.38	13.17	20.54	17.14	21.12	24.23		
Y79AA1002062	4.33	5.18	8.15	8.54	6.66	5.51		
Y79AA1002065	33.54	39.97	72.6	49.46	30.04	41.81		
Y79AA1002067	10.11	11.64	17.24	16.25	9.42	8.13		
Y79AA1002069	0.97	1.79	0.54	1.55	1.44	0.66		
Y79AA1002070	10.16	33.47	44.36	52.16	71.15	73.35	*	+
Y79AA1002074	38.55	74.38	179.6	165.55	282.48	224.96		
Y79AA1002076	0.48	9.71	2.89	2.86	3.34	1.91		
Y79AA1002083	1.2	7.48	2.03	2.73	1.75	2.06		
Y79AA1002084	1.79	2.59	4.54	3.73	3.73	2.98		
Y79AA1002086	0.96	1.78	1.71	2.77	1.88	1.43		

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Y79AA1002087	11.18	14.9	27.67	33.34	30.01	23.08		
Y79AA1002089	1.18	3.46	2.13	1.46	2.92	3.26		
Y79AA1002093	2.19	5.48	5.25	5.28	5.68	6.17		
Y79AA1002101	1.11	8.58	2.98	6.54	5.58	6.6		
Y79AA1002103	1.47	10.22	3.39	4.43	6.49	4.7		
Y79AA1002115	4.34	9.78	7.37	7.45	7.03	6.95		
Y79AA1002121	1.55	2.16	2.18	1.67	2.55	2.31		
Y79AA1002125	6.67	7.08	9.29	8.81	6.4	7.6		
Y79AA1002129	1.64	6.23	7.84	5.41	2.2	4.93		
Y79AA1002131	0.9	3.25	0.78	0.77	1.29	1.15		
Y79AA1002139	0.69	5.02	1.04	1.83	1.53	1.34		
Y79AA1002144	25.99	29.62	51.01	42.61	51.16	43.17		
Y79AA1002177	1.72	5.97	4.33	4.79	3.09	4.73		
Y79AA1002183	10.44	13.89	17.69	27.61	29.67	28.92	**	+
Y79AA1002202	3.97	7.15	8.34	18.27	10.12	17.85	*	+
Y79AA1002204	0.53	0.99	1.56	1.7	2.2	1.54		
Y79AA1002206	2.63	5.36	7.28	4.35	2.95	1.49		
Y79AA1002208	4.26	6.54	3.94	6.88	6.3	3.96		
Y79AA1002209	1.8	6.34	2.88	4.38	3.74	4.57		
Y79AA1002210	0.41	4.14	2.09	1.8	2.24	1.65		
Y79AA1002211	2.25	5.39	3.85	5.71	5.3	4.5		
Y79AA1002213	1.15	4.13	6.53	7.38	7.54	7.43		
Y79AA1002215	18.7	18.69	26.61	17.72	15.59	9.62		
Y79AA1002220	3.78	3.38	2.87	4.89	4.19	4.14	*	+
Y79AA1002226	8.54	8.9	9.75	13.06	14.2	4.41		
Y79AA1002229	1.35	3.88	3.38	2.95	2.79	2.67		
Y79AA1002234	3.24	6.82	3.94	4.29	7.74	6.88		
Y79AA1002235	5.6	7.55	6.43	8.78	9.74	9.47	*	+
Y79AA1002246	0.59	5.06	2.41	3.94	2.54	4.27		

Y79AA1002258	0.72	7.26	2.92	3.99	4.19	2.7		
Y79AA1002279	17.79	19.12	27.8	16.52	19.13	11.5		
Y79AA1002292	1.68	2.1	3.22	2.96	3.91	2.73		
Y79AA1002298	0.76	2.52	1.32	2.03	2.77	1.06		
Y79AA1002307	1.05	4.35	1.79	0.76	1.05	1.2		
Y79AA1002309	1.15	4.19	2.3	2.21	1.78	2.55		
Y79AA1002311	2.84	7.35	3.43	5.71	6.04	5.45		
Y79AA1002334	1.72	6.54	2.95	4.77	4.19	3.35		
Y79AA1002351	1.27	5.5	2.89	3.5	3.38	3.06		
Y79AA1002355	12.83	12.25	28.96	22.94	22.07	21.02		
Y79AA1002361	2.22	2.27	3.26	2.47	4.54	1.55		
Y79AA1002365	0.66	2.04	2.26	1.97	3.51	2.25		
Y79AA1002373	1.17	3.93	2.42	1.59	1.97	1.43		
Y79AA1002376	110.81	135.82	249.8	205.99	213.25	191.69		
Y79AA1002378	1.9	4.8	4.91	2.2	3.6	3		
Y79AA1002381	8.65	14.11	19.19	18.84	21.52	17.97		
Y79AA1002388	7.05	9.99	18.24	15.88	21.51	19.99		
Y79AA1002399	1.79	4.25	3.74	4.62	4.08	3.47		
Y79AA1002407	3.05	4.16	3.13	4.66	5.77	4.5	*	+
Y79AA1002413	3.21	6.78	8.05	6.46	8.32	6.87		
Y79AA1002416	1.46	5	2.74	2.49	3.44	3.55		
Y79AA1002429	5.5	8.15	7.27	8	11.11	8.01		
Y79AA1002431	0.92	4.43	0.48	0.79	1.78	0.89		
Y79AA1002433	1.27	5.9	3.24	4.8	3.84	5.58		
Y79AA1002445	4.01	5.34	5.76	3.1	4.89	5.41		
Y79AA1002461	0.63	2.45	1.79	1.19	2.71	1.41		
Y79AA1002466	39.02	70.71	94.5	91.12	82.27	94.71		
Y79AA1002471	4.44	6.67	6.08	7.43	8.06	10.49		
Y79AA1002472	2.41	6.16	5.99	6.8	8.39	4.06		

Y79AA1002474	1.93	8.27	4.31	4.89	6.52	7.13
Y79AA1002482	3.52	6.66	10.37	9.02	11.81	8.69
Y79AA1002487	1.38	4.12	2.46	1.96	3.01	2.56
Y79AA1002490	10.37	9.91	16.35	11.11	12.88	16.86
Y79AA1002493	1.96	4.07	6.14	6.5	8.9	4.1
ZRV6C1006278	0.61	4.08	2.22	1.81	1.58	2.11

【 0 8 1 7 】

実施例 16. オリゴキャップ法で作製された cDNA ライブラリーからの新規 cDNA クロンの選抜

オリゴキャップ法で作製された cDNA ライブラリーから得られたクローンの 5' 末端配列中に開始コドンから始まる 50 アミノ酸以上の蛋白質コード領域が推定される 54 クローン、HEMBA1000497、HEMBA1001750、HEMBA1003854、HEMBA1004193、HEMBA1004860、HEMBA1005572、HEMBA1006038、HEMBA1006092、HEMBA1006406、HEMBA1006650、HEMBA1006812、HEMBA100672、HEMBA1001197、HEMBA1001871、MAMMA1001252、MAMMA1002094、NT2RM4000634、NT2RM4000657、NT2RM4000783、NT2RM4000857、NT2RM4001178、NT2RM4002420、NT2RP2000198、NT2RP2000551、NT2RP2000660、NT2RP2001214、NT2RP2001460、NT2RP2001756、NT2RP2002056、NT2RP2002677、NT2RP2002755、NT2RP2002843、NT2RP2003101、NT2RP2003799、NT2RP2004095、NT2RP2004732、NT2RP2004920、NT2RP2005454、NT2RP2005776、NT2RP2005806、NT2RP2005882、NT2RP3001282、NT2RP3001723、NT2RP3002099、NT2RP3003155、NT2RP3004028、OVARC1000008、OVARC1000724、OVARC1000751、OVARC1001029、PLACE1000814、PLACE1003030、PLACE1005549、PLACE1007218 を新たに選抜した。

中でも HEMBA1000497、HEMBA1003854、HEMBA1004193、HEMBA1006812、HEMBA1001871、NT2RM4000657、NT2RM4001178、NT2RP2001756、NT2RP2002677、NT2RP2002755、NT2RP2002843、NT2RP2004095、NT2RP2004920、NT2RP2005806、NT2RP3001282、NT2RP3002099、NT2RP3003155、OVARC1000724、OVARC1001029、PLACE1000814、PLACE1003030、PLACE1005549、PLACE1007218 の 23 クローンは 100 アミノ酸以上の蛋白質コード領域が推定され、蛋白質コード領域を含む確率が非常に高いことが

示された。

【 0 8 1 8 】

各クローンの最大ATGpr1値を表 4 5 4 に示す。HEMBA1006812、HEMBB1001871、NT2RP3001282は最大ATGpr1値が0.3より大であるため全長である確率が高いが、その他HEMBA1000497、HEMBA1001750、HEMBA1003854、HEMBA1004193、HEMBA1004860、HEMBA1005572、HEMBA1006038、HEMBA1006092、HEMBA1006406、HEMBA1006650、HEMBB1000672、HEMBB1001197、MAMMA1001252、MAMMA1002094、NT2RM4000634、NT2RM4000657、NT2RM4000783、NT2RM4000857、NT2RM4001178、NT2RM4002420、NT2RP2000198、NT2RP2000551、NT2RP2000660、NT2RP2001214、NT2RP2001460、NT2RP2001756、NT2RP2002056、NT2RP2002677、NT2RP2002755、NT2RP2002843、NT2RP2003101、NT2RP2003799、NT2RP2004095、NT2RP2004732、NT2RP2004920、NT2RP2005454、NT2RP2005776、NT2RP2005806、NT2RP2005882、NT2RP3001723、NT2RP3002099、NT2RP3003155、NT2RP3004028、OVARC1000008、OVARC1000724、OVARC1000751、OVARC1001029、PLACE1000814、PLACE1003030、PLACE1005549、PLACE1007218は最大ATGpr1値が0.3以下であるため全長率が低いとされるものの依然全長である可能性はある。

表 4 5 5 (表 2 と同じ内容を表す) 中に 5 4 クローンにおける 5' 側と 3' 側を規定する塩基配列を示す配列番号と、そのポリヌクレオチドをインサートとして含む実施例で取得したプラスミドクローンの対応関係を示す。5' 配列 配列名の右側が 5' 配列の配列番号であり、3' 配列 配列名の右側が 3' 配列の配列番号である。

選抜された 54 クローンの 5' 末端配列を Swiss-Prot に対して、5' 末端配列、3' 末端配列を GenBank、UniGene に対して相同性検索した。それぞれの検索結果は、明細書の最後に相同性検索結果データ 7 ~ 1 1 として示した。

【 0 8 1 9 】

得られたトップヒットデータからは、少なくとも、分泌・膜蛋白質、糖蛋白質、シグナル伝達関連蛋白質、転写関連蛋白質、疾患関連蛋白質、蛋白質合成・輸送関連蛋白質のいずれかのカテゴリーに属する蛋白質をコードすると推定されるクローンが 7 クローンあった。いずれも該カテゴリーに属する既知蛋白質と比較

的相同性の低いとされるクローンであった。ここでいう「比較的相同性が低い」とは、「比較的相同性が高い」条件（Swiss-Protデータベースの既知配列との比較において、Identityが60%以上、かつP値が 10^{-10} 以下のスコアである）は満たさないが、Swiss-Protデータベースの既知配列との比較において、比較配列の長さが55塩基以上、かつIdentityが25%以上、かつP値が 10^{-6} 以下のスコアであることを示す。

7クローンのうち、分泌・膜蛋白質のカテゴリーに属する蛋白質をコードすると推定されるクローンはHEMBB1001871, NT2RM4000857の2クローンであった（他のカテゴリーに重複して属するクローン）。糖蛋白質のカテゴリーに属する蛋白質をコードすると推定されるクローンはHEMBB1001871, NT2RM4000857の2クローンであった（他のカテゴリーに重複して属するクローン）。シグナル伝達関連蛋白質のカテゴリーに属する蛋白質をコードすると推定されるクローンはPLACE1005549の1クローンであった。転写関連蛋白質のカテゴリーに属する蛋白質をコードすると推定されるクローンはHEMBA1005572, NT2RP2001756, NT2RP2005776の3クローンであった。疾患関連蛋白質のカテゴリーに属する蛋白質をコードすると推定されるクローンはNT2RM4000857の1クローンであった（他のカテゴリーに重複して属するクローン）。蛋白質合成・輸送関連蛋白質のカテゴリーに属する蛋白質をコードすると推定されるクローンはHEMBA1001750の1クローンであった（実施例12.参照）。

【0 8 2 0】

【表 4 5 4】

実施例16で選抜されたクローンの最大ATGpr1値

クローン名	配列名	最大 ATGpr1値
HEMBA1000497	F-HEMBA1000497	0.25
HEMBA1001750	F-HEMBA1001750	0.08
HEMBA1003854	F-HEMBA1003854	0.23

HEMBA1004193	F-HEMBA1004193	0.22
HEMBA1004860	F-HEMBA1004860	0.29
HEMBA1005572	F-HEMBA1005572	0.24
HEMBA1006038	F-HEMBA1006038	0.29
HEMBA1006092	F-HEMBA1006092	0.28
HEMBA1006406	F-HEMBA1006406	0.26
HEMBA1006650	F-HEMBA1006650	0.22
HEMBA1006812	F-HEMBA1006812	0.71
HEMBB1000672	F-HEMBB1000672	0.24
HEMBB1001197	F-HEMBB1001197	0.22
HEMBB1001871	F-HEMBB1001871	0.94
MAMMA1001252	F-MAMMA1001252	0.29
MAMMA1002094	F-MAMMA1002094	0.28
NT2RM4000634	F-NT2RM4000634	0.07
NT2RM4000657	F-NT2RM4000657	0.24
NT2RM4000783	F-NT2RM4000783	0.22
NT2RM4000857	F-NT2RM4000857	0.12
NT2RM4001178	F-NT2RM4001178	0.27
NT2RM4002420	F-NT2RM4002420	0.06
NT2RP2000198	F-NT2RP2000198	0.15
NT2RP2000551	F-NT2RP2000551	0.07
NT2RP2000660	F-NT2RP2000660	0.22
NT2RP2001214	F-NT2RP2001214	0.26
NT2RP2001460	F-NT2RP2001460	0.07
NT2RP2001756	F-NT2RP2001756	0.17
NT2RP2002056	F-NT2RP2002056	0.12
NT2RP2002677	F-NT2RP2002677	0.14
NT2RP2002755	F-NT2RP2002755	0.12
NT2RP2002843	F-NT2RP2002843	0.11

NT2RP2003101	F-NT2RP2003101	0.13
NT2RP2003799	F-NT2RP2003799	0.24
NT2RP2004095	F-NT2RP2004095	0.16
NT2RP2004732	F-NT2RP2004732	0.18
NT2RP2004920	F-NT2RP2004920	0.15
NT2RP2005454	F-NT2RP2005454	0.09
NT2RP2005776	F-NT2RP2005776	0.19
NT2RP2005806	F-NT2RP2005806	0.27
NT2RP2005882	F-NT2RP2005882	0.11
NT2RP3001282	F-NT2RP3001282	0.39
NT2RP3001723	F-NT2RP3001723	0.22
NT2RP3002099	F-NT2RP3002099	0.20
NT2RP3003155	F-NT2RP3003155	0.29
NT2RP3004028	F-NT2RP3004028	0.13
OVARC1000008	F-OVARC1000008	0.23
OVARC1000724	F-OVARC1000724	0.27
OVARC1000751	F-OVARC1000751	0.28
OVARC1001029	F-OVARC1001029	0.25
PLACE1000814	F-PLACE1000814	0.21
PLACE1003030	F-PLACE1003030	0.26
PLACE1005549	F-PLACE1005549	0.16
PLACE1007218	F-PLACE1007218	0.30

【 0 8 2 1 】

【 表 4 5 5 】

クローン名	5' 末端配列	5' 末端	3' 末端配列	3' 末端
	配列名	配列番号	配列名	配列番号

HEMBA1000497	F-HEMBA1000497	16111	R-HEMBA1000497	16165
HEMBA1001750	F-HEMBA1001750	16112	R-HEMBA1001750	16166
HEMBA1003854	F-HEMBA1003854	16113	R-HEMBA1003854	16167
HEMBA1004193	F-HEMBA1004193	16114	R-HEMBA1004193	16168
HEMBA1004860	F-HEMBA1004860	16115	R-HEMBA1004860	16169
HEMBA1005572	F-HEMBA1005572	16116	R-HEMBA1005572	16170
HEMBA1006038	F-HEMBA1006038	16117	R-HEMBA1006038	16171
HEMBA1006092	F-HEMBA1006092	16118	R-HEMBA1006092	16172
HEMBA1006406	F-HEMBA1006406	16119	R-HEMBA1006406	16173
HEMBA1006650	F-HEMBA1006650	16120	R-HEMBA1006650	16174
HEMBA1006812	F-HEMBA1006812	16121	R-HEMBA1006812	16175
HEMBB1000672	F-HEMBB1000672	16122	R-HEMBB1000672	16176
HEMBB1001197	F-HEMBB1001197	16123	R-HEMBB1001197	16177
HEMBB1001871	F-HEMBB1001871	16124	R-HEMBB1001871	16178
MAMMA1001252	F-MAMMA1001252	16125	R-MAMMA1001252	16179
MAMMA1002094	F-MAMMA1002094	16126	R-MAMMA1002094	16180
NT2RM4000634	F-NT2RM4000634	16127	R-NT2RM4000634	16181
NT2RM4000657	F-NT2RM4000657	16128	R-NT2RM4000657	16182
NT2RM4000783	F-NT2RM4000783	16129	R-NT2RM4000783	16183
NT2RM4000857	F-NT2RM4000857	16130	R-NT2RM4000857	16184
NT2RM4001178	F-NT2RM4001178	16131	R-NT2RM4001178	16185
NT2RM4002420	F-NT2RM4002420	16132	R-NT2RM4002420	16186
NT2RP2000198	F-NT2RP2000198	16133	R-NT2RP2000198	16187
NT2RP2000551	F-NT2RP2000551	16134	R-NT2RP2000551	16188
NT2RP2000660	F-NT2RP2000660	16135	R-NT2RP2000660	16189
NT2RP2001214	F-NT2RP2001214	16136	R-NT2RP2001214	16190
NT2RP2001460	F-NT2RP2001460	16137	R-NT2RP2001460	16191
NT2RP2001756	F-NT2RP2001756	16138	R-NT2RP2001756	16192
NT2RP2002056	F-NT2RP2002056	16139	R-NT2RP2002056	16193

NT2RP2002677	F-NT2RP2002677	16140	R-NT2RP2002677	16194
NT2RP2002755	F-NT2RP2002755	16141	R-NT2RP2002755	16195
NT2RP2002843	F-NT2RP2002843	16142	R-NT2RP2002843	16196
NT2RP2003101	F-NT2RP2003101	16143	R-NT2RP2003101	16197
NT2RP2003799	F-NT2RP2003799	16144	R-NT2RP2003799	16198
NT2RP2004095	F-NT2RP2004095	16145	R-NT2RP2004095	16199
NT2RP2004732	F-NT2RP2004732	16146	R-NT2RP2004732	16200
NT2RP2004920	F-NT2RP2004920	16147	R-NT2RP2004920	16201
NT2RP2005454	F-NT2RP2005454	16148	R-NT2RP2005454	16202
NT2RP2005776	F-NT2RP2005776	16149	R-NT2RP2005776	16203
NT2RP2005806	F-NT2RP2005806	16150	R-NT2RP2005806	16204
NT2RP2005882	F-NT2RP2005882	16151	R-NT2RP2005882	16205
NT2RP3001282	F-NT2RP3001282	16152	R-NT2RP3001282	16206
NT2RP3001723	F-NT2RP3001723	16153	R-NT2RP3001723	16207
NT2RP3002099	F-NT2RP3002099	16154	R-NT2RP3002099	16208
NT2RP3003155	F-NT2RP3003155	16155	R-NT2RP3003155	16209
NT2RP3004028	F-NT2RP3004028	16156	R-NT2RP3004028	16210
OVARC1000008	F-OVARC1000008	16157	R-OVARC1000008	16211
OVARC1000724	F-OVARC1000724	16158	R-OVARC1000724	16212
OVARC1000751	F-OVARC1000751	16159	R-OVARC1000751	16213
OVARC1001029	F-OVARC1001029	16160	R-OVARC1001029	16214
PLACE1000814	F-PLACE1000814	16161	R-PLACE1000814	16215
PLACE1003030	F-PLACE1003030	16162	R-PLACE1003030	16216
PLACE1005549	F-PLACE1005549	16163	R-PLACE1005549	16217
PLACE1007218	F-PLACE1007218	16164	R-PLACE1007218	16218

【 0 8 2 2 】

実施例 1 7 . 推定アミノ酸配列に対するシグナル配列、膜貫通領域および機能ドメインの検索

全長塩基配列から推定されたアミノ酸配列に対して、アミノ末端のシグナル配列の有無と膜貫通領域の有無を予測、さらに蛋白質の機能ドメイン（モチーフ）検索を行った。アミノ末端のシグナル配列についてはPSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)] を、膜貫通領域についてはSOSUI [T. Hirokawa et.al. Bioinformatics, 14: 378-379 (1998)]（三井情報開発株式会社販売）を用いて解析を行った。機能ドメインの検索についてはPfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) を用いた。PSORTやSOSUIにより、アミノ末端のシグナル配列や膜貫通領域が予測されたアミノ酸配列は分泌、膜蛋白質であると予測された。また、Pfamによる機能ドメイン検索において、ある機能ドメインにヒットしたアミノ酸配列はヒットデータをもとに、例えばPROSITE(<http://www.expasy.ch/cgi-bin/prosite-list.pl>)にある機能カテゴリー分類を参照にしてその蛋白質の機能予測することができる。また、PROSITEでの機能ドメインの検索も可能である。

各ソフトウェアによる検索結果を以下に示す。

【 0 8 2 3 】

PSORTにより推定アミノ酸配列にシグナル配列を検出されたクローンは、以下の通りであった。

HEMBA1001052, HEMBA1001407, HEMBA1002486, HEMBA1002661, HEMBA1002818, HEMBA1002876, HEMBA1003086, HEMBA1003711, HEMBA1004752, HEMBA1005991, HEMBA1006067, HEMBA1006173, HEMBA1006198, HEMBA1006789, HEMBA1006921, HEMBB1000054, HEMBB1000175, HEMBB1002692, MAMMA1000798, MAMMA1002427, MAMMA1002881, MAMMA1003035, NT2RM1000035, NT2RM1000742, NT2RM1000811, NT2RM1000905, NT2RM1001008, NT2RM2000287, NT2RM2000609, NT2RM2001613, NT2RM4000634, NT2RM4000778, NT2RM4002339, NT2RM4002460, NT2RP1000782, NT2RP1000856, NT2RP1001247, NT2RP1001546, NT2RP1001569, NT2RP2001597, NT2RP2002537, NT2RP2004142, NT2RP2005752, NT2RP2005812, NT2RP3001084, NT2RP3001589, NT2RP3002163, NT2RP3002650, NT2RP3003145, NT2RP3003242, NT2RP3003621, NT2RP3004282, NT2RP3004503, NT2RP4000051, NT2RP4000151, NT2RP4000243, NT2RP4000259, NT2RP4000323, NT2RP4000417, NT2RP4001064, NT2RP4001117, NT2RP40017

30, NT2RP4001739, NT2RP4002075, NT2RP5003500, OVARC1001154, PLACE1000611
 , PLACE1003030, PLACE1003044, PLACE1003369, PLACE1003596, PLACE1004258,
 PLACE1005086, PLACE1006239, PLACE1006754, PLACE1006829, PLACE1007954, PL
 ACE1008424, PLACE1008533, PLACE1008693, PLACE1010622, PLACE1010942, PLAC
 E2000176, PLACE2000341, PLACE2000379, PLACE2000427, PLACE2000477, PLACE4
 000431, PLACE4000593, THYRO1000156, THYRO1001134, THYRO1001287, Y79AA100
 0258, Y79AA1001874, Y79AA1002399
 HEMBB1001871, HEMBB1001925, MAMMA1000778, MAMMA1000897, MAMMA1001080, NT
 2RP2004300, NT2RP3002985, NT2RP3003059, OVARC1000689, OVARC1000890, PLAC
 E1005162, PLACE3000399, PLACE3000455, PLACE4000247, PLACE4000259, PLACE4
 000494

【 0 8 2 4 】

SOSUIにより推定アミノ酸配列に膜貫通領域を検出されたクローンは、以下の
 通りであった。

HEMBA1000005, HEMBA1000356, HEMBA1000518, HEMBA1000531, HEMBA1000637, HE
 MBA1000719, HEMBA1000817, HEMBA1000822, HEMBA1000870, HEMBA1000991, HEMB
 A1001052, HEMBA1001085, HEMBA1001286, HEMBA1001351, HEMBA1001407, HEMBA1
 001446, HEMBA1001510, HEMBA1001515, HEMBA1001557, HEMBA1001746, HEMBA100
 2092, HEMBA1002125, HEMBA1002150, HEMBA1002166, HEMBA1002462, HEMBA10024
 77, HEMBA1002486, HEMBA1002609, HEMBA1002659, HEMBA1002661, HEMBA1002780
 , HEMBA1002818, HEMBA1002876, HEMBA1002921, HEMBA1003077, HEMBA1003079,
 HEMBA1003086, HEMBA1003096, HEMBA1003281, HEMBA1003286, HEMBA1003711, HE
 MBA1003742, HEMBA1003803, HEMBA1004143, HEMBA1004146, HEMBA1004341, HEMB
 A1004461, HEMBA1004577, HEMBA1004637, HEMBA1004752, HEMBA1004756, HEMBA1
 004850, HEMBA1004889, HEMBA1004923, HEMBA1004930, HEMBA1005029, HEMBA100
 5035, HEMBA1005050, HEMBA1005552, HEMBA1005588, HEMBA1005616, HEMBA10059
 91, HEMBA1006036, HEMBA1006067, HEMBA1006293, HEMBA1006492, HEMBA1006502
 , HEMBA1006659, HEMBA1006758, HEMBA1006789, HEMBA1006921, HEMBA1006926,
 HEMBA1007203, HEMBB1000050, HEMBB1000054, HEMBB1000556, HEMBB1000593, HE

MBBI000631, HEMBB1000763, HEMBB1000827, HEMBB1000915, HEMBB1000975, HEMBB1001112, HEMBB1001177, HEMBB1001302, HEMBB1001348, HEMBB1001962, HEMBB1002142, HEMBB1002190, HEMBB1002247, HEMBB1002387, HEMBB1002550, HEMBB1002600, HEMBB1002692, MAMMA1000129, MAMMA1000133, MAMMA1000277, MAMMA1000278, MAMMA1000410, MAMMA1000416, MAMMA1000472, MAMMA1000714, MAMMA1000731, MAMMA1000734, MAMMA1000798, MAMMA1000842, MAMMA1000956, MAMMA1001008, MAMMA1001030, MAMMA1001139, MAMMA1001154, MAMMA1001388, MAMMA1001411, MAMMA1001487, MAMMA1001751, MAMMA1001771, MAMMA1002461, MAMMA1002524, MAMMA1002598, MAMMA1002684, MAMMA1002769, MAMMA1002890, MAMMA1002938, MAMMA1003146, NT2RM1000035, NT2RM1000037, NT2RM1000062, NT2RM1000131, NT2RM1000257, NT2RM1000260, NT2RM1000355, NT2RM1000648, NT2RM1000742, NT2RM1000800, NT2RM1000811, NT2RM1000857, NT2RM1000867, NT2RM1000882, NT2RM1001008, NT2RM1001115, NT2RM1001139, NT2RM2000259, NT2RM2000395, NT2RM2000402, NT2RM2000407, NT2RM2000422, NT2RM2000566, NT2RM2000581, NT2RM2000609, NT2RM2001370, NT2RM2001393, NT2RM2001499, NT2RM2001613, NT2RM2001648, NT2RM2001659, NT2RM2001671, NT2RM2001718, NT2RM2001760, NT2RM2001785, NT2RM2001823, NT2RM2001930, NT2RM2001950, NT2RM2001998, NT2RM2002049, NT2RM4000046, NT2RM4000233, NT2RM4000433, NT2RM4000520, NT2RM4000634, NT2RM4000674, NT2RM4000700, NT2RM4000764, NT2RM4000795, NT2RM4000820, NT2RM4000857, NT2RM4001032, NT2RM4001054, NT2RM4001455, NT2RM4001813, NT2RM4001930, NT2RM4001987, NT2RM4002054, NT2RM4002073, NT2RM4002145, NT2RM4002146, NT2RM4002194, NT2RM4002339, NT2RM4002438, NT2RM4002446, NT2RM4002452, NT2RM4002460, NT2RM4002493, NT2RM4002571, NT2RP1000191, NT2RP1000358, NT2RP1000418, NT2RP1000547, NT2RP1000609, NT2RP1000677, NT2RP1000767,

【 0 8 2 5 】

NT2RP1000782, NT2RP1000856, NT2RP1001113, NT2RP1001247, NT2RP1001286, NT2RP1001310, NT2RP1001311, NT2RP1001313, NT2RP1001385, NT2RP1001449, NT2RP1001546, NT2RP1001569, NT2RP2000032, NT2RP2000040, NT2RP2000070, NT2RP2

000091, NT2RP2000114, NT2RP2000120, NT2RP2000173, NT2RP2000175, NT2RP2000195, NT2RP2000248, NT2RP2000270, NT2RP2000283, NT2RP2000289, NT2RP2000459, NT2RP2000516, NT2RP2000842, NT2RP2000892, NT2RP2001081, NT2RP2001268, NT2RP2001295, NT2RP2001366, NT2RP2001576, NT2RP2001581, NT2RP2001597, NT2RP2001947, NT2RP2001991, NT2RP2002025, NT2RP2002312, NT2RP2002385, NT2RP2002479, NT2RP2002537, NT2RP2002643, NT2RP2002701, NT2RP2002740, NT2RP2002857, NT2RP2003125, NT2RP2003297, NT2RP2003433, NT2RP2003446, NT2RP2003466, NT2RP2003629, NT2RP2003777, NT2RP2003781, NT2RP2004041, NT2RP2004194, NT2RP2004270, NT2RP2004681, NT2RP2004775, NT2RP2004799, NT2RP2004936, NT2RP2005012, NT2RP2005159, NT2RP2005227, NT2RP2005270, NT2RP2005344, NT2RP2005509, NT2RP2005752, NT2RP2005781, NT2RP2005784, NT2RP2005812, NT2RP2006069, NT2RP2006100, NT2RP2006141, NT2RP2006261, NT2RP2006571, NT2RP3000092, NT2RP3000134, NT2RP3000333, NT2RP3000393, NT2RP3000439, NT2RP3000441, NT2RP3000531, NT2RP3000685, NT2RP3000826, NT2RP3000852, NT2RP3001126, NT2RP3001176, NT2RP3001260, NT2RP3001355, NT2RP3001383, NT2RP3001426, NT2RP3001453, NT2RP3001497, NT2RP3001538, NT2RP3001716, NT2RP3001727, NT2RP3001739, NT2RP3001799,

【 0 8 2 6 】

NT2RP3001943, NT2RP3001944, NT2RP3002002, NT2RP3002014, NT2RP3002054, NT2RP3002108, NT2RP3002163, NT2RP3002351, NT2RP3002455, NT2RP3002549, NT2RP3002628, NT2RP3002650, NT2RP3002687, NT2RP3002701, NT2RP3002869, NT2RP3002969, NT2RP3003008, NT2RP3003071, NT2RP3003101, NT2RP3003145, NT2RP3003302, NT2RP3003353, NT2RP3003409, NT2RP3003716, NT2RP3003918, NT2RP3004207, NT2RP3004454, NT2RP3004503, NT2RP4000051, NT2RP4000151, NT2RP4000243, NT2RP4000259, NT2RP4000323, NT2RP4000500, NT2RP4000560, NT2RP4000588, NT2RP4000713, NT2RP4000724, NT2RP4000833, NT2RP4000878, NT2RP4000907, NT2RP4000925, NT2RP4000928, NT2RP4000973, NT2RP4000989, NT2RP4001057, NT2RP4001064, NT2RP4001079, NT2RP4001117, NT2RP4001138, NT2RP4001150, NT2RP4001174, NT2RP4001274, NT2RP4001345, NT2RP4001372, NT2RP4001373, NT2RP400

-----1379, NT2RP4001498, NT2RP4001547, NT2RP4001571, NT2RP4001644, NT2RP40016

77, NT2RP4001803, NT2RP4001822, NT2RP4001975, NT2RP4002052, NT2RP4002075
, NT2RP5003500, NT2RP5003506, NT2RP5003522, NT2RP5003534, OVARC1000151,
OVARC1000241, OVARC1000335, OVARC1000700, OVARC1000722, OVARC1000751, OV
ARC1000850, OVARC1000924, OVARC1000936, OVARC1000959, OVARC1000984, OVAR
C1001034, OVARC1001129, OVARC1001381, OVARC1001391, OVARC1001453, OVARC1
001476, OVARC1001506, OVARC1001610, OVARC1001702, OVARC1001703, OVARC100
1713, OVARC1001745, OVARC1001767, OVARC1002127, OVARC1002158, OVARC10021
65, PLACE1000014, PLACE1000401,

【 0 8 2 7 】

PLACE1000562, PLACE1000611, PLACE1000656, PLACE1000712, PLACE1000909, PL
ACE1000948, PLACE1001241, PLACE1001257, PLACE1001377, PLACE1001517, PLAC
E1001610, PLACE1001771, PLACE1001817, PLACE1001983, PLACE1002213, PLACE1
002395, PLACE1002500, PLACE1002714, PLACE1002722, PLACE1002794, PLACE100
2851, PLACE1002908, PLACE1003045, PLACE1003238, PLACE1003296, PLACE10033
69, PLACE1003493, PLACE1003537, PLACE1003553, PLACE1003768, PLACE1003771
, PLACE1003903, PLACE1004197, PLACE1004258, PLACE1004270, PLACE1004289,
PLACE1004473, PLACE1004743, PLACE1004840, PLACE1004969, PLACE1005086, PL
ACE1005206, PLACE1005313, PLACE1005530, PLACE1005595, PLACE1005623, PLAC
E1005763, PLACE1005884, PLACE1005934, PLACE1006225, PLACE1006754, PLACE1
006901, PLACE1006935, PLACE1006956, PLACE1007014, PLACE1007111, PLACE100
7243, PLACE1007274, PLACE1007282, PLACE1007317, PLACE1007375, PLACE10073
86, PLACE1007409, PLACE1007484, PLACE1007583, PLACE1007632, PLACE1007645
, PLACE1007852, PLACE1007877, PLACE1008331, PLACE1008424, PLACE1008531,
PLACE1008532, PLACE1008568, PLACE1008715, PLACE1009045, PLACE1009319, PL
ACE1009338, PLACE1009368, PLACE1009493, PLACE1009639, PLACE1009708, PLAC
E1009731, PLACE1010089, PLACE1010231, PLACE1010321, PLACE1010622, PLACE1
010811, PLACE1010917, PLACE1010954, PLACE1011090, PLACE1011214, PLACE101
1221, PLACE1011399, PLACE1011492, PLACE1011646, PLACE1011749, PLACE20000

34, PLACE2000111, PLACE2000176,

【 0 8 2 8 】

PLACE2000187, PLACE2000341, PLACE2000379, PLACE2000425, PLACE2000458, PLACE3000020, PLACE3000218, PLACE3000226, PLACE3000244, PLACE3000413, PLACE4000052, PLACE4000129, PLACE4000300, PLACE4000387, PLACE4000581, PLACE4000593, PLACE4000650, THYRO1000394, THYRO1000395, THYRO1000570, THYRO1000748, THYRO1000756, THYRO1001134, THYRO1001271, THYRO1001401, THYRO1001534, THYRO1001541, THYRO1001809, Y79AA1000258, Y79AA1000420, Y79AA1000469, Y79AA1000734, Y79AA1000800, Y79AA1000976, Y79AA1001023, Y79AA1001177, Y79AA1001394, Y79AA1001603, Y79AA1001647, Y79AA1001846, Y79AA1001874, Y79AA1002139, Y79AA1002351, Y79AA1002399, Y79AA1002416, HEMBA1004055, HEMBB1001630, HEMBB1001872, HEMBB1002044, HEMBB1002383, MAMMA1000778, MAMMA1000859, MAMMA1000897, MAMMA1001073, MAMMA1002009, MAMMA1002844, MAMMA1002947, MAMMA1003089, NT2RM1000092, NT2RM1000833, NT2RP2002105, NT2RP2003668, NT2RP2006184, NT2RP3001282, NT2RP3002810, NT2RP3002985, NT2RP3003059, NT2RP3003576, NT2RP3003665, NT2RP3003799, NT2RP3003828, NT2RP3003992, NT2RP3004051, NT2RP3004155, OVARC1000890, OVARC1001117, OVARC1001329, PLACE1001761, PLACE1002437, PLACE1004793, PLACE1005611, PLACE1005898, PLACE1009935, PLACE1011896, PLACE2000132, PLACE2000335, PLACE3000373, PLACE3000406, PLACE4000250, PLACE4000487, PLACE4000494, THYRO1001320, THYRO1001537, THYRO1001828, Y79AA1001384

【 0 8 2 9 】

Pfamにより推定アミノ酸配列に機能ドメインを検出されたクローン名とヒットした機能ドメイン名は以下の通りであった。検索結果は、クローン名//機能ドメイン名のように示した。複数の機能ドメインがヒットした場合には//で区切って並記した。

HEMBA1000005//DnaJ, prokaryotic heat shock protein

HEMBA1000020//Tubulin

HEMBA1000129//Helicases conserved C-terminal domain

HEMBA1000156//RNA recognition motif. (aka-RRM, RBD, or-RNP-domain)-----
 HEMBA1000158//Fork head domain, eukaryotic transcription factors //Zinc
 finger, C2H2 type
 HEMBA1000303//Src homology domain 3 //Zinc finger, C3HC4 type (RING fing
 er)
 HEMBA1000411//Ank repeat
 HEMBA1000491//Ras family (contains ATP/GTP binding P-loop)
 HEMBA1000531//Heat shock hsp70 proteins
 HEMBA1000561//Zinc finger, C2H2 type
 HEMBA1000608//Src homology domain 3
 HEMBA1000919//WD domain, G-beta repeats
 HEMBA1001043//Ank repeat
 HEMBA1001088//LIM domain containing proteins
 HEMBA1001137//Zinc finger, C2H2 type
 HEMBA1001174//ADP-ribosylation factors (Arf family) (contains ATP/GTP bi
 nding P-loop)
 HEMBA1001247//WW/rsp5/WWP domain containing proteins
 HEMBA1001286//Sushi domain
 HEMBA1001510//Basic region plus leucine zipper transcription factors
 HEMBA1001515//Reverse transcriptase (RNA-dependent DNA polymerase)
 HEMBA1001661//Cadherin
 HEMBA1001723//WD domain, G-beta repeats
 HEMBA1001744//Eukaryotic protein kinase domain
 HEMBA1001804//Zinc finger, C2H2 type
 HEMBA1001819//Zinc finger, C2H2 type
 HEMBA1001847//Zinc finger, C2H2 type
 HEMBA1002035//Bromodomain
 HEMBA1002102//Ank repeat
 HEMBA1002161//Myosin head (motor domain) (contains ATP/GTP binding P-loo

p)

HEMBA1002177//GATA family of transcription factors //Zinc finger, C2H2 type

HEMBA1002212//Eukaryotic protein kinase domain

HEMBA1002215//LIM domain containing proteins

HEMBA1002419//RNA recognition motif. (aka RRM, RBD, or RNP domain)

HEMBA1002547//Kazal-type serine protease inhibitor domain //Laminin EGF-like (Domains III and V)

HEMBA1002768//Src homology domain 3

HEMBA1002810//WW/rsp5/WWP domain containing proteins

HEMBA1002818//EGF-like domain

HEMBA1002935//Zinc finger, C2H2 type

HEMBA1002939//Ank repeat

HEMBA1002973//3' 5' -cyclic nucleotide phosphodiesterases

HEMBA1003077//Fibronectin type III domain

HEMBA1003250//Eukaryotic protein kinase domain

HEMBA1003257//Zinc finger, C2H2 type

HEMBA1003281//IG superfamily

HEMBA1003291//Eukaryotic protein kinase domain

HEMBA1003433//Forkhead-associated (FHA) domain

HEMBA1003545//Homeobox domain //LIM domain containing proteins

HEMBA1003591//RNA recognition motif. (aka RRM, RBD, or RNP domain)

HEMBA1003684//Zinc finger, C2H2 type

HEMBA1003953//Zinc finger, C2H2 type

HEMBA1004202//Ras family (contains ATP/GTP binding P-loop)

HEMBA1004227//Protein phosphatase 2C

HEMBA1004321//Zinc finger, C2H2 type

HEMBA1004356//RNA recognition motif. (aka RRM, RBD, or RNP domain)

HEMBA1004408//Peptidyl-prolyl cis-trans isomerases

HEMBA1004596//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 HEMBA1004734//Ubiquitin-conjugating enzymes
 HEMBA1004973//Fibronectin type III domain
 HEMBA1005009//Actins
 HEMBA1005101//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 HEMBA1005581//EGF-like domain //Laminin G domain
 HEMBA1005732//Polyprenyl synthetases
 HEMBA1005737//EF hand
 HEMBA1006248//Zinc finger, C2H2 type
 HEMBA1006284//Ubiquitin family
 HEMBA1006293//IG superfamily
 HEMBA1006344//Band 4.1 family
 HEMBA1006445//Ras family (contains ATP/GTP binding P-loop)
 HEMBA1006492//Ank repeat
 HEMBA1006559//Zinc finger, C3HC4 type (RING finger)
 HEMBA1006708//WD domain, G-beta repeats
 HEMBA1006737//Ank repeat
 HEMBA1006758//Cadherin
 HEMBA1006941//Thioredoxins
 HEMBA1007243//Purine/pyrimidine phosphoribosyl transferases
 HEMBA1007300//3'5'-cyclic nucleotide phosphodiesterases
 HEMBB1000083//IG superfamily
 HEMBB1000317//EGF-like domain //Thrombospondin type 1 domain
 HEMBB1000556//Actinin-type actin-binding domain containing proteins //LI
 M domain containing proteins
 HEMBB1000725//Ras family (contains ATP/GTP binding P-loop)
 HEMBB1000781//Eukaryotic protein kinase domain
 HEMBB1000915//Thrombospondin type 1 domain
 HEMBB1000927//EF hand

HEMBB1000947//Double-stranded RNA binding motif
 HEMBB1001112//eubacterial secY protein
 HEMBB1001175//Ank repeat
 HEMBB1001234//WW/rsp5/WWP domain containing proteins
 HEMBB1001282//Ank repeat
 HEMBB1001294//Ras family (contains ATP/GTP binding P-loop)
 HEMBB1001339//Forkhead-associated (FHA) domain
 HEMBB1001673//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type
 (RING finger)
 HEMBB1001802//Intermediate filament proteins
 HEMBB1001839//Zinc finger, C2H2 type
 HEMBB1002217//Zinc finger, C2H2 type
 HEMBB1002342//Thioredoxins
 HEMBB1002600//4 transmembrane segments integral membrane proteins
 MAMMA1000173//Src homology domain 3
 MAMMA1000388//Zinc finger, C2H2 type
 MAMMA1000402//Reverse transcriptase (RNA-dependent DNA polymerase)
 MAMMA1000612//WD domain, G-beta repeats
 MAMMA1000672//Serine carboxypeptidases
 MAMMA1000731//SNF2 and others N-terminal domain
 MAMMA1001008//Eukaryotic aspartyl proteases
 MAMMA1001041//Actinin-type actin-binding domain containing proteins
 MAMMA1001059//DEAD and DEAH box helicases //Helicases conserved C-termin
 al domain
 MAMMA1001105//Zinc finger, C2H2 type
 MAMMA1001260//Zinc finger, C3HC4 type (RING finger)
 MAMMA1001576//Tubulin
 MAMMA1001735//Tubulin
 MAMMA1001768//ATPases associated with various cellular activities (AAA)

MAMMA1001837//Zinc finger, C2H2 type
 MAMMA1002170//Ribosomal protein S5
 MAMMA1002385//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 MAMMA1002619//Ubiquitin carboxyl-terminal hydrolases family 2
 MAMMA1002637//Kinesin light chain repeat
 MAMMA1002650//Zinc finger, C2H2 type
 MAMMA1002671//AMP-binding enzymes
 MAMMA1002869//LIM domain containing proteins
 MAMMA1002881//SCP-like extracellular Proteins
 MAMMA1002937//Zinc finger, C2H2 type
 MAMMA1002938//Multicopper oxidases
 MAMMA1003011//Core histones H2A, H2B, H3 and H4
 MAMMA1003057//WD domain, G-beta repeats
 MAMMA1003127//Myosin head (motor domain) (contains ATP/GTP binding P-loop)
 NT2RM1000086//Zinc finger, C3HC4 type (RING finger)
 NT2RM1000199//CUB domain //Sushi domain
 NT2RM1000256//Glutamine amidotransferases class-II
 NT2RM1000499//Ank repeat
 NT2RM1000555//'Cold-shock' DNA-binding domain containing proteins
 NT2RM1000666//'Cold-shock' DNA-binding domain containing proteins //Zinc finger, CCHC class
 NT2RM1000772//WD domain, G-beta repeats
 NT2RM1000826//'Cold-shock' DNA-binding domain containing proteins
 NT2RM1000850//Ank repeat //Eukaryotic protein kinase domain
 NT2RM1000852//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 NT2RM1000882//Heme-binding domain in cytochrome b5 and oxidoreductases
 NT2RM1000885//Zinc finger, C3HC4 type (RING finger)

NT2RM1001059//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RM1001072//C2 domain //Phosphatidylinositol-specific phospholipase C,
 X domain //Phosphatidylinositol-specific phospholipase C, Y domain
 NT2RM2000092//Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RM2000101//Zinc finger, C3HC4 type (RING finger)
 NT2RM2000191//3'5'-cyclic nucleotide phosphodiesterases
 NT2RM2000422//Sodium:neurotransmitter symporter family
 NT2RM2000490//C2 domain
 NT2RM2000566//Integrins alpha chain
 NT2RM2000577//tRNA synthetases class I
 NT2RM2000594//C-5 cytosine-specific DNA methylases
 NT2RM2000691//Actins
 NT2RM2000735//Zinc finger, C2H2 type
 NT2RM2000740//Helicases conserved C-terminal domain
 NT2RM2000951//FGGY family of carbohydrate kinases
 NT2RM2001324//LIM domain containing proteins
 NT2RM2001499//Amino acid permeases
 NT2RM2001547//DnaJ, prokaryotic heat shock protein //Thioredoxins
 NT2RM2001613//eubacterial secY protein
 NT2RM2001670//Zinc finger, C2H2 type
 NT2RM2001700//Acyl-CoA dehydrogenases
 NT2RM2001730//Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RM2001813//WD domain, G-beta repeats
 NT2RM2001823//Helicases conserved C-terminal domain //SNF2 and others N-
 terminal domain
 NT2RM2001896//Cytochrome C oxidase subunit II
 NT2RM2001989//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RM2001997//Thioredoxins
 NT2RM2002088//KH domain family of RNA binding proteins.

-----NT2RM2002100//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

NT2RM2002109//IG superfamily

NT2RM4000046//Zinc finger, C3HC4 type (RING finger)

NT2RM4000104//Zinc finger, C2H2 type

NT2RM4000167//Kinesin motor domain

NT2RM4000191//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

NT2RM4000202//Zinc finger, C2H2 type

NT2RM4000229//PH (pleckstrin homology) domain

NT2RM4000344//ATPases associated with various cellular activities (AAA)

NT2RM4000356//Ras family (contains ATP/GTP binding P-loop)

NT2RM4000471//Aminotransferases class-V

NT2RM4000496//ATPases associated with various cellular activities (AAA)

NT2RM4000611//WD domain, G-beta repeats

NT2RM4000657//C2 domain //Phosphatidylinositol-specific phospholipase C, Y domain

NT2RM4000712//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2

NT2RM4000733//Forkhead-associated (FHA) domain

NT2RM4000734//Zinc finger, C2H2 type

NT2RM4000751//Zinc finger, C2H2 type

NT2RM4000795//Carboxylesterases

NT2RM4000996//Zinc finger, C2H2 type

NT2RM4001054//eubacterial secY protein

NT2RM4001140//Homeobox domain

NT2RM4001178//DEAD and DEAH box helicases

NT2RM4001200//Zinc finger, C2H2 type

NT2RM4001313//Phosphatidylinositol 3- and 4-kinases

NT2RM4001316//Acyl-CoA-dehydrogenases
 NT2RM4001320//Src homology domain 3
 NT2RM4001411//PH (pleckstrin homology) domain //Src homology domain 2
 NT2RM4001454//PH (pleckstrin homology) domain
 NT2RM4001483//Zinc finger, C2H2 type
 NT2RM4001629//Src homology domain 3
 NT2RM4001758//Eukaryotic protein kinase domain
 NT2RM4001810//Zinc finger, C2H2 type
 NT2RM4001813//Lectin C-type domain short and long forms
 NT2RM4001823//Zinc finger, C2H2 type
 NT2RM4001828//Zinc finger, C2H2 type
 NT2RM4001979//Zinc finger, C2H2 type
 NT2RM4001987//IG superfamily
 NT2RM4002013//WD domain, G-beta repeats
 NT2RM4002073//AMP-binding enzymes
 NT2RM4002093//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RM4002145//IG superfamily
 NT2RM4002287//Fibronectin type III domain
 NT2RM4002527//WD domain, G-beta repeats
 NT2RM4002623//tRNA synthetases class II
 NT2RP1000101//Zinc finger, C2H2 type
 NT2RP1000202//Ank repeat
 NT2RP1000272//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP1000363//PH (pleckstrin homology) domain
 NT2RP1000376//Ank repeat
 NT2RP1000470//DEAD and DEAH box helicases
 NT2RP1000478//Tubulin
 NT2RP1000522//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2

NT2RP1000677//Kazal-type serine-protease inhibitor domain..

NT2RP1000701//WD domain, G-beta repeats

NT2RP1000733//Elongation factor Tu family (contains ATP/GTP binding P-loop)

NT2RP1000782//4 transmembrane segments integral membrane proteins

NT2RP1000833//3' 5' -cyclic nucleotide phosphodiesterases

NT2RP1000856//4 transmembrane segments integral membrane proteins

NT2RP1000947//Ubiquitin-conjugating enzymes

NT2RP1000959//60s Acidic ribosomal protein

NT2RP1000966//RNA recognition motif. (aka RRM, RBD, or RNP domain)

NT2RP1001033//Tubulin

NT2RP1001080//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

NT2RP1001177//Core histones H2A, H2B, H3 and H4

NT2RP1001247//Transforming growth factor beta like domain

NT2RP1001294//WD domain, G-beta repeats

NT2RP1001302//WD domain, G-beta repeats

NT2RP1001313//Heme-binding domain in cytochrome b5 and oxidoreductases

NT2RP1001457//WD domain, G-beta repeats

NT2RP1001546//4 transmembrane segments integral membrane proteins

NT2RP2000008//Zinc finger, C2H2 type

NT2RP2000040//C2 domain

NT2RP2000045//DnaJ, prokaryotic heat shock protein

NT2RP2000054//Zinc finger, C3HC4 type (RING finger)

NT2RP2000070//Cadherin

NT2RP2000126//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain

NT2RP2000153//RNA recognition motif. (aka RRM, RBD, or RNP domain)

NT2RP2000224//PH (pleckstrin homology) domain

NT2RP2000257//Mitochondrial carrier proteins
 NT2RP2000329//Adenylate kinases
 NT2RP2000414//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP2000448//PH (pleckstrin homology) domain
 NT2RP2000660//ATPases associated with various cellular activities (AAA)
 NT2RP2000668//Eukaryotic protein kinase domain
 NT2RP2000710//tRNA synthetases class II
 NT2RP2000764//Aminotransferases class-V
 NT2RP2000842//7 transmembrane receptor (rhodopsin family)
 NT2RP2000880//Elongation factor Tu family (contains ATP/GTP binding P-loop)
 NT2RP2000931//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP2000932//Ank repeat
 NT2RP2001081//C2 domain
 NT2RP2001174//Zinc finger, C2H2 type
 NT2RP2001397//Cyclins
 NT2RP2001520//Mitochondrial carrier proteins
 NT2RP2001597//Zinc finger, C3HC4 type (RING finger)
 NT2RP2001740//Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RP2001748//Polyprenyl synthetases
 NT2RP2001756//Zinc finger, C2H2 type
 NT2RP2001839//Eukaryotic protein kinase domain
 NT2RP2001900//Actins
 NT2RP2001991//Sodium:neurotransmitter symporter family
 NT2RP2002058//WD domain, G-beta repeats
 NT2RP2002124//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RP2002185//Ubiquitin family
 NT2RP2002208//Zinc finger, C3HC4 type (RING finger)

NT2RP2002256//Cytochrome P450
 NT2RP2002479//ABC transporters
 NT2RP2002503//Zinc finger, C2H2 type
 NT2RP2002520//Ank repeat
 NT2RP2002591//Zinc finger, C2H2 type
 NT2RP2002741//Src homology domain 3
 NT2RP2002929//WD domain, G-beta repeats
 NT2RP2002939//Zinc finger, C2H2 type
 NT2RP2002959//Ubiquitin-conjugating enzymes
 NT2RP2002980//Ribosomal protein S10
 NT2RP2003137//Ubiquitin family
 NT2RP2003164//Eukaryotic protein kinase domain
 NT2RP2003228//MCM2/3/5 family
 NT2RP2003243//Fibronectin type III domain
 NT2RP2003272//Ubiquitin family
 NT2RP2003307//Kinesin light chain repeat
 NT2RP2003401//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquiti
 n carboxyl-terminal hydrolases family 2
 NT2RP2003433//eubacterial secY protein
 NT2RP2003480//Zinc finger, C2H2 type
 NT2RP2003713//Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RP2003737//Ubiquitin-conjugating enzymes
 NT2RP2003777//Zinc finger, C3HC4 type (RING finger)
 NT2RP2003840//Ubiquitin-conjugating enzymes
 NT2RP2003857//Ank repeat
 NT2RP2003981//Zinc finger, C3HC4 type (RING finger)
 NT2RP2004170//WD domain, G-beta repeats
 NT2RP2004187//Zinc finger, C2H2 type
 NT2RP2004232//Phorbol esters / diacylglycerol binding domain //PH (pleck

strin homology) domain //Eukaryotic protein kinase domain
 NT2RP2004389//Ribosomal protein S9
 NT2RP2004538//PH (pleckstrin homology) domain
 NT2RP2004568//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 NT2RP2004710//WW/rsp5/WWP domain containing proteins
 NT2RP2004768//Eukaryotic protein kinase domain
 NT2RP2004933//Eukaryotic protein kinase domain
 NT2RP2004961//Zinc finger, C2H2 type
 NT2RP2005003//Zinc finger, C3HC4 type (RING finger)
 NT2RP2005012//DnaJ, prokaryotic heat shock protein
 NT2RP2005126//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 NT2RP2005139//Ank repeat
 NT2RP2005140//PH (pleckstrin homology) domain
 NT2RP2005239//Aminotransferases class-V
 NT2RP2005288//Regulator of chromosome condensation (RCC1)
 NT2RP2005293//PH (pleckstrin homology) domain
 NT2RP2005325//Homeobox domain //LIM domain containing proteins
 NT2RP2005344//E1-E2 ATPases
 NT2RP2005465//Mitochondrial carrier proteins
 NT2RP2005525//Forkhead-associated (FHA) domain
 NT2RP2005531//Band 4.1 family
 NT2RP2005557//Bacterial mutT protein
 NT2RP2005654//DnaJ, prokaryotic heat shock protein
 NT2RP2005701//Zinc finger, C3HC4 type (RING finger)
 NT2RP2005722//Zinc finger, C2H2 type
 NT2RP2005752//TNFR/NGFR cysteine-rich region
 NT2RP2005763//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

al domain

NT2RP2005767//HMG (high mobility group) box

NT2RP2006312//HMG (high mobility group) box

NT2RP2006464//HMG (high mobility group) box

NT2RP2006571//Cytochrome P450

NT2RP3000050//Zinc finger, C2H2 type

NT2RP3000068//PH (pleckstrin homology) domain

NT2RP3000085//Biotin-requiring enzymes //Carbamoyl-phosphate synthase (C
PSase)

NT2RP3000299//Src homology domain 3

NT2RP3000359//Adenylate kinases

NT2RP3000366//Ras family (contains ATP/GTP binding P-loop)

NT2RP3000403//WW/rsp5/WWP domain containing proteins

NT2RP3000487//WW/rsp5/WWP domain containing proteins

NT2RP3000512//Homeobox domain

NT2RP3000527//Zinc finger, C2H2 type

NT2RP3000531//IG superfamily

NT2RP3000590//Zinc finger, C3HC4 type (RING finger)

NT2RP3000603//Helix-loop-helix DNA-binding domain

NT2RP3000605//Zinc finger, C2H2 type

NT2RP3000632//Zinc finger, C2H2 type

NT2RP3000742//Phosphatidylinositol-specific phospholipase C, X domain //
Phosphatidylinositol-specific phospholipase C, Y domain

NT2RP3000759//ADP-ribosylation factors (Arf family) (contains ATP/GTP bi
nding P-loop)

NT2RP3000825//EGF-like domain

NT2RP3000869//ATPases associated with various cellular activities (AAA)

NT2RP3000994//Double-stranded RNA binding motif

NT2RP3001057//Zinc finger, C2H2 type

NT2RP3001084//PH (pleckstrin homology) domain
 NT2RP3001120//Zinc finger, C2H2 type
 NT2RP3001140//Thrombospondin type 1 domain
 NT2RP3001150//Forkhead-associated (FHA) domain
 NT2RP3001155//HMG (high mobility group) box
 NT2RP3001214//Zinc finger, C2H2 type
 NT2RP3001268//Zinc finger, C2H2 type
 NT2RP3001338//Zinc finger, C2H2 type
 NT2RP3001355//Mitochondrial carrier proteins
 NT2RP3001398//Zinc finger, C2H2 type
 NT2RP3001426//DnaJ, prokaryotic heat shock protein
 NT2RP3001453//ABC transporters
 NT2RP3001457//PH (pleckstrin homology) domain
 NT2RP3001472//HMG (high mobility group) box
 NT2RP3001495//Alcohol/other dehydrogenases, short chain type //WW/rsp5/W
 WP domain containing proteins
 NT2RP3001497//Zinc finger, C3HC4 type (RING finger)
 NT2RP3001724//Helicases conserved C-terminal domain
 NT2RP3001792//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP3001943//Zinc finger, C3HC4 type (RING finger)
 NT2RP3001944//Zinc finger, C3HC4 type (RING finger)
 NT2RP3002007//ATPases associated with various cellular activities (AAA)
 NT2RP3002054//Low-density lipoprotein receptor domain class A
 NT2RP3002151//Elongation factor Tu family (contains ATP/GTP binding P-loop)
 NT2RP3002399//MCM2/3/5 family
 NT2RP3002501//Serine/threonine dehydratases
 NT2RP3002602//Thioredoxins
 NT2RP3002628//DnaJ, prokaryotic heat shock protein //Thioredoxins

NT2RP3002663//PH (pleckstrin homology) domain
 NT2RP3002909//Ank repeat
 NT2RP3002953//Cadherin
 NT2RP3002969//AMP-binding enzymes
 NT2RP3003061//Ank repeat
 NT2RP3003145//Zinc carboxypeptidases
 NT2RP3003230//WD domain, G-beta repeats
 NT2RP3003251//Zinc finger, C3HC4 type (RING finger)
 NT2RP3003278//Ank repeat //Zinc finger, C2H2 type
 NT2RP3003282//PH (pleckstrin homology) domain
 NT2RP3003311//PH (pleckstrin homology) domain
 NT2RP3003385//Ank repeat //Chaperonins clpA/B
 NT2RP3003589//Ras family (contains ATP/GTP binding P-loop)
 NT2RP3003621//CUB domain //Kringle domain
 NT2RP3003701//Thrombospondin type 1 domain
 NT2RP3003716//Fibronectin type III domain
 NT2RP3003809//ATPases associated with various cellular activities (AAA)
 NT2RP3004016//Zinc finger, C3HC4 type (RING finger)
 NT2RP3004207//CUB domain //Sushi domain
 NT2RP3004209//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin
 carboxyl-terminal hydrolases family 2
 NT2RP3004242//PH (pleckstrin homology) domain
 NT2RP3004262//DnaJ, prokaryotic heat shock protein
 NT2RP3004566//Zinc finger, C2H2 type
 NT2RP3004569//Ank repeat
 NT2RP3004594//HMG (high mobility group) box
 NT2RP3004617//Zinc finger, C3HC4 type (RING finger)
 NT2RP4000259//Glutathione peroxidases
 NT2RP4000370//Prokaryotic-type class I peptide chain release factors

NT2RP4000376//WD domain, G-beta repeats
NT2RP4000398//Zinc finger, C2H2 type
NT2RP4000455//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type
(RING finger)
NT2RP4000457//Ubiquitin carboxyl-terminal hydrolases family 2
NT2RP4000518//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
NT2RP4000588//Actinin-type actin-binding domain containing proteins
NT2RP4000614//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP4000648//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type
(RING finger)
NT2RP4000837//Zinc finger, C2H2 type
NT2RP4000839//WD domain, G-beta repeats
NT2RP4000865//Zinc finger, C2H2 type
NT2RP4000907//Fibronectin type III domain //IG superfamily
NT2RP4000925//Fibronectin type III domain
NT2RP4000927//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
NT2RP4000973//DnaJ, prokaryotic heat shock protein //Thioredoxins
NT2RP4001079//E1-E2 ATPases
NT2RP4001080//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP4001117//eubacterial secY protein
NT2RP4001150//Fibronectin type III domain
NT2RP4001213//Zinc finger, C2H2 type
NT2RP4001219//Thioredoxins
NT2RP4001235//Zinc finger, CCHC class
NT2RP4001433//Zinc finger, C2H2 type
NT2RP4001498//Ank repeat
NT2RP4001568//Ank repeat

NT2RP4001644//Eukaryotic protein kinase-domain
 NT2RP4001725//WD domain, G-beta repeats
 NT2RP4001753//Zinc finger, C2H2 type
 NT2RP4001790//Zinc finger, C2H2 type
 NT2RP4001822//4 transmembrane segments integral membrane proteins
 NT2RP4001823//Fibrinogen beta and gamma chains, C-terminal globular domain
 in
 NT2RP4001893//Ank repeat
 NT2RP4001896//WD domain, G-beta repeats
 NT2RP4001927//WD domain, G-beta repeats
 NT2RP4001938//Zinc finger, C2H2 type
 NT2RP4002047//Elongation factor Tu family (contains ATP/GTP binding P-loop)
 NT2RP4002078//Zinc finger, C2H2 type
 NT2RP4002408//Eukaryotic protein kinase domain
 NT2RP4002905//Cyclins
 NT2RP5003477//WD domain, G-beta repeats
 OVARC1000006//Core histones H2A, H2B, H3 and H4
 OVARC1000085//Proteasome A-type and B-type
 OVARC1000148//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 OVARC1000556//Eukaryotic protein kinase domain
 OVARC1000649//PH (pleckstrin homology) domain //Src homology domain 2
 OVARC1000746//Double-stranded RNA binding motif
 OVARC1000885//Alcohol/other dehydrogenases, short chain type
 OVARC1000937//Cyclins
 OVARC1000999//Ank repeat
 OVARC1001154//Granulins
 OVARC1001180//Ubiquitin family
 OVARC1001306//Helix-loop-helix DNA-binding domain

OVARC1001577//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 OVARC1001731//Tropomyosins
 OVARC1001943//Zinc finger, C2H2 type
 OVARC1002050//Spectrin alpha chain, repeated domain
 OVARC1002112//Core histones H2A, H2B, H3 and H4
 OVARC1002138//ATPases associated with various cellular activities (AAA)
 OVARC1002182//WD domain, G-beta repeats
 PLACE1000014//Zinc finger, C3HC4 type (RING finger)
 PLACE1000040//Ras family (contains ATP/GTP binding P-loop)
 PLACE1000050//Zinc finger, C2H2 type
 PLACE1000081//PH (pleckstrin homology) domain
 PLACE1000142//Enoyl-CoA hydratase/isomerase
 PLACE1000401//IG superfamily
 PLACE1000406//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 PLACE1000420//Bacterial mutT protein
 PLACE1000706//Bromodomain
 PLACE1000769//KH domain family of RNA binding proteins
 PLACE1000786//PH (pleckstrin homology) domain
 PLACE1000863//Ribosomal protein S4
 PLACE1000909//Ank repeat
 PLACE1000972//Src homology domain 3
 PLACE1000979//Zinc finger, C2H2 type
 PLACE1001304//Zinc finger, C2H2 type
 PLACE1001387//Src homology domain 3
 PLACE1001632//Zinc finger, C2H2 type
 PLACE1001672//Aminotransferases class-III pyridoxal-phosphate
 PLACE1001716//Zinc finger, CCHC class
 PLACE1001739//DEAD and DEAH box helicases //Helicases conserved C-termin
 al domain

PLACE1001781//Phosphoglucosmutase and phosphomannosmutase phosphoserine
 PLACE1001869//FGGY family of carbohydrate kinases
 PLACE1002438//Zinc finger, C2H2 type
 PLACE1002450//Zinc finger, C2H2 type
 PLACE1002474//EGF-like domain //von Willebrand factor type A domain
 PLACE1002499//Zinc finger, C3HC4 type (RING finger)
 PLACE1002532//Homeobox domain
 PLACE1002571//Actins
 PLACE1002685//Src homology domain 2
 PLACE1002722//7 transmembrane receptor (rhodopsin family)
 PLACE1002775//Bromodomain
 PLACE1002834//Zinc finger, C2H2 type
 PLACE1003100//Alcohol/other dehydrogenases, short chain type
 PLACE1003174//Ubiquitin-conjugating enzymes
 PLACE1003238//7 transmembrane receptor (rhodopsin family)
 PLACE1003302//Zinc finger, C2H2 type
 PLACE1003334//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 PLACE1003366//C2 domain
 PLACE1003394//Ras family (contains ATP/GTP binding P-loop)
 PLACE1003420//Mitochondrial carrier proteins
 PLACE1003493//C1q domain
 PLACE1003519//KH domain family of RNA binding proteins
 PLACE1003723//Src homology domain 2
 PLACE1003738//Zinc finger, C2H2 type
 PLACE1003888//C2 domain //Phosphatidylinositol-specific phospholipase C,
 X domain //Phosphatidylinositol-specific phospholipase C, Y domain
 PLACE1004128//WD domain, G-beta repeats
 PLACE1004358//PH (pleckstrin homology) domain
 PLACE1004428//Acyl-CoA dehydrogenases

PLACE1004437//Isocitrate and isopropylmalate dehydrogenases
 PLACE1004506//LIM domain containing proteins
 PLACE1004674//EF hand
 PLACE1004918//L-lactate dehydrogenases
 PLACE1005243//Eukaryotic protein kinase domain
 PLACE1005305//Adenylate kinases
 PLACE1005327//Src homology domain 3
 PLACE1005530//Zinc finger, C3HC4 type (RING finger)
 PLACE1005646//Helicases conserved C-terminal domain
 PLACE1005656//Ribonucleotide reductases
 PLACE1005966//WD domain, G-beta repeats
 PLACE1006157//Sushi domain
 PLACE1006196//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 PLACE1006438//Zinc finger, C2H2 type
 PLACE1006626//Double-stranded RNA binding motif
 PLACE1006754//IG superfamily
 PLACE1006829//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 PLACE1006917//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 PLACE1006956//ABC transporters
 PLACE1006958//Heat shock hsp70 proteins
 PLACE1007375//C2 domain
 PLACE1007488//PH (pleckstrin homology) domain
 PLACE1007511//Intermediate filament proteins
 PLACE1007537//Ank repeat
 PLACE1007544//Zinc finger, C2H2 type
 PLACE1007547//Zinc finger, C3HC4 type (RING finger)
 PLACE1007598//Zinc finger, C2H2 type

PLACE1007697//ABC transporters
 PLACE1007958//3' 5'-cyclic nucleotide phosphodiesterases
 PLACE1007969//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 PLACE1008201//Zinc finger, C2H2 type
 PLACE1008429//Ank repeat
 PLACE1008465//Zinc finger, C2H2 type
 PLACE1008650//WD domain, G-beta repeats
 PLACE1009020//Aminotransferases class-V
 PLACE1009094//von Willebrand factor type C domain
 PLACE1009099//Zinc finger, C2H2 type
 PLACE1009246//LIM domain containing proteins
 PLACE1009468//WD domain, G-beta repeats
 PLACE1009476//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 PLACE1009524//PH (pleckstrin homology) domain
 PLACE1009596//WD domain, G-beta repeats
 PLACE1009622//Double-stranded RNA binding motif
 PLACE1009861//Cysteine proteases
 PLACE1009925//Helicases conserved C-terminal domain
 PLACE1009992//CUB domain //EGF-like domain //Sushi domain //Trypsin
 PLACE1010053//Double-stranded RNA binding motif
 PLACE1010089//Ubiquitin carboxyl-terminal hydrolases family 2
 PLACE1010702//Zinc finger, C2H2 type
 PLACE1010833//EF hand
 PLACE1010926//Src homology domain 3
 PLACE1010960//Actins
 PLACE1011041//Src homology domain 3
 PLACE1011046//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain

PLACE1011114//Helicases conserved C-terminal domain
PLACE1011160//Zinc finger, C3HC4 type (RING finger)
PLACE1011263//Ank repeat
PLACE1011433//Zinc finger, C2H2 type
PLACE1011576//Zinc finger, C2H2 type
PLACE1011923//Eukaryotic protein kinase domain
PLACE2000034//Fibronectin type III domain //IG superfamily
PLACE2000072//Zinc finger, C2H2 type
PLACE2000111//IG superfamily
PLACE2000164//WD domain, G-beta repeats
PLACE2000216//PH (pleckstrin homology) domain
PLACE2000341//Sodium:solute symporter family
PLACE2000371//Src homology domain 2
PLACE2000373//Thrombospondin type 1 domain
PLACE2000398//IG superfamily
PLACE2000427//Helicases conserved C-terminal domain
PLACE2000458//Cadherin
PLACE3000020//Guanylate cyclases
PLACE3000169//Zinc finger, C2H2 type
PLACE4000014//Helicases conserved C-terminal domain
PLACE4000052//ABC transporters
PLACE4000192//Zinc finger, C2H2 type
PLACE4000211//Bromodomain
PLACE4000431//Helicases conserved C-terminal domain
PLACE4000522//Ank repeat
PLACE4000581//EGF-like domain //Sushi domain
PLACE4000654//Ubiquitin-conjugating enzymes
THYR01000072//IG superfamily
THYR01000242//Zinc finger, C2H2 type

THYRO1000288//Zinc-binding metalloprotease domain
 THYRO1000488//Zinc finger, C3HC4 type (RING finger)
 THYRO1000501//Zinc finger, C3HC4 type (RING finger)
 THYRO1000666//Kinesin motor domain
 THYRO1000748//Src homology domain 3
 THYRO1000926//3' 5'-cyclic nucleotide phosphodiesterases
 THYRO1001661//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 THYRO1001671//Ubiquitin family
 Y79AA1000037//Zinc finger, C3HC4 type (RING finger)
 ● Y79AA1000214//Core histones H2A, H2B, H3 and H4
 Y79AA1000342//Zinc finger, C2H2 type
 Y79AA1000349//Double-stranded RNA binding motif
 Y79AA1000627//Zinc finger, C2H2 type
 Y79AA1000705//Helicases conserved C-terminal domain
 Y79AA1000752//KH domain family of RNA binding proteins
 Y79AA1000833//Tubulin
 Y79AA1001048//Acyl-CoA dehydrogenases
 Y79AA1001391//Homeobox domain
 Y79AA1001394//ATPases associated with various cellular activities (AAA)
 ● Y79AA1001493//Ubiquitin-conjugating enzymes
 Y79AA1001613//Zinc finger, C2H2 type
 Y79AA1001874//TNFR/NGFR cysteine-rich region
 Y79AA1002027//Ubiquitin-conjugating enzymes
 Y79AA1002139//DnaJ, prokaryotic heat shock protein
 Y79AA1002208//Ank repeat
 Y79AA1002246//C2 domain
 Y79AA1002307//Fibronectin type III domain
 Y79AA1002472//Zinc finger, C2H2 type
 HEMBA1003538//CUB domain

HEMBA1003645//WD domain, G-beta repeats //Src homology domain 3
HEMBA1005206//Glutathione S-transferases.
HEMBA1006521//Alcohol/other dehydrogenases, short chain type
HEMBB1001482//Zinc finger, C2H2 type
HEMBB1001915//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
HEMBB1002044//Cadherin
MAMMA1000183//Zinc finger, C2H2 type
MAMMA1000897//von Willebrand factor type A domain
MAMMA1001080//IG superfamily
MAMMA1002498//IG superfamily
MAMMA1002573//KH domain family of RNA binding proteins
MAMMA1002617//Zinc finger, C2H2 type
NT2RM1000833//eubacterial secY protein
NT2RM2001797//Zinc finger, C2H2 type
NT2RP1001013//Zinc finger, C2H2 type
NT2RP2001233//Zinc finger, C2H2 type
NT2RP2001440//14-3-3 proteins
NT2RP2002105//7 transmembrane receptor (rhodopsin family)
NT2RP3001723//Laminin G domain
NT2RP3001938//Eukaryotic protein kinase domain
NT2RP3002330//Elongation factor Tu family (contains ATP/GTP binding P-loop)
NT2RP3003133//Zinc finger, C2H2 type
NT2RP3003500//Eukaryotic protein kinase domain
NT2RP3003799//C2 domain
NT2RP3003800//Eukaryotic protein kinase domain
NT2RP3004013//Double-stranded RNA binding motif
NT2RP3004125//Zinc finger, C2H2 type

OVARC1001244//Bromodomain
OVARC1001496//D-isomer specific 2-hydroxyacid dehydrogenases
PLACE1000007//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
PLACE1001118//Zinc finger, C2H2 type
PLACE1010310//Zinc finger, C2H2 type
PLACE1011896//wnt family of developmental signaling proteins
PLACE3000124//Src homology domain 2
PLACE4000100//D-isomer specific 2-hydroxyacid dehydrogenases
PLACE4000259//Helicases conserved C-terminal domain
PLACE4000261//Bromodomain
SKNMC1000013//ABC transporters
SKNMC1000091//Basic region plus leucine zipper transcription factors
THYRO1000343//Src homology domain 3
THYRO1000569//Zinc finger, C2H2 type
THYRO1001189//Zinc finger, C2H2 type
Y79AA1002103//Zinc finger, C2H2 type
PLACE3000350//Eukaryotic protein kinase domain
PLACE4000156//Zinc finger, C2H2 type

【 0 8 3 0 】

【発明の効果】

本発明により、5601にも及ぶ新規な全長cDNAと、このcDNAを合成することができるプライマーが提供された。全長cDNAの分離が進んでいないヒトにおいて、新規な全長cDNAを提供した意義は大きい。本発明のcDNAは全長であるため、翻訳開始点を含み、蛋白質の機能解析において有用な情報を与える。

これらのcDNAは、分泌蛋白質、膜蛋白質、シグナル伝達関連蛋白質、Glycoprotein関連蛋白質、転写関連蛋白質などを含む生体において重要な機能を持つ蛋白質をコードしていることが考えられ、また、多くの疾患に関連していることが予想される。疾患に関連した遺伝子や蛋白質は、診断マーカー、発現や活性を制御

する医薬品の開発、あるいは遺伝子治療のターゲットになるなど医薬品の開発等に有効である。

【0831】

相同性検索結果データ1.

5'末端クローン配列に対するSwissProt相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのDefinition、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのOrganism、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

ここでP値とは、配列間の類似性を統計的に起こりうる確率を考慮してスコアで示したもので、一般に値が小さいと類似性が高い(Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272)。

F-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.8e-85:244:75//MUS MUSCULUS (MOUSE).//Q61712

F-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T RNA LIGASE) (LEURS).//7.6e-57:231:53//CAENORHABDITIS ELEGANS.//Q09996

F-HEMBA1000020//TUBULIN BETA CHAIN.//1.0e-92:143:80//AJELLOMYCES CAPSULATA (HISTOPLASMA CAPSULATUM).//P41742

F-HEMBA1000030//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.021:136:33//PLASMODIUM KNOWLESI (STRAIN NURI).//P04922

F-HEMBA1000042//METALLOTHIONEIN 10-II (MT-10-II).//0.71:64:32//MYTILUS EDULIS (BLUE MUSSEL).//P80247

F-HEMBA1000046//PROTEIN Q300.//0.92:40:37//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1000050//COMPETENCE PROTEIN S.//0.50:28:35//BACILLUS SUBTILIS://P
80355

F-HEMBA1000076//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.86
:41:41//HOMO SAPIENS (HUMAN).//P56385

F-HEMBA1000111

F-HEMBA1000129//UVSW PROTEIN (DAR PROTEIN).//0.023:68:33//BACTERIOPHAGE
T4.//P20703

F-HEMBA1000141//YSY6 PROTEIN.//0.90:29:37//SACCHAROMYCES CEREVISIAE (BAK
ER'S YEAST).//P38374

F-HEMBA1000150//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.4e-16:47:70/
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1000156//IMMEDIATE-EARLY PROTEIN.//8.1e-07:143:28//HERPESVIRUS SA
IMIRI (STRAIN 11).//Q01042

F-HEMBA1000158//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//7.9e-11:129:4
0//HOMO SAPIENS (HUMAN).//Q93074

F-HEMBA1000168//INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).//0.00055:86:
36//MUS MUSCULUS (MOUSE).//P81122

F-HEMBA1000180//VPU PROTEIN (U ORF PROTEIN).//0.22:73:28//CHIMPANZEE IMM
UNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286

F-HEMBA1000185//RAS-1 PROTEIN.//5.1e-10:121:29//NEUROSPORA CRASSA.//P221
26

F-HEMBA1000193//PROLINE-RICH PEPTIDE P-B.//0.00078:56:41//HOMO SAPIENS (
HUMAN).//P02814

F-HEMBA1000201//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.00061:49:42//MUS
MUSCULUS (MOUSE).//P05142

F-HEMBA1000213

F-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INT
ERACTING PROTEIN).//1.6e-59:115:53//MUS MUSCULUS (MOUSE).//Q61221

F-HEMBA1000227//SUPPRESSOR PROTEIN SRP40.//0.00059:135:22//SACCHAROMYCES

CEREVISIAE (BAKER'S YEAST).//P32583
 F-HEMBA1000231//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I./
 /0.024:60:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264
 F-HEMBA1000243//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0038:125:34//HO
 MO SAPIENS (HUMAN).//P08547
 F-HEMBA1000244//HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC R
 EGION.//3.1e-17:149:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P4048
 0
 F-HEMBA1000251
 F-HEMBA1000264//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TY
 PE 58.//P26552
 F-HEMBA1000280//SHORT NEUROTOXIN 1 (TOXIN C-6).//0.98:58:31//NAJA NAJA K
 AOUTHIA (MONOCLED COBRA) (NAJA NAJA SIAMENSIS).//P14613
 F-HEMBA1000282//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.14:26:65//HOM
 O SAPIENS (HUMAN).//P39188
 F-HEMBA1000288
 F-HEMBA1000290//HYPOTHETICAL 14 KD PROTEIN IN TVRI-6 REPETITIVE REGION./
 /3.8e-06:98:39//HOMO SAPIENS (HUMAN).//P10516
 F-HEMBA1000302
 F-HEMBA1000303//HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III.
 //1.3e-05:69:42//CAENORHABDITIS ELEGANS.//Q03601
 F-HEMBA1000304//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.021:18:83//H
 OMO SAPIENS (HUMAN).//P39194
 F-HEMBA1000307//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//7.1e-06:235:2
 5//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922
 F-HEMBA1000327
 F-HEMBA1000333//SRP1 PROTEIN.//1.0:159:30//SCHIZOSACCHAROMYCES POMBE (FI
 SSION YEAST).//Q10193
 F-HEMBA1000338//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.8e-26:36:83/

/HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1000351
 F-HEMBA1000355//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.99:22:50//HOMO
 SAPIENS (HUMAN).//P02811
 F-HEMBA1000356//IMMEDIATE-EARLY PROTEIN IE180.//0.11:82:36//PSEUDORABIES
 VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
 F-HEMBA1000357//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-35:105:74
 //HOMO SAPIENS (HUMAN).//P39192
 F-HEMBA1000366//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//1.0:28:4
 2//ARCHAEOGLOBUS FULGIDUS.//028646
 F-HEMBA1000369//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//0.013:140:26//
 HOMO SAPIENS (HUMAN).//P78352
 F-HEMBA1000376//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR
 ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.8e-08:66:42//MUS MUSCULUS (
 MOUSE).//P11369
 F-HEMBA1000387//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//1
 .5e-15:177:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414
 F-HEMBA1000390//PARATHYMOSIN.//0.0071:61:29//HOMO SAPIENS (HUMAN).//P209
 62
 F-HEMBA1000392//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.1e-30:92:69/
 /HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1000396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-23:64:57//HO
 MO SAPIENS (HUMAN).//P08547
 F-HEMBA1000411
 F-HEMBA1000418
 F-HEMBA1000422//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.3e-10:90:53//
 HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1000428//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-12:72:55//HO
 MO SAPIENS (HUMAN).//P08547

F-HEMBA1000434

F-HEMBA1000442//GENE 11 PROTEIN.//1.0:28:46//SPIROPLASMA VIRUS SPV1-R8A2
B.//P15902

F-HEMBA1000456//26S PROTEASOME REGULATORY SUBUNIT MTS4 (19S REGULATORY C
AP REGION OF 26S PROTEASE SUBUNIT 2).//0.077:118:28//SCHIZOSACCHAROMYCES
POMBE (FISSION YEAST).//P87048

F-HEMBA1000459//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA
KINASE (EC 2.7.1.-) (HRI).//4.8e-62:102:78//ORYCTOLAGUS CUNICULUS (RABBI
T).//P33279

F-HEMBA1000460//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:24:50//BACTERIOPHA
GE ALPHA-3.//P31280

F-HEMBA1000464

F-HEMBA1000469//PILI PROTEIN.//1.0:27:44//PSEUDOMONAS AERUGINOSA.//P4350
2

F-HEMBA1000488//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//1.1e-07:90:38/
/HOMO SAPIENS (HUMAN).//Q13105

F-HEMBA1000490//PLECTIN.//0.74:254:25//RATTUS NORVEGICUS (RAT).//P30427

F-HEMBA1000491//RAS-RELATED PROTEIN M-RAS.//3.0e-14:100:36//RATTUS NORVE
GICUS (RAT).//P97538

F-HEMBA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-20:81:54/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000504

F-HEMBA1000505//NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).//0.00028:128:32/
/HOMO SAPIENS (HUMAN).//Q02410

F-HEMBA1000508//CHITIN SYNTHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCO
SAMINYL TRANSFERASE 3).//0.61:132:25//SACCHAROMYCES CEREVISIAE (BAKER'S
YEAST).//P29465

F-HEMBA1000518

F-HEMBA1000519//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.8e-37:68:75/

/HOMO SAPIENS (HUMAN).//P39189
 F-HEMBA1000520//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.2e-09:75:49/
 /HOMO SAPIENS (HUMAN).//P39192
 F-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//1.5e-35:257:36//MUS MUSC
 ULUS (MOUSE).//Q01755
 F-HEMBA1000531//HEAT SHOCK PROTEIN 70 B2.//1.6e-14:72:44//ANOPHELES ALBI
 MANUS (NEW WORLD MALARIA MOSQUITO).//P41827
 F-HEMBA1000534//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/9.7e-32:96:78/
 /HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1000540//LANTIBIOTIC LACTICIN 481 PRECURSOR (LACTOCOCCIN DR).//1.
 0:12:75//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P36
 499
 F-HEMBA1000542//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.0089
 :79:31//MUS MUSCULUS (MOUSE).//P15265
 F-HEMBA1000545//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.0e-83:256:66//H
 OMO SAPIENS (HUMAN).//P08547
 F-HEMBA1000555//TRANSLATION INITIATION FACTOR IF-2.//3.6e-06:252:22//SAC
 CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730
 F-HEMBA1000557
 F-HEMBA1000561//ZINC FINGER PROTEIN 81 (FRAGMENT).//9.1e-18:200:28//HOMO
 SAPIENS (HUMAN).//P51508
 F-HEMBA1000563
 F-HEMBA1000568
 F-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//1.0e-40:137:54//HOMO SAPIENS
 (HUMAN).//Q14444
 F-HEMBA1000575
 F-HEMBA1000588
 F-HEMBA1000591//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:41:92/
 /HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000592//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.18:128:23//HOMO SAPIENS (HUMAN).//Q02224

F-HEMBA1000594//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III./ /0.93:24:54//CAENORHABDITIS ELEGANS.//P41997

F-HEMBA1000604//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00010:49:55// HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-55:179:6 1//HOMO SAPIENS (HUMAN).//043295

F-HEMBA1000622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-21:94:62// HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000636//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.34:73:36 //VOLVOX CARTERI.//P21997

F-HEMBA1000637//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0057:76:38//HOMO SAPIENS (HUMAN).//P04281

F-HEMBA1000655

F-HEMBA1000657//ZINC FINGER PROTEIN GCS1.//1.5e-07:66:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197

F-HEMBA1000662//METALLOTHIONEIN-II (MT-II).//0.79:33:39//CRICETULUS GRIS EUS (CHINESE HAMSTER).//P02799

F-HEMBA1000673//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.1e-17:86:59/ /HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1000682//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] .//3.0e-13:45:44//MUS MUSCULUS (MOUSE).//P11369

F-HEMBA1000686//HYPOTHETICAL 48.0 KD PROTEIN C1B3.08 IN CHROMOSOME I.//4 .5e-07:79:34//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013873

F-HEMBA1000702

F-HEMBA1000705//PROTEIN Q300.//0.80:25:44//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1000719//MYOSIN IC HEAVY CHAIN.//0.0026:115:44//ACANTHAMOEBA CAST

ELLANII (AMOEBA).//P10569
 F-HEMBA1000722
 F-HEMBA1000726//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//7.4e-32:83:77
 //HOMO SAPIENS (HUMAN).//P39191
 F-HEMBA1000727//ZINC FINGER PROTEIN CTH2 (YTIS11 PROTEIN).//0.73:26:46//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47977
 F-HEMBA1000747
 F-HEMBA1000749//HYPOTHETICAL PROTEIN HI1484.//1.0:42:35//HAEMOPHILUS INF
 LUENZAE.//P44211
 F-HEMBA1000752//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.0e-08:84:39//HOMO
 SAPIENS (HUMAN).//P10267
 F-HEMBA1000769
 F-HEMBA1000773//PAIRED BOX PROTEIN PAX-4.//1.0:107:33//HOMO SAPIENS (HUM
 AN).//043316
 F-HEMBA1000774//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.3e-23:92:63//
 HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1000791
 F-HEMBA1000817//PROLACTIN RECEPTOR PRECURSOR (PRL-R).//0.079:87:29//CERV
 US ELAPHUS (RED DEER).//Q28235
 F-HEMBA1000822
 F-HEMBA1000827//HYPOTHETICAL 8.4 KD PROTEIN.//0.98:48:39//VACCINIA VIRUS
 (STRAIN COPENHAGEN).//P20546
 F-HEMBA1000843//HYPOTHETICAL 7.3 KD PROTEIN D1044.5 IN CHROMOSOME III.//
 0.92:46:34//CAENORHABDITIS ELEGANS.//P41953
 F-HEMBA1000851//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC
 HOMEBOX PROTEIN 2).//0.048:39:51//HOMO SAPIENS (HUMAN).//P52951
 F-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//4.0e-24:2
 9:100//HOMO SAPIENS (HUMAN).//P51689
 F-HEMBA1000867

F-HEMBA1000869//PROBABLE E5 PROTEIN.//0.99:70:27//HUMAN PAPILLOMAVIRUS TYPE 18.//P06792

F-HEMBA1000870//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.79:43:32//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333

F-HEMBA1000872//GAR2 PROTEIN.//0.89:70:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-HEMBA1000876//DEFENSIN.//0.89:34:38//ALLOMYRINA DICHOTOMA.//Q10745

F-HEMBA1000908//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.69:43:37//HOMO SAPIENS (HUMAN).//P30808

F-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B3 (MAGE-B3 ANTIGEN).//5.1e-08:44:38//HOMO SAPIENS (HUMAN).//O15480

F-HEMBA1000918//60S RIBOSOMAL PROTEIN L37-A (YL35) (FRAGMENT).//1.0:19:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P22667

F-HEMBA1000919//69 KD PARAFLAGELLAR ROD PROTEIN (69 KD PFR PROTEIN) (PFR-A/PFR-B).//0.29:116:30//TRYPANOSOMA BRUCEI BRUCEI.//P22225

F-HEMBA1000934

F-HEMBA1000942//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.85:27:59//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000943

F-HEMBA1000946//STO-2 PROTEIN.//0.82:82:30//CAENORHABDITIS ELEGANS.//Q19958

F-HEMBA1000960//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.0097:29:72//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1000968//METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-IIIA AND MT-20-IIIB).//0.047:45:37//MYTILUS EDULIS (BLUE MUSSEL).//P80253

F-HEMBA1000971//HYPOTHETICAL BHLF1 PROTEIN.//0.038:172:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEMBA1000972

F-HEMBA1000974//HYPOTHETICAL PROTEIN MG441.//0.98:66:28//MYCOPLASMA GENI

TALIUM.//P47679

F-HEMBA1000975//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.028:57:36//HOMO SAPIENS (HUMAN).//P25067

F-HEMBA1000985

F-HEMBA1000986//SUBMANDIBULAR GLAND SECRETORY GLX-RICH PROTEIN CB PRECURSOR (GRP-CB) (CONTIGUOUS REPEAT POLYPEPTIDE) (CRP).//0.13:91:34//RATTUS NORVEGICUS (RAT).//P08462

F-HEMBA1000991//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//5.6e-05:37:45//CAENORHABDITIS ELEGANS.//Q1896

4

F-HEMBA1001007//HYPOTHETICAL PROTEIN KIAA0179.//0.27:72:41//HOMO SAPIENS (HUMAN).//Q14684

F-HEMBA1001008//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.4e-25:61:70//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1001009//CUTICLE COLLAGEN 34.//0.044:214:29//CAENORHABDITIS ELEGANS.//P34687

F-HEMBA1001017//SYNDECAN-3 PRECURSOR (N-SYNDECAN) (NEUROGLYCAN).//5.0e-85:191:84//RATTUS NORVEGICUS (RAT).//P33671

F-HEMBA1001019

F-HEMBA1001020//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.7e-24:49:73//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1001022

F-HEMBA1001024//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.0e-11:61:59//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1001026//HYPOTHETICAL PROTEIN BB0073.//0.94:63:34//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51100

F-HEMBA1001043//INVOLUCRIN.//0.0036:238:25//SAGUINUS OEDIPUS (COTTON-TOP TAMARIN).//P24712

F-HEMBA1001051//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.3e-32:95:75/

/HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1001052//CURROMYCIN RESISTANCE PROTEIN.//1.0:31:38//STREPTOMYCES
HYGROSCOPICUS.//P16961

F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.4)
(N- ACETYL GALACTOSAMINE-6-SULFATE SULFATASE) (GALACTOSE-6-SULFATE SULFA
TASE) (GALNAC6S SULFATASE) (CHONDROITIN SULFATASE) (CHONDROITINASE).//3.2
e-132:249:94//HOMO SAPIENS (HUMAN).//P34059

F-HEMBA1001060

F-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//8.3e-23:51:96
//HOMO SAPIENS (HUMAN).//P02461

F-HEMBA1001077//AUTOIMMUNE REGULATOR (APECED PROTEIN).//3.4e-06:37:56//H
OMO SAPIENS (HUMAN).//043918

F-HEMBA1001080//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP
34.5).//0.0012:70:38//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P3
7319

F-HEMBA1001085//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP
5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//0.00018:76:32//MUS MUSCULU
S (MOUSE).//Q60676

F-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTE
IN).//3.5e-50:176:57//HOMO SAPIENS (HUMAN).//P48059

F-HEMBA1001094

F-HEMBA1001099//LIGHT-HARVESTING PROTEIN B800/850/890, ALPHA-2 CHAIN (EH
A-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN) (FRAGMENT).//1.0:15:
60//ECTOTHIORHODOSPIRA HALOPHILA.//P80101

F-HEMBA1001109//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//6.7e-37:102:82
//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1001121//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.036:49:46//HOMO
SAPIENS (HUMAN).//P08547

F-HEMBA1001122

F-HEMBA1001123

F-HEMBA1001133//HYPOTHETICAL 9.4 KD PROTEIN (ORF2).//0.86:29:41//FELINE
IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO) (FIV), AND FELINE IMMUNODEFIC
IENCY VIRUS (ISOLATE PETALUMA) (FIV).//P19033

F-HEMBA1001137//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.0e
-22:103:52//HOMO SAPIENS (HUMAN).//P51523

F-HEMBA1001140//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.032:94:36//HOMO
SAPIENS (HUMAN).//P53420

F-HEMBA1001172

F-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//2.9e-78:179:79/
/RATTUS NORVEGICUS (RAT).//P51646

F-HEMBA1001197//MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35
C) (FRAGMENT).//0.051:96:32//CERCOCEBUS ATERRIMUS, AND MACACA SYLVANUS (
BARBARY APE).//Q95145

F-HEMBA1001208

F-HEMBA1001213

F-HEMBA1001226//PROTEASOME COMPONENT C8 (EC 3.4.99.46) (MACROPAIN SUBUNI
T C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8).//1.5e-08:24:91/
/HOMO SAPIENS (HUMAN).//P25788

F-HEMBA1001235//FIBRONECTIN (FN) (FRAGMENT).//0.76:50:38//ORYCTOLAGUS CU
NICULUS (RABBIT).//Q28749

F-HEMBA1001247//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00052:16
:81//VOLVOX CARTERI.//P21997

F-HEMBA1001257//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//1.6e-68:178
:77//RATTUS NORVEGICUS (RAT).//P70473

F-HEMBA1001265//MANNAN ENDO-1,4-BETA-MANNOSIDASE A PRECURSOR (EC 3.2.1.7
8) (BETA- MANNANASE A) (1,4-BETA-D-MANNAN MANNANOHYDROLASE A).//0.67:23:
60//PIROMYCES SP.//P55296

F-HEMBA1001281//HYPOTHETICAL 8.9 KD PROTEIN YCF34 (ORF76).//0.83:48:35//

PORPHYRA PURPUREA.//P51229
 F-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//1.3e-07
 :185:29//CAVIA PORCELLUS (GUINEA PIG).//Q60401
 F-HEMBA1001289//METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.//0.00018:15
 9:30//RATTUS NORVEGICUS (RAT).//P31422
 F-HEMBA1001294
 F-HEMBA1001299//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.3e-07:27:77/
 /HOMO SAPIENS (HUMAN).//P39195
 F-HEMBA1001302//45 KD CALCIUM-BINDING PROTEIN PRECURSOR (STROMAL CELL-DE
 RIVED FACTOR 4) (SDF-4).//3.3e-61:150:76//MUS MUSCULUS (MOUSE).//Q61112
 F-HEMBA1001303
 F-HEMBA1001310//HYPOTHETICAL PROTEIN KIAA0161.//2.7e-10:170:27//HOMO SAP
 IENS (HUMAN).//P50876
 F-HEMBA1001319
 F-HEMBA1001323
 F-HEMBA1001326//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REG
 ION.//1.1e-39:144:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601
 F-HEMBA1001327
 F-HEMBA1001330
 F-HEMBA1001351//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDIN
 G PROTEIN (VAP-33).//1.9e-37:155:46//APLYSIA CALIFORNICA (CALIFORNIA SEA
 HARE).//Q16943
 F-HEMBA1001361//RUBREDOXIN (RD).//0.95:44:29//ALCALIGENES EUTROPHUS.//P3
 1912
 F-HEMBA1001375//AEROLYSIN REGULATORY PROTEIN.//0.013:45:33//AEROMONAS SO
 BRIA.//P09165
 F-HEMBA1001377//SPERM PROTAMINE P1.//1.0:22:40//PLANIGALE MACULATA SINUA
 LIS (COMMON PLANIGALE).//018746
 F-HEMBA1001383//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.60:

37:29//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).
 //P12506
 F-HEMBA1001387//GTP-BINDING PROTEIN TC10.//6.6e-43:83:92//HOMO SAPIENS (HUMAN).//P17081
 F-HEMBA1001388//HYPOTHETICAL PROTEIN KIAA0136 (FRAGMENT).//0.00088:46:45
 //HOMO SAPIENS (HUMAN).//Q14149
 F-HEMBA1001391
 F-HEMBA1001398//CLOACIN (EC 3.1.-.-) (RIBONUCLEASE).//1.0:59:37//ESCHERICHIA COLI.//P00645
 F-HEMBA1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.2
 5:41:34//HOMO SAPIENS (HUMAN).//P22531
 F-HEMBA1001407//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4
 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.0e-09:129:40//
 HOMO SAPIENS (HUMAN).//P04280
 F-HEMBA1001411//HYPOTHETICAL 34.9 KD PROTEIN IN CYSJ-ENO INTERGENIC REGION (O313).//0.95:88:31//ESCHERICHIA COLI.//P55140
 F-HEMBA1001413//SOX-12 PROTEIN (FRAGMENT).//0.95:46:32//MUS MUSCULUS (MOUSE).//Q04890
 F-HEMBA1001415//HISTONE H5.//0.43:95:29//GALLUS GALLUS (CHICKEN).//P02259
 F-HEMBA1001432//LANTIBIOTIC NISIN A PRECURSOR.//0.77:46:32//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068
 F-HEMBA1001433//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.8e-09:132:31//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-HEMBA1001435//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-31:84:77//HOMO SAPIENS (HUMAN).//P39189
 F-HEMBA1001442
 F-HEMBA1001446//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.71:41:39//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734

F-HEMBA1001450//PROLINE-RICH PROTEIN LAS17.//0.13:127:27//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//Q12446

F-HEMBA1001454//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.57:38:47/
/HANSENULA WINGEI (YEAST).//P48882

F-HEMBA1001455//CHEMOTAXIS PROTEIN CHEA (EC 2.7.3.-).//0.98:124:25//BORR
ELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//Q44737

F-HEMBA1001463//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.8e-32:62:67/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1001476//NUCLEOPORIN NUP159 (NUCLEAR PORE PROTEIN NUP159).//6.8e-
09:252:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40477

F-HEMBA1001478

F-HEMBA1001497//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-33:105:72
//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1001510//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.3e-37:54:81/
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1001515//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-63:223:57//H
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1001517

F-HEMBA1001522//TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE.//0.78:150:22//CO
TURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P49437

F-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//1.6e-06:
130:29//CLOSTRIDIUM PASTEURIANUM.//P29166

F-HEMBA1001533//PROBABLE E5A PROTEIN.//0.73:35:37//HUMAN PAPILLOMAVIRUS
TYPE 6A.//Q84296

F-HEMBA1001557//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3' REGION.//1.5e-07:
99:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-HEMBA1001566//HYPOTHETICAL PROTEIN BB0692.//0.91:27:44//BORRELIA BURGD
ORFERI (LYME DISEASE SPIROCHETE).//051635

F-HEMBA1001569//SYNAPTOSOMAL VESICLE ASSOCIATED MEMBRANE PROTEIN 2

(VAMP-2).//2.2e-50:110:95//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE)
 .//P19065

F-HEMBA1001570//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.3e-33:107:72
 //HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001579//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-14:111:39//DRO
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-HEMBA1001581

F-HEMBA1001585

F-HEMBA1001589//PROBABLE DNA-BINDING PROTEIN (AGNOPROTEIN).//0.98:51:33/
 /HUMAN ADENOVIRUS TYPE 2.//P03263

F-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//3.0e-124:274:85//HOMO SAPI
 ENS (HUMAN).//Q14141

F-HEMBA1001608//RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA+)/DICARBOX
 YLATE COTRANSPORTER).//0.99:28:39//ORYCTOLAGUS CUNICULUS (RABBIT).//Q286
 15

F-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//4
 .3e-45:222:46//SPIRODELA POLYRRHIZA.//P42803

F-HEMBA1001635//FIBRILLARIN.//0.10:72:38//CAENORHABDITIS ELEGANS.//Q2205
 3

F-HEMBA1001636//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8C/8D.//0.75:38:47//H
 OMO SAPIENS (HUMAN).//Q09155

F-HEMBA1001640//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-06:80:41//
 HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1001647//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA
 FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.075:165:32//HOMO SAPIENS
 (HUMAN).//000268

F-HEMBA1001651//GOLGIN-95.//6.8e-05:141:24//HOMO SAPIENS (HUMAN).//Q0837
 9

F-HEMBA1001655//PROLINE-RICH PROTEIN LAS17.//0.19:97:30//SACCHAROMYCES C

EREVISIAE (BAKER'S YEAST).//Q12446

F-HEMBA1001658//TETRAHYDROMETHANOPTERIN S-METHYLTRANSFERASE 12 KD SUBUNIT
T (EC 2.1.1.86) (N5-METHYLTETRAHYDROMETHANOPTERIN--COENZYME M METHYLTRAN
SFERASE 12 KD SUBUNIT).//1.0:29:44//METHANOBACTERIUM THERMOAUTOTROPHICUM
(STRAIN MARBURG / DSM 2133).//Q50773

F-HEMBA1001661//CELLULOSE COMPLEMENTING PROTEIN.//0.35:87:33//ACETOBACTE
R XYLINUM (ACETOBACTER PASTEURIANUS).//P37697

F-HEMBA1001672//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//2.7e-10:216:35
//PLASMODIUM CYNOMOLGI (STRAIN BEROK).//P08672

F-HEMBA1001675//NODULIN 20 PRECURSOR (N-20).//0.98:36:44//GLYCINE MAX (S
OYBEAN).//P08960

F-HEMBA1001678//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.2e-13:62:64/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001681//HYPOTHETICAL 41.5 KD PROTEIN IN P6.5-VP48 INTERGENIC REG
ION (P40) (ORF3) (ORF102).//1.0:51:39//ORGYIA PSEUDOTSUGATA MULTICAPSID
POLYHEDROSIS VIRUS (OPMNPV).//P24653

F-HEMBA1001702//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.017:5
4:37//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-HEMBA1001709//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REG
ION.//0.59:109:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042

F-HEMBA1001711

F-HEMBA1001712//HYPOTHETICAL 6.9 KD PROTEIN IN 100 KD PROTEIN REGION.//0
.54:44:34//HUMAN ADENOVIRUS TYPE 41.//P23690

F-HEMBA1001714//ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR.//1.2e-19:60:7
5//RATTUS NORVEGICUS (RAT).//Q03344

F-HEMBA1001718//HYPOTHETICAL PROTEIN UL63.//1.0:54:37//HUMAN CYTOMEGALOV
IRUS (STRAIN AD169).//P16820

F-HEMBA1001723//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN
IN SIS1-MRPL2 INTERGENIC REGION.//5.1e-26:90:53//SACCHAROMYCES CEREVISIA

E (BAKER'S YEAST).//P41318

F-HEMBA1001731//HYPOTHETICAL 16.6 KD PROTEIN.//0.71:49:32//AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 52/70) (IBDV).//P25221

F-HEMBA1001734

F-HEMBA1001744//SCY1 PROTEIN.//2.1e-11:182:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009

F-HEMBA1001745//HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR.//1.0:36:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53116

F-HEMBA1001746//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.94:48:35//MYCOBACTERIUM LEPRAE.//P38388

F-HEMBA1001761

F-HEMBA1001781//ZINC FINGER PROTEIN 19 (ZINC FINGER PROTEIN KOX12) (FRAGMENT).//0.028:47:40//HOMO SAPIENS (HUMAN).//P17023

F-HEMBA1001784//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.00068:32:46//CAENORHABDITIS ELEGANS.//Q11116

F-HEMBA1001791//METALLOTHIONEIN (MT).//1.0:34:35//PLEURONECTES PLATESSA (PLAICE).//P07216

F-HEMBA1001800//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//1.5e-14:60:48//MUS MUSCULUS (MOUSE).//P16372

F-HEMBA1001803

F-HEMBA1001804//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//9.3e-17:56:57//ORYZA SATIVA (RICE).//P25074

F-HEMBA1001808//PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG (HU-ANTIGEN D).//0.75:97:31//RATTUS NORVEGICUS (RAT).//009032

F-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//4.5e-11:206:36//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-HEMBA1001815//60S RIBOSOMAL PROTEIN L37-B (YL27) (FRAGMENT).//0.34:30:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P05733

F-HEMBA1001819//ZINC FINGER PROTEIN 135.//2.6e-102:262:66//HOMO SAPIENS (HUMAN).//P52742

F-HEMBA1001820

F-HEMBA1001822//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).//1.2e-18:251:33//MUS MUSCULUS (MOUSE).//P42567

F-HEMBA1001824//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN). //4.7e-11:124:37//OVIS ARIES (SHEEP).//P26372

F-HEMBA1001835

F-HEMBA1001844//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-14:36:63/ /HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//2.7e-36:135:51//MUS MUSCULUS (MOUSE).//Q07230

F-HEMBA1001861

F-HEMBA1001864//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H).//1.0:31:38//ESCHERICHIA COLI.//P07965

F-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//9.7e-42:234:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332

F-HEMBA1001869//HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I. //5.3e-13:65:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10362

F-HEMBA1001888//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.85:62:37//STREPTOMYCES FRADIAE.//P26800

F-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.8e-20:250:29//RATTUS NORVEGICUS (RAT).//Q63342

F-HEMBA1001910//EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT).//0.94:44:38//CAE NORHABDITIS ELEGANS.//061955

F-HEMBA1001912//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.7e-07:53:62// HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1001913//GCN20 PROTEIN.//1.8e-21:68:60//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P43535

F-HEMBA1001915//KLEE PROTEIN (KCRB3 PROTEIN).//0.94:64:21//ESCHERICHIA C
OLI.//Q52280

F-HEMBA1001918

F-HEMBA1001921

F-HEMBA1001939//CHLOROPLAST 50S RIBOSOMAL PROTEIN L24.//1.0:47:31//ODONT
ELLA SINENSIS.//P49560

F-HEMBA1001940//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0017:31:77//H
OMO SAPIENS (HUMAN).//P39188

F-HEMBA1001942//HIBERNATION-ASSOCIATED PLASMA PROTEIN HP-27 PRECURSOR (H
IBERNATOR- SPECIFIC BLOOD COMPLEX, 27 KD SUBUNIT).//1.0:77:28//TAMIAS AS
IATICUS (CHIPMUNK).//Q06577

F-HEMBA1001945//HYPOTHETICAL 4.6 KD PROTEIN IN GP47-AGT INTERGENIC REGIO
N (ORF E).//1.0:35:37//BACTERIOPHAGE T4.//P32269

F-HEMBA1001950//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.43:18:44/
/DROSOPHILA YAKUBA (FRUIT FLY).//P03933

F-HEMBA1001960//HOMEBOX PROTEIN HOX-C5 (HOX-3D) (CP11).//0.17:12:66//HO
MO SAPIENS (HUMAN).//Q00444

F-HEMBA1001962//HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5' REGION.//1.0:30:36
//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53056

F-HEMBA1001964

F-HEMBA1001967//HYPOTHETICAL PROTEIN UL61.//0.027:111:36//HUMAN CYTOMEGA
LOVIRUS (STRAIN AD169).//P16818

F-HEMBA1001979

F-HEMBA1001987//HYPOTHETICAL 11.2 KD PROTEIN (ORF117).//1.0:83:32//ORGYI
A PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10356

F-HEMBA1001991//NEUROTOXIN 1 (TOXIN ATX-I).//0.99:31:45//ANEMONIA SULCAT
A (SNAKE-LOCKS SEA ANEMONE).//P01533

F-HEMBA1002003//GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-SPECIFIC (EC 1.2.1.12) (GAPDH).//5.5e-07:109:32//MUS MUSCULUS (MOUSE).//Q64467
F-HEMBA1002008
F-HEMBA1002018//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.83:66:33//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377
F-HEMBA1002022//INSULIN.//1.0:59:32//SQUALUS ACANTHIAS (SPINY DOGFISH).//P12704
F-HEMBA1002035//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//8.3e-15:64:40//HOMO SAPIENS (HUMAN).//Q92794
F-HEMBA1002039//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.0070:70:40//HOMO SAPIENS (HUMAN).//Q92558
F-HEMBA1002049//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-07:37:75//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002084
F-HEMBA1002092//SPT23 PROTEIN.//0.12:208:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35210
F-HEMBA1002100
F-HEMBA1002102//ANKYRIN.//1.4e-12:106:35//MUS MUSCULUS (MOUSE).//Q02357
F-HEMBA1002113//EARLY NODULIN 20 PRECURSOR (N-20).//0.073:155:32//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329
F-HEMBA1002119//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.85:22:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-HEMBA1002125//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].//0.35:111:33//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338
F-HEMBA1002139//HYPOTHETICAL 12.4 KD PROTEIN IN SEC17-QCR1 INTERGENIC REGION.//0.88:72:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38192
F-HEMBA1002144
F-HEMBA1002150//THROMBOMODULIN (FETOMODULIN) (TM) (FRAGMENT).//4.8e-10:65:46//BOS TAURUS (BOVINE).//P06579

F-HEMBA1002151//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.24:146:28/
/SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-HEMBA1002153//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0
.93:58:25//APIS MELLIFERA (HONEYBEE).//P34859

F-HEMBA1002160//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.1e-21:94:65/
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4e-5
1:180:56//SUS SCROFA (PIG).//P79293

F-HEMBA1002162//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.1e-40:102:75
//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1002166//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-13:133:45/
/HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002177//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.0014:153
:26//HOMO SAPIENS (HUMAN).//P52746

F-HEMBA1002185

F-HEMBA1002189//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.86:46:45//HO
MO SAPIENS (HUMAN).//P39194

F-HEMBA1002191//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.037:14:57//DROSO
PHILA MELANOGASTER (FRUIT FLY).//Q01644

F-HEMBA1002199

F-HEMBA1002204

F-HEMBA1002212//DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE
DSOR1 (EC 2.7.1.-) (DOWNSTREAM OF RAF) (MAPKK).//3.2e-13:201:30//DROSOP
HILA MELANOGASTER (FRUIT FLY).//Q24324

F-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.1e-62:14
7:84//MUS MUSCULUS (MOUSE).//P47226

F-HEMBA1002226//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-26:168:44/
/HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002229//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//6.8e-18:68:72

//HOMO SAPIENS (HUMAN).//P39190
 F-HEMBA1002237//EAMZP30-47 PROTEIN (FRAGMENT).//0.96:21:61//EIMERIA ACER
 VULINA.//P21959
 F-HEMBA1002241//METALLOTHIONEIN (MT).//0.95:25:48//PARACENTROTUS LIVIDUS
 (COMMON SEA URCHIN).//P80367
 F-HEMBA1002253//METALLOTHIONEIN-II (MT-II).//0.97:27:48//MESOCRICETUS AU
 RATUS (GOLDEN HAMSTER).//P17808
 F-HEMBA1002257
 F-HEMBA1002265//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.95:24:50//DROSOP
 HILA MELANOGASTER (FRUIT FLY).//Q01644
 F-HEMBA1002267//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.94:33:33//GALLUS
 GALLUS (CHICKEN).//Q90667
 F-HEMBA1002270
 F-HEMBA1002321//HYPOTHETICAL IMMUNITY REGION PROTEIN 14.//0.99:22:40//BA
 CTERIOPHAGE PHI-105.//P10437
 F-HEMBA1002328
 F-HEMBA1002337
 F-HEMBA1002341//P53-BINDING PROTEIN 53BP2 (FRAGMENT).//3.7e-55:109:96//M
 US MUSCULUS (MOUSE).//Q62415
 F-HEMBA1002348//PROBABLE E5 PROTEIN.//0.43:30:50//HUMAN PAPILLOMAVIRUS T
 YPE 35.//P27226
 F-HEMBA1002349
 F-HEMBA1002363//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.7e-105:278:71//XE
 NOPUS LAEVIS (AFRICAN CLAWED FROG).//P50533
 F-HEMBA1002381//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.3e-24:69:73//
 HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1002389//EARLY NODULIN 20 PRECURSOR (N-20).//0.16:110:31//MEDICAG
 O TRUNCATULA (BARREL MEDIC).//P93329
 F-HEMBA1002417//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)./

/2.6e-51:187:56//MUS MUSCULUS (MOUSE).//P39447
 F-HEMBA1002419//PROLINE-RICH PEPTIDE P-B.//1.0:18:61//HOMO SAPIENS (HUMAN).//P02814
 F-HEMBA1002430//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION.//0.042:41:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140
 F-HEMBA1002439//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.99:47:29//CALYPTROSPHAERA SPHAEROIDEA.//P41548
 F-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.1e-24:109:55//HOMO SAPIENS (HUMAN).//Q00994
 F-HEMBA1002460
 F-HEMBA1002462//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.00025:80:30//HOMO SAPIENS (HUMAN).//P81489
 F-HEMBA1002469//PUTATIVE TUMOR SUPPRESSOR LUCA15.//0.0012:110:33//HOMO SAPIENS (HUMAN).//P52756
 F-HEMBA1002475//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.37:106:33//MUS MUSCULUS (MOUSE).//P05143
 F-HEMBA1002477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-34:96:71//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1002486
 F-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//2.9e-31:110:39//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P48732
 F-HEMBA1002498//SFT2 PROTEIN.//1.0:54:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38166
 F-HEMBA1002503//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.0e-06:49:63//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1002508//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-22:169:44//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBA1002513//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//0.00017:79:35//CAENORHABDITIS ELEGANS.//Q20296

F-HEMBA1002515

F-HEMBA1002538//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//1.0:
53:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P81449

F-HEMBA1002542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.7e-32:96:75//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002547//AGRIN PRECURSOR.//2.5e-100:218:80//RATTUS NORVEGICUS (RA
T).//P25304

F-HEMBA1002552//HEP27 PROTEIN (PROTEIN D).//9.5e-12:29:82//HOMO SAPIENS
(HUMAN).//Q13268

F-HEMBA1002555//COLLAGEN ALPHA 1(III) CHAIN.//2.4e-15:207:36//BOS TAURUS
(BOVINE).//P04258

F-HEMBA1002558//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0:34:50//HOM
O SAPIENS (HUMAN).//P39193

F-HEMBA1002561//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-05:49:46//NY
CTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBA1002569//SINGLE-STRANDED DNA-BINDING PROTEIN P12.//0.97:60:33//BA
CTERIOPHAGE PRD1.//P17637

F-HEMBA1002583

F-HEMBA1002590//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-15:54:55//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002592//HISTIDINE-RICH PROTEIN.//0.99:39:28//PLASMODIUM FALCIPAR
UM (ISOLATE FCM17 / SENEGAL).//P14586

F-HEMBA1002609//SSM4 PROTEIN.//1.9e-12:135:29//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P40318

F-HEMBA1002621//CYTOCHROME B6-F COMPLEX 3.5 KD SUBUNIT (CYTOCHROME B6-F
COMPLEX SUBUNIT 6).//1.0:20:55//ZEA MAYS (MAIZE).//P19445

F-HEMBA1002624//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOP
ROTEIN).//0.0035:124:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-HEMBA1002628

F-HEMBA1002629//IMMEDIATE-EARLY PROTEIN IE180.//0.84:80:36//PSEUDORABIES
VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-HEMBA1002645//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-16:57:68/
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1002651

F-HEMBA1002659//CUTICLE COLLAGEN 2.//0.0077:77:38//CAENORHABDITIS ELEGAN
S.//P17656

F-HEMBA1002661//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.3e-89:116:72//H
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1002666//BETA CRYSTALLIN A4.//0.18:58:44//GALLUS GALLUS (CHICKEN)
.//P49152

F-HEMBA1002678

F-HEMBA1002679//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//5.7e-06:219:27//P
LASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816

F-HEMBA1002688//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.1e-0
7:198:32//NEPHILA CLAVIPES (ORB SPIDER).//P46804

F-HEMBA1002696//COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAG
EN) (LC COLLAGEN).//0.16:158:33//HOMO SAPIENS (HUMAN).//Q02388

F-HEMBA1002703//HYPOTHETICAL BHLF1 PROTEIN.//0.78:147:29//EPSTEIN-BARR V
IRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEMBA1002712//11.2 KD PROTEIN (ORF 103).//0.029:75:34//BACTERIOPHAGE P
F1.//P25133

F-HEMBA1002716//50S RIBOSOMAL PROTEIN L28.//1.0:44:27//BACILLUS SUBTILIS
.//P37807

F-HEMBA1002728//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.4e-18:56:75/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1002730//HYPOTHETICAL PROTEIN MJ0316.//0.097:84:35//METHANOCOCCUS
JANNASCHII.//Q57764

F-HEMBA1002742//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.97:26:50//

SUS SCROFA (PIG).//P27917
 F-HEMBA1002746//CALPHOTIN.//0.35:65:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02910
 F-HEMBA1002748//PLATELET GLYCOPROTEIN IB BETA CHAIN PRECURSOR (GP-IB BETA) (GPIBB).//1.0:74:32//MUS MUSCULUS (MOUSE).//P56400
 F-HEMBA1002750//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.0e-15:49:75//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1002768//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//0.00036:197:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09746
 F-HEMBA1002770//UTEROGLOBIN PRECURSOR (BLASTOKININ).//0.23:88:27//ORYCTOLAGUS CUNICULUS (RABBIT).//P02779
 F-HEMBA1002777//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.00018:67:43//MUS MUSCULUS (MOUSE).//P06798
 F-HEMBA1002779//HYPOTHETICAL 17.6 KD PROTEIN IN NPR1-RPS3 INTERGENIC REGION.//0.70:30:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53880
 F-HEMBA1002780//OLFACTORY RECEPTOR 3 (K10) (FRAGMENT).//1.0:31:45//MUS MUSCULUS (MOUSE).//Q60879
 F-HEMBA1002794//HMG-Y RELATED PROTEIN B (SB16B PROTEIN) (FRAGMENT).//0.0044:66:37//GLYCINE MAX (SOYBEAN).//Q10370
 F-HEMBA1002801
 F-HEMBA1002810//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.00033:116:31//CAENORHABDITIS ELEGANS.//Q09202
 F-HEMBA1002816//HYPOTHETICAL 47.1 KD PROTEIN C9G1.13C IN CHROMOSOME I.//1.0e-17:68:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14308
 F-HEMBA1002818//FIBULIN-2 PRECURSOR.//2.1e-27:92:44//MUS MUSCULUS (MOUSE).//P37889
 F-HEMBA1002826//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//0.28:46:34//BACTERIOPHAGE T4.//P16012
 F-HEMBA1002833

F-HEMBA1002850//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//
 METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//047493
 F-HEMBA1002863//PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I
 8.1 KD PROTEIN) (P30 PROTEIN) (PSI-E).//0.84:37:43//SYNECHOCYSTIS SP. (S
 TRAIN PCC 6803).//P12975
 F-HEMBA1002876//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.74:58:34//MUS MUSCULUS
 (MOUSE).//Q06666
 F-HEMBA1002886
 F-HEMBA1002896//HOMEODOMAIN PROTEIN HOX-B3 (HOX-2G) (HOX-2.7).//4.7e-05:84:
 35//HOMO SAPIENS (HUMAN).//P14651
 F-HEMBA1002921//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.21:
 42:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RF/HAT ISOLATE) (HIV-1).//P0
 5908
 F-HEMBA1002924//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.85:75:22//ARABIDOPSIS
 THALIANA (MOUSE-EAR CRESS).//Q42377
 F-HEMBA1002934//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.4e-31:92:72//
 HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1002935//GASTRULA ZINC FINGER PROTEIN XLCGF58.1 (FRAGMENT).//7.7e
 -06:187:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18730
 F-HEMBA1002937//SUPPRESSOR PROTEIN SRP40.//0.00031:150:24//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P32583
 F-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./
 /5.2e-25:225:33//HOMO SAPIENS (HUMAN).//P16157
 F-HEMBA1002944
 F-HEMBA1002951//TRICHOHYALIN.//0.0011:220:24//HOMO SAPIENS (HUMAN).//Q07
 283
 F-HEMBA1002954//PROBABLE E8 PROTEIN.//0.98:49:32//BOVINE PAPILLOMAVIRUS
 TYPE 4.//P08352
 F-HEMBA1002968//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)

.//0.93:41:34//DROSOPHILA SECHELLIA (FRUIT FLY).//018417
 F-HEMBA1002970//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.00010:35:62/
 /HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1002971//INSULIN.//1.0:31:35//HYDROLAGUS COLLIEI (SPOTTED RATFISH
) (PACIFIC RATFISH), AND CHIMAERA MONSTROSA (RABBIT FISH).//P09536
 F-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1
 .4.17) (DPDE4).//3.0e-29:63:100//RATTUS NORVEGICUS (RAT).//P14646
 F-HEMBA1002997//HYPOTHETICAL 106.5 KD PROTEIN IN CTT1-PRP31 INTERGENIC R
 EGION.//1.0e-08:211:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5325
 3
 F-HEMBA1002999//SUPPRESSOR PROTEIN SRP40.//0.026:175:23//SACCHAROMYCES C
 EREVISIAE (BAKER'S YEAST).//P32583
 F-HEMBA1003021//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-36:102:70
 //HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1003033//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.029:75:29//MY
 COBACTERIUM TUBERCULOSIS.//P71779
 F-HEMBA1003034//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//6.3e-23:144:46
 //HOMO SAPIENS (HUMAN).//P39192
 F-HEMBA1003035//HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC RE
 GION.//0.99:55:30//BACILLUS SUBTILIS.//P54457
 F-HEMBA1003037//DNA-BINDING PROTEIN INHIBITOR ID-4.//0.17:42:40//HOMO SA
 PIENS (HUMAN).//P47928
 F-HEMBA1003041//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)
 .//0.69:28:46//HOMO SAPIENS (HUMAN).//P30808
 F-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR
 (EC 3.4.24.64) (BETA-MPP) (P-52).//7.9e-124:253:96//HOMO SAPIENS (HUMAN
).//075439
 F-HEMBA1003064//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.
 25:263:22//TRYPANOSOMA BRUCEI BRUCEI.//P04540

F-HEMBA1003067//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//4.1e-05:189:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-HEMBA1003071//CUTICLE COLLAGEN 40.//6.0e-07:126:38//CAENORHABDITIS ELEGANS.//P34804

F-HEMBA1003077//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.4e-12:139:34//HOMO SAPIENS (HUMAN).//Q06828

F-HEMBA1003078//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] .//7.2e-05:60:40//MUS MUSCULUS (MOUSE).//P11369

F-HEMBA1003079//PROTEIN Q300.//0.0012:16:87//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1003083//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.3e-32:95:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003086

F-HEMBA1003096//PROTAMINE 1A (IRIDINE 1A).//0.36:20:40//SALMO IRIDEUS (RAINBOW TROUT).//P02328

F-HEMBA1003098//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-09:43:72//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003117//PUTATIVE CUTICLE COLLAGEN C09G5.5.//1.0:88:38//CAENORHABDITIS ELEGANS.//Q09456

F-HEMBA1003129//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.61:63:25//APIS MELLIFERA (HONEYBEE).//P34859

F-HEMBA1003133//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.48:79:37//HOMO SAPIENS (HUMAN).//P25067

F-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//3.6e-25:190:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

F-HEMBA1003142

F-HEMBA1003148//HYPOTHETICAL 56.4 KD PROTEIN IN RPL30-CWH41 INTERGENIC REGION PRECURSOR.//0.068:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53189

F-HEMBA1003166//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.8e-13:54:66//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1003175//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.015:147:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//2.6e-51:164:47//BACILLUS SUBTILIS.//035020

F-HEMBA1003197

F-HEMBA1003199//HOMEBOX PROTEIN HOX-A4 (HOX-1D) (HOX-1.4).//0.00049:83:38//HOMO SAPIENS (HUMAN).//Q00056

F-HEMBA1003202//SPERM PROTAMINE P1.//0.98:53:28//PLANIGALE GILESI (FLAT-SKULLED MARSUPIAL MOUSE).//018747

F-HEMBA1003204//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.2e-22:42:80//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003212//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.6e-18:74:71//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1003220//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-18:56:78//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003222//HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION.//0.0018:159:27//BACILLUS SUBTILIS.//P46327

F-HEMBA1003229//DIHYDRODIPICOLINATE SYNTHASE 1 PRECURSOR (EC 4.2.1.52) (DHDPS).//1.0:85:28//TRITICUM AESTIVUM (WHEAT).//P24846

F-HEMBA1003235//TROPOMYOSIN.//8.3e-07:109:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088

F-HEMBA1003250

F-HEMBA1003257//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.5e-07:27:74//OWENIA FUSIFORMIS.//P21260

F-HEMBA1003273

F-HEMBA1003276

F-HEMBA1003278

F-HEMBA1003281//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0053:116:36//GALL
US GALLUS (CHICKEN).//P17277

F-HEMBA1003286//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//0.9
6:37:35//SULFOLOBUS ACIDOCALDARIUS.//P39472

F-HEMBA1003291//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN
(EC 2.7.1.-) (AMPK ALPHA-2 CHAIN) (FRAGMENT).//3.3e-15:68:39//SUS SCROF
A (PIG).//Q28948

F-HEMBA1003296//PULMONARY SURFACTANT-ASSOCIATED PROTEIN B (SP-B) (6 KD P
ROTEIN) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)).//0.98:49
:28//BOS TAURUS (BOVINE).//P15781

F-HEMBA1003304//MITOCHONDRIAL RIBOSOMAL PROTEIN S19.//0.99:36:30//PROTOT
HECA WICKERHAMII.//P46750

F-HEMBA1003309//HYPOTHETICAL 7.9 KD PROTEIN.//0.69:54:37//VACCINIA VIRUS
(STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P04306

F-HEMBA1003314//MIXED LINEAGE KINASE 2 (EC 2.7.1.-) (FRAGMENT).//2.3e-06
:143:22//HOMO SAPIENS (HUMAN).//Q02779

F-HEMBA1003322//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-30:53:77/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003327

F-HEMBA1003328//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGME
NT).//0.53:21:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV
-1).//P04612

F-HEMBA1003330//LONG NEUROTOXIN 3 (TOXIN VN2).//1.0:26:34//DENDROASPIS P
OLYLEPIS POLYLEPIS (BLACK MAMBA).//P25667

F-HEMBA1003348//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.5e-09:56:66/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003369//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.00
42:97:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602

F-HEMBA1003370//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.0e-18:99:53//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003373

F-HEMBA1003376//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.7e-16:60:75/
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003380//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.8e-10:50:68//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003384

F-HEMBA1003395//PROBABLE E5 PROTEIN.//0.62:64:29//HUMAN PAPILLOMAVIRUS T
YPE 16.//P06927

F-HEMBA1003402//HYPOTHETICAL 12.0 KD PROTEIN IN TUB1-CPR3 INTERGENIC REG
ION PRECURSOR.//0.89:74:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q
04521

F-HEMBA1003403//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRA
GMENT).//0.0010:69:33//RATTUS NORVEGICUS (RAT).//P10164

F-HEMBA1003408//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//4.8e-06
:93:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968

F-HEMBA1003417//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHOND
ROCALCIN].//0.0021:140:34//MUS MUSCULUS (MOUSE).//P28481

F-HEMBA1003418//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI
NG FACTOR SRP75).//1.7e-14:188:33//HOMO SAPIENS (HUMAN).//Q08170

F-HEMBA1003433//DNA REPAIR PROTEIN XRS2.//1.0:88:35//SACCHAROMYCES CEREV
ISIAE (BAKER'S YEAST).//P33301

F-HEMBA1003447//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRA
GMENT).//0.0061:69:33//RATTUS NORVEGICUS (RAT).//P10164

F-HEMBA1003461//SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).//2.3e-0
9:239:33//NEPHILA CLAVIPES (ORB SPIDER).//P19837

F-HEMBA1003463//METALLOTHIONEIN-A (MTA) (FRAGMENT).//1.0:40:35//SPHAEREC
HINUS GRANULARIS (PURPLE SEA URCHIN).//Q26497

F-HEMBA1003480//FUSARIC ACID RESISTANCE PROTEIN FUSB.//0.0043:96:32//BUR
KHOLDERIA CEPACIA (PSEUDOMONAS CEPACIA).//P24127

F-HEMBA1003528//36.4 KD PROLINE-RICH PROTEIN.//6.4e-15:167:33//LYCOPERSI
CON ESCULENTUM (TOMATO).//Q00451

F-HEMBA1003531//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-18:56:78/
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.5e
-28:136:47//HOMO SAPIENS (HUMAN).//P00736

F-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//9.2e-105
:217:85//RATTUS NORVEGICUS (RAT).//P50480

F-HEMBA1003548

F-HEMBA1003555//HYPOTHETICAL 31.9 KD PROTEIN IN BET1-PAN1 INTERGENIC REG
ION.//8.7e-57:180:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40558

F-HEMBA1003556//HYPOTHETICAL 19.2 KD PROTEIN IN COX-REP INTERGENIC REGIO
N (ORF5) (ORF21).//0.53:97:25//BACTERIOPHAGE HP1.//P51706

F-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-
2 SUBUNIT (G GAMMA-I).//1.8e-32:71:100//BOS TAURUS (BOVINE).//P16874

F-HEMBA1003568//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//4.1e-19:1
26:31//HOMO SAPIENS (HUMAN).//P14373

F-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//3.9e-83:143:74//HOM
O SAPIENS (HUMAN).//Q13330

F-HEMBA1003571//HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D).//1.0:64:2
5//STAPHYLOCOCCUS AUREUS.//P03860

F-HEMBA1003579//CYTOTOXIN 1 (CYTOTOXIN V-II-1) (TOXIN V(II)1).//1.0:41:2
9//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01448

F-HEMBA1003581//TALIN.//3.7e-36:52:98//MUS MUSCULUS (MOUSE).//P26039

F-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//

1.6e-05:91:31//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P19682
 F-HEMBA1003595//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REG
 ION.//1.0:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182
 F-HEMBA1003597
 F-HEMBA1003598//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//4.9e-10:
 85:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333
 F-HEMBA1003615//PUTATIVE MINOR COAT PROTEIN (ORF43).//0.086:10:70//BACTE
 RIOPHAGE PHI-LF.//Q07482
 F-HEMBA1003617//HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I.//
 4.4e-13:58:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10169
 F-HEMBA1003621//LONG NEUROTOXIN 1 (NEUROTOXIN A).//0.096:40:37//OPHIOPHA
 GUS HANNAH (KING COBRA) (NAJA HANNAH).//P01387
 F-HEMBA1003622
 F-HEMBA1003630
 F-HEMBA1003637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-13:47:74//
 HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1003640//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.87:25:64//HO
 MO SAPIENS (HUMAN).//P39193
 F-HEMBA1003645//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN
 C14B1.4 IN CHROMOSOME III.//1.8e-10:157:26//CAENORHABDITIS ELEGANS.//Q17
 963
 F-HEMBA1003646//SERINE-ARGININE PROTEIN 55 (SRP55) (ENHANCER OF DEFORMED
) (52-KD BRACKETING PROTEIN) (B52 PROTEIN).//4.9e-05:207:27//DROSOPHILA
 MELANOGASTER (FRUIT FLY).//P26686
 F-HEMBA1003656
 F-HEMBA1003662//PROLINE-RICH PEPTIDE P-B.//0.57:17:52//HOMO SAPIENS (HUM
 AN).//P02814
 F-HEMBA1003667//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.0e-16:43:72/
 /HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003679

F-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//3.9e-08:137:27//CAENORHABDITIS ELEGANS.//P34629

F-HEMBA1003684//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//2.1e-20:127:40//MUS MUSCULUS (MOUSE).//Q60821

F-HEMBA1003690//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//3.0e-85:201:78//HOMO SAPIENS (HUMAN).//P56524

F-HEMBA1003692//CELL DIVISION CONTROL PROTEIN 1.//0.13:69:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40986

F-HEMBA1003711//CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E ANTIGEN).//0.021:153:26//HOMO SAPIENS (HUMAN).//P06731

F-HEMBA1003714//ABAECIN.//0.99:34:32//BOMBUS PASCUORUM.//P81463

F-HEMBA1003715

F-HEMBA1003720//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4e-34:155:56//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1003725//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-27:181:41//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1003729//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.0037:103:33//HOMO SAPIENS (HUMAN).//P23246

F-HEMBA1003733//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-54:210:58//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1003742//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.066:72:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-HEMBA1003758

F-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.5e-51:220:52//MUS MUSCULUS (MOUSE).//Q61221

F-HEMBA1003773

F-HEMBA1003783

F-HEMBA1003784

F-HEMBA1003799//SHORT NEUROTOXIN 1 (TOXIN AA C).//0.95:27:37//ACANTHOPHIS ANTARCTICUS (COMMON DEATH ADDER).//P01434

F-HEMBA1003803//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].//0.46:96:34//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338

F-HEMBA1003804//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.019:30:50//HOMO SAPIENS (HUMAN).//P30808

F-HEMBA1003805//HYPOTHETICAL 75.0 KD PROTEIN B0280.11 IN CHROMOSOME III.//1.8e-20:109:47//CAENORHABDITIS ELEGANS.//P42083

F-HEMBA1003807

F-HEMBA1003827//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.1e-09:23:78//OWENIA FUSIFORMIS.//P21260

F-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//2.0e-31:134:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484

F-HEMBA1003838//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.9e-22:39:76//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1003856

F-HEMBA1003864//HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION.//1.5e-15:194:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36151

F-HEMBA1003866//PROTEIN A39.//0.0027:72:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062

F-HEMBA1003879//80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80).//2.9e-16:22:100//HOMO SAPIENS (HUMAN).//Q09161

F-HEMBA1003880//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:39:38//FELIS SILVESTRIUS (CAT).//P48896

F-HEMBA1003885//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.5e-28:47:76//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1003893//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//1.7e-57:215:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5321

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F-HEMBA1003902

F-HEMBA1003908

F-HEMBA1003926//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.3e-10:60:63//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003937//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.1e-29:68:64/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003939//PROTEIN Q300.//0.0025:24:62//MUS MUSCULUS (MOUSE).//Q027
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F-HEMBA1003942//EXCITATORY INSECT TOXIN BJXTR-IT PRECURSOR (BJ-XTRIT).//
0.084:67:31//BUTHOTUS JUDAICUS (SCORPION) (HOTTENTOTTA JUDAICA).//P56637

F-HEMBA1003950//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGI
ON (071).//0.95:26:34//ESCHERICHIA COLI.//P46878

F-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAG
MENT).//2.5e-17:89:46//MUS MUSCULUS (MOUSE).//P16372

F-HEMBA1003958//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-23:43:76//HO
MO SAPIENS (HUMAN).//P08547

F-HEMBA1003959

F-HEMBA1003976//HYPOTHETICAL PROTEIN KIAA0076 (HA0936).//0.99:88:28//HOM
O SAPIENS (HUMAN).//Q14999

F-HEMBA1003978//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.9
8:19:57//HOMO SAPIENS (HUMAN).//P22531

F-HEMBA1003985//LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE)
(LYSRS) (FRAGMENT).//1.0:40:32//MYCOBACTERIUM LEPRAE.//P46861

F-HEMBA1003987//HYPOTHETICAL PROTEIN UL66.//0.27:65:33//HUMAN CYTOMEGALO
VIRUS (STRAIN AD169).//P16822

F-HEMBA1003989//MALE SPECIFIC SPERM PROTEIN MST84DB.//5.2e-05:64:40//DRO
SOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-HEMBA1004000//PROTEIN Q300.//0.00042:17:82//MUS MUSCULUS (MOUSE).//Q02

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F-HEMBA1004011//ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR (CG RP-I).//0.47:106:32//HOMO SAPIENS (HUMAN).//P06881

F-HEMBA1004012//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIP ID-BINDING PROTEIN).//0.96:36:33//PARAMECIUM TETRAURELIA.//P16001

F-HEMBA1004015//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III./ /0.00018:90:34//CAENORHABDITIS ELEGANS.//P41997

F-HEMBA1004024//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.1e-34:75:80/ /HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1004038

F-HEMBA1004042

F-HEMBA1004045//40S RIBOSOMAL PROTEIN S27A.//1.0:20:55//ASPARAGUS OFFICI NALIS (GARDEN ASPARAGUS).//P31753

F-HEMBA1004048//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3e-06:158:35//M US MUSCULUS (MOUSE).//P05143

F-HEMBA1004049//32 KD HEAT SHOCK PROTEIN (4-1 PROTEIN).//0.098:106:32//D ICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54658

F-HEMBA1004055//HYPOTHETICAL PROTEIN HI0258/259.//0.87:133:23//HAEMOPHIL US INFLUENZAE.//P43974

F-HEMBA1004056//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//3.3e-25:39:64 //HOMO SAPIENS (HUMAN).//P39191

F-HEMBA1004074//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.9e-08:35:68// HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004086

F-HEMBA1004097//IMMEDIATE-EARLY PROTEIN IE4 (IE68) (FRAGMENT).//0.71:95: 35//HERPES SIMPLEX VIRUS (TYPE 2).//P14379

F-HEMBA1004111//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-26:84:64// HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//2.8e-34:108:63//HOMO SAPIE

NS (HUMAN).//Q14141
 F-HEMBA1004132//HYPOTHETICAL PROTEIN HI1736.//1.0:44:34//HAEMOPHILUS INF
 LUENZAE.//P44300
 F-HEMBA1004133//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.89:21:57//MYCO
 BACTERIUM TUBERCULOSIS.//Q10826
 F-HEMBA1004138//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.016:39:4
 1//MEDICAGO SATIVA (ALFALFA).//P11728
 F-HEMBA1004143//CYTOCHROME C OXIDASE POLYPEPTIDE VIII PRECURSOR (EC 1.9.
 3.1).//0.93:34:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P04039
 F-HEMBA1004146//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.63:52:36//HOMO
 SAPIENS (HUMAN).//P02811
 F-HEMBA1004150//METALLOTHIONEIN-II (MT-II).//1.0:20:45//MUS MUSCULUS (MO
 USE).//P02798
 F-HEMBA1004164//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.0e-13:57:71/
 /HOMO SAPIENS (HUMAN).//P39195
 F-HEMBA1004168//V-TYPE SODIUM ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (NA(+
)- TRANSLOCATING ATPASE SUBUNIT F).//0.00035:90:34//ENTEROCOCCUS HIRAE./
 /P43437
 F-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//5.1e-1
 4:115:31//CAENORHABDITIS ELEGANS.//P34529
 F-HEMBA1004200
 F-HEMBA1004202//YPT1-RELATED PROTEIN 1.//2.5e-24:96:52//SCHIZOSACCHAROMY
 CES POMBE (FISSION YEAST).//P11620
 F-HEMBA1004203//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.2e-09:48:64/
 /HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1004207//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC RE
 GION (ORF70).//0.98:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
 F-HEMBA1004225//METALLOTHIONEIN-II.//1.0:30:33//CANDIDA GLABRATA (YEAST)
 (TORULOPSIS GLABRATA).//P15114

F-HEMBA1004227//PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KI
AA0015).//5.9e-06:109:33//HOMO SAPIENS (HUMAN).//P49593

F-HEMBA1004238//VERY HYPOTHETICAL XYLU PROTEIN.//0.98:39:38//ESCHERICHIA
COLI.//P05056

F-HEMBA1004241//SOX-13 PROTEIN (FRAGMENT).//0.66:36:38//MUS MUSCULUS (MO
USE).//Q04891

F-HEMBA1004246

F-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-
EARLY PROTEIN CL-6).//1.0e-43:98:84//RATTUS NORVEGICUS (RAT).//Q08755

F-HEMBA1004264//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.014:
160:28//NEPHILA CLAVIPES (ORB SPIDER).//P46804

F-HEMBA1004267//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.8e-52:56:83/
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1004272

F-HEMBA1004274//HYPOTHETICAL 13.0 KD PROTEIN F59B2.10 IN CHROMOSOME III.
//0.00084:33:54//CAENORHABDITIS ELEGANS.//P34485

F-HEMBA1004275//HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REG
ION.//9.3e-06:125:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40034

F-HEMBA1004276//BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN
BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP
105A).//3.7e-30:239:32//HOMO SAPIENS (HUMAN).//Q10567

F-HEMBA1004286//CUTICLE COLLAGEN 34.//0.0027:71:38//CAENORHABDITIS ELEGA
NS.//P34687

F-HEMBA1004289//PTR3 PROTEIN (SSY3 PROTEIN).//1.0:76:28//SACCHAROMYCES C
EREVISIAE (BAKER'S YEAST).//P43606

F-HEMBA1004295//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)
.//0.075:58:39//HOMO SAPIENS (HUMAN).//P30808

F-HEMBA1004306//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.020:132:30//ORG
YIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-HEMBA1004312//EARLY PROTEIN I73R.//0.99:65:32//AFRICAN SWINE FEVER VIR
US (STRAIN BA71V) (ASFV).//P27946

F-HEMBA1004321//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK1
0).//4.3e-43:133:44//MUS MUSCULUS (MOUSE).//Q61967

F-HEMBA1004323

F-HEMBA1004327//SMALL PROLINE-RICH PROTEIN 2-1.//0.027:48:43//HOMO SAPIE
NS (HUMAN).//P35326

F-HEMBA1004330//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1).//0.46:70:34//HOM
O SAPIENS (HUMAN).//Q05925

F-HEMBA1004334//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.7e-05:83:34//HO
MO SAPIENS (HUMAN).//P08547

F-HEMBA1004335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.0e-24:41:80/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1004341//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.8e-06:148:35//M
US MUSCULUS (MOUSE).//P05143

F-HEMBA1004353//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.2e-29:57:80/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1004354//CHL1 PROTEIN.//0.017:40:40//SACCHAROMYCES CEREVISIAE (BA
KER'S YEAST).//P22516

F-HEMBA1004356

F-HEMBA1004366//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00045:49:46//HO
MO SAPIENS (HUMAN).//P08547

F-HEMBA1004372//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME
I.//1.0:125:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263

F-HEMBA1004389//HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC RE
GION.//0.76:170:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04893

F-HEMBA1004394

F-HEMBA1004396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.2e-10:72:51//HO
MO SAPIENS (HUMAN).//P08547

F-HEMBA1004405

F-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPI
ASE) (ROTAMASE) (CYCLOPHILIN-10).//2.7e-29:146:48//CAENORHABDITIS ELEGAN
S.//P52017

F-HEMBA1004429//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//0.0019:47:59/
/HOMO SAPIENS (HUMAN).//P39191

F-HEMBA1004433//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-20:47:68/
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1004460//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.2e-64:134:69
//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1004461//METALLOTHIONEIN-LIKE PROTEIN 1.//1.0:39:35//PISUM SATIVU
M (GARDEN PEA).//P20830

F-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INT
ERACTING PROTEIN).//9.7e-43:101:48//MUS MUSCULUS (MOUSE).//Q61221

F-HEMBA1004482//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34).//1.0:41:36//CANDID
A GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P05040

F-HEMBA1004499//TUBULIN BETA CHAIN.//0.00021:55:36//CAENORHABDITIS ELEGA
NS.//P52275

F-HEMBA1004502

F-HEMBA1004506//HYPOTHETICAL PROTEIN ORF-1137.//5.3e-11:119:35//MUS MUSC
ULUS (MOUSE).//P11260

F-HEMBA1004507//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP.62) (SF3A66).//0.
00072:90:37//HOMO SAPIENS (HUMAN).//Q15428

F-HEMBA1004509//HYPOTHETICAL 52.2 KD PROTEIN IN MPRI-GCN20 INTERGENIC RE
GION.//6.3e-28:169:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43589

F-HEMBA1004534//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE F
ILAMIN) (FILAMIN 1).//1.3e-80:226:66//HOMO SAPIENS (HUMAN).//P21333

F-HEMBA1004538//HYPOTHETICAL PROTEIN MJ0764.//0.96:28:35//METHANOCOCCUS
JANNASCHII.//Q58174

F-HEMBA1004542//METALLOTHIONEIN (MT).//0.78:36:41//GADUS MORHUA (ATLANTIC COD).//P51902

F-HEMBA1004554

F-HEMBA1004560//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//4.2e-15:56:69//HOMO SAPIENS (HUMAN).//Q92556

F-HEMBA1004573//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.65:31:58//PLASMODIUM BERGHEI.//P06915

F-HEMBA1004577//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.9e-08:35:80//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1004586//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.6e-08:64:54//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1004596//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (HNRNP C) (HNRNP CORE PROTEIN C) (FRAGMENT).//0.00057:88:31//RATTUS NORVEGICUS (RAT).//P17132

F-HEMBA1004604//COLLAGEN ALPHA 2(XI) CHAIN PRECURSOR (FRAGMENT).//0.045:37:45//MUS MUSCULUS (MOUSE).//Q64739

F-HEMBA1004610//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.3e-11:73:54//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004617

F-HEMBA1004629

F-HEMBA1004631//HYPOTHETICAL 7.8 KD PROTEIN IN WAPA-LICT INTERGENIC REGION.//1.0:36:38//BACILLUS SUBTILIS.//P42303

F-HEMBA1004632//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING 8.0 KD POLYPEPTIDE).//0.86:48:35//SYNECHOCOCCUS ELONGATUS NAEGELI.//P20453

F-HEMBA1004637//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.7e-32:159:42//CAENORHABDITIS ELEGANS.//P34535

F-HEMBA1004638//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.8e-06:50:46//OWENIA FUSIFORMIS.//P21260

F-HEMBA1004666//TOXIN S6C4.//1.0:36:30//DENDROASPIS JAMESONI KAIMOSAE (E
ASTERN JAMESON' S MAMBA).//P25682

F-HEMBA1004669//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI
NG FACTOR SRP75).//1.6e-12:105:42//HOMO SAPIENS (HUMAN).//Q08170

F-HEMBA1004670//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.5e-06:62:45//
HOMO SAPIENS (HUMAN).//P02452

F-HEMBA1004672//HYPOTHETICAL PROTEIN MJ0437.//0.95:37:29//METHANOCOCCUS
JANNASCHII.//Q57879

F-HEMBA1004693//MYOSIN HEAVY CHAIN; NONMUSCLE TYPE B (CELLULAR MYOSIN HE
AVY CHAIN, TYPE B) (NMMHC-B).//0.00035:217:23//HOMO SAPIENS (HUMAN).//P3
5580

F-HEMBA1004697//IMMUNOGLOBULIN G BINDING PROTEIN H PRECURSOR (PROTEIN H)
.//0.058:118:30//STREPTOCOCCUS PYOGENES.//P50470

F-HEMBA1004705//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.8e-09:43:72//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004709//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.8e-18:50:84/
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1004711//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2).//0
.0027:148:30//HOMO SAPIENS (HUMAN).//O00321

F-HEMBA1004725//CUTICLE COLLAGEN 2.//0.0051:41:41//CAENORHABDITIS ELEGAN
S.//P17656

F-HEMBA1004730//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:210:37//H
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1004733//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-07:50:62//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBI
QUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9e-39:143
:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743

F-HEMBA1004736//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.1e-60:210:61//H

OMO SAPIENS (HUMAN).//P08547
 F-HEMBA1004748
 F-HEMBA1004751//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.8e-20:88:63//
 HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1004752//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.
 0043:126:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-HEMBA1004753//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.8e-28:47:78/
 /HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1004756//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REG
 ION.//0.22:77:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981
 F-HEMBA1004758
 F-HEMBA1004763//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.1e-06:5
 8:43//OWENIA FUSIFORMIS.//P21260
 F-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:298:53//H
 OMO SAPIENS (HUMAN).//P08547
 F-HEMBA1004770
 F-HEMBA1004771
 F-HEMBA1004776//GRANULIN 1.//0.78:28:42//CYPRINUS CARPIO (COMMON CARP)./
 /P81013
 F-HEMBA1004778
 F-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//6.9e-20:74:63//HOMO SAPIE
 NS (HUMAN).//P50851
 F-HEMBA1004803//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:58:86//HO
 MO SAPIENS (HUMAN).//P08547
 F-HEMBA1004806//HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGENIC RE
 GION (ORF182).//0.72:75:33//CYANOPHORA PARADOXA.//P48324
 F-HEMBA1004807
 F-HEMBA1004816
 F-HEMBA1004820//HEMOLYMPH TRYPSIN INHIBITOR A (BPI-TYPE) (FRAGMENT).//1.

0:50:38//MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).//P26226
 F-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.0e
 -76:171:91//CANIS FAMILIARIS (DOG).//Q00004
 F-HEMBA1004850//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.0e-05:64:43/
 /BOS TAURUS (BOVINE).//P25508
 F-HEMBA1004863//TOXIN C13S1C1 PRECURSOR.//0.38:52:30//DENDROASPIS ANGUST
 ICEPS (EASTERN GREEN MAMBA).//P18329
 F-HEMBA1004864//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGME
 NT).//0.89:24:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV
 -1).//P04612
 F-HEMBA1004865
 F-HEMBA1004880
 F-HEMBA1004889//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.
 66:23:47//HOMO SAPIENS (HUMAN).//P22532
 F-HEMBA1004900
 F-HEMBA1004909
 F-HEMBA1004918//CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 (FRAGMENT).//0.56:3
 7:32//SPINACIA OLERACEA (SPINACH).//P09597
 F-HEMBA1004923//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.5e-24:44:68//
 HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1004929//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.97:39:38/
 /STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997
 F-HEMBA1004930//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.6e-15:64:59//HO
 MO SAPIENS (HUMAN).//P08547
 F-HEMBA1004933//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.34:58:4
 1//HOMO SAPIENS (HUMAN).//P50552
 F-HEMBA1004934
 F-HEMBA1004944
 F-HEMBA1004954//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//0.

58:78:30//PARAMECIUM TETRAURELIA.//P15579
 F-HEMBA1004956//HYPOTHETICAL 18.8 KD PROTEIN (ORF4).//0.98:57:31//PARAMECIUM TETRAURELIA.//P15605
 F-HEMBA1004960//HYPOTHETICAL 12.6 KD PROTEIN (ORFJ) (RETRON EC67).//1.0:58:27//ESCHERICHIA COLI.//P21324
 F-HEMBA1004972
 F-HEMBA1004973//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:55:30//HOMO SAPIENS (HUMAN).//P22531
 F-HEMBA1004977
 F-HEMBA1004978
 F-HEMBA1004980//MOTILIN PRECURSOR.//0.088:79:31//MACACA MULATTA (RHESUS MACAQUE).//018811
 F-HEMBA1004983//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES).//0.87:51:31//BUCHNERA APHIDICOLA.//Q59176
 F-HEMBA1004995//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2).//0.17:52:40//HOMO SAPIENS (HUMAN).//Q02080
 F-HEMBA1005008//METALLOTHIONEIN (MT).//1.0:52:32//CRASSOSTREA VIRGINICA (EASTERN OYSTER).//P23038
 F-HEMBA1005009//ACTIN.//3.5e-27:171:38//CANDIDA ALBICANS (YEAST).//P14235
 F-HEMBA1005019//HYPOTHETICAL PROTEIN HI1222.//0.13:58:31//HAEMOPHILUS INFLUENZAE.//P44129
 F-HEMBA1005029//P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).//0.76:72:31//GALLUS GALLUS (CHICKEN).//P32250
 F-HEMBA1005035//HOMEBOX PROTEIN HB9.//0.0086:60:40//HOMO SAPIENS (HUMAN).//P50219
 F-HEMBA1005039//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.47:49:32//HOMO SAPIENS (HUMAN).//P22532

F-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//1.5e-19:39:100//MUS MUSCULUS (MOUSE).//P35290

F-HEMBA1005050//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.074:34:44//BOS TAURUS (BOVINE).//P25508

F-HEMBA1005062

F-HEMBA1005066//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-44:126:65//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005075//SUPPRESSOR PROTEIN SRP40.//0.35:96:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1005079//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//3.6e-20:75:64//HOMO SAPIENS (HUMAN).//P39191

F-HEMBA1005083//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.00015:72:34//BOS TAURUS (BOVINE).//P25508

F-HEMBA1005101//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1).//4.8e-10:176:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48809

F-HEMBA1005113

F-HEMBA1005123//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-24:99:60//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005133//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.11:22:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

F-HEMBA1005149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.7e-16:59:71//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005152//GENOME POLYPROTEIN 2 [CONTAINS: HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 70 KD PROTEIN].//1.0:77:27//BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1) (BAYMV).//Q01207

F-HEMBA1005159//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.40:53:33//APIS MELLIFERA (HONEYBEE).//P34859

F-HEMBA1005185//MYOSIN IB HEAVY CHAIN.//0.011:58:48//DICTYOSTELIUM DISCOMIDEUM (SLIME MOLD).//P34092

F-HEMBA1005201//HYPOTHETICAL 56.6 KD PROTEIN C16C9.03 IN CHROMOSOME I.//
 3.9e-67:241:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09817
 F-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.8e
 -124:257:95//CANIS FAMILIARIS (DOG).//Q00004
 F-HEMBA1005206//CUTICLE COLLAGEN 1.//0.010:118:33//CAENORHABDITIS ELEGAN
 S.//P08124
 F-HEMBA1005219//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.99:85:40//HOMO
 SAPIENS (HUMAN).//P23246
 F-HEMBA1005223//HYPOTHETICAL GENE 1.05 PROTEIN.//0.31:75:28//BACTERIOPHA
 GE T3.//P07715
 F-HEMBA1005232//HYPOTHETICAL 7.8 KD PROTEIN.//0.99:48:29//VACCINIA VIRUS
 (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P20544
 F-HEMBA1005241//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-28:138:55
 //HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1005244//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0
 14:39:41//HOMO SAPIENS (HUMAN).//P22531
 F-HEMBA1005251//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.55:15:46/
 /DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362
 F-HEMBA1005252//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.0
 88:33:42//ZEA MAYS (MAIZE).//P43401
 F-HEMBA1005274
 F-HEMBA1005275//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.96:42:45//HOM
 O SAPIENS (HUMAN).//P39188
 F-HEMBA1005293//PROBABLE COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BE
 TA'-COP).//0.55:98:30//CAENORHABDITIS ELEGANS.//Q20168
 F-HEMBA1005296//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.095:75:34//HO
 MO SAPIENS (HUMAN).//Q02817
 F-HEMBA1005304//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.4e-33:103:74
 //HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1005311//PERIOD CLOCK PROTEIN (FRAGMENT).//0.99:45:31//DROSOPHILA
SALTANS (FRUIT FLY).//Q04536

F-HEMBA1005314//HYPOTHETICAL 6.3 KD PROTEIN T19C3.3 IN CHROMOSOME III.//
0.98:30:30//CAENORHABDITIS ELEGANS.//Q10009

F-HEMBA1005315//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-05:35:51//HO
MO SAPIENS (HUMAN).//P08547

F-HEMBA1005318//OLFACTORY RECEPTOR-LIKE PROTEIN COR8 (FRAGMENT).//0.57:4
4:38//GALLUS GALLUS (CHICKEN).//Q98913

F-HEMBA1005331//IMMEDIATE-EARLY PROTEIN IE180.//0.57:106:33//PSEUDORABIE
S VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-HEMBA1005338//CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).//1.8e-5
5:199:59//GALLUS GALLUS (CHICKEN).//P05099

F-HEMBA1005353//CHLOROPLAST 30S RIBOSOMAL PROTEIN S17.//0.88:33:36//PORP
HYRA PURPUREA.//P51305

F-HEMBA1005359//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.1e
-68:255:48//HOMO SAPIENS (HUMAN).//P51522

F-HEMBA1005367//ALPHA-AMYLASE INHIBITOR AAI.//1.0:25:40//AMARANTHUS HYPO
CHONDRIACUS (PRINCE'S FEATHER).//P80403

F-HEMBA1005372

F-HEMBA1005374//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:92:75/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005382//APOLIPOPROTEIN C-II (APO-CII).//0.99:39:33//BOS TAURUS (
BOVINE).//P19034

F-HEMBA1005389//HYPOTHETICAL 70.0 KD PROTEIN IN DNAK 3' REGION (ORF4).//0
.82:164:31//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//
P42377

F-HEMBA1005394//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION
.//0.98:44:38//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV
).//P41703

F-HEMBA1005403//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.066:64:29
//MUS MUSCULUS (MOUSE).//P07978

F-HEMBA1005408//50S RIBOSOMAL PROTEIN L33.//0.77:32:25//BACILLUS SUBTILI
S.//Q06798

F-HEMBA1005410//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR
ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] .//0.0065:38:52//MUS MUSCULUS (M
OUSE).//P11369

F-HEMBA1005411//TOXIN S4C8.//0.16:46:28//DENDROASPIS JAMESONI KAIMOSAE (E
ASTERN JAMESON'S MAMBA).//P25683

F-HEMBA1005423//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-D
EPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//4.3e-09:29:96//HOMO SAPIENS
(HUMAN).//P42773

F-HEMBA1005426//TOXIN C10S2C2.//0.99:49:34//DENDROASPIS ANGUSTICEPS (EAS
TERN GREEN MAMBA).//P25684

F-HEMBA1005443//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:78:60//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005447//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:57:31/
/DASYPUS NOVMCINCTUS (NINE-BANDED ARMADILLO).//021329

F-HEMBA1005468//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRA
GMENTS).//0.68:41:31//ARTEMIA SALINA (BRINE SHRIMP).//P19040

F-HEMBA1005469

F-HEMBA1005472//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-39:142:70//H
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1005474//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.8e-10:44:68/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005475//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD
) (SNRP70).//9.2e-14:179:33//HOMO SAPIENS (HUMAN).//P08621

F-HEMBA1005497

F-HEMBA1005500//60S RIBOSOMAL PROTEIN L37.//0.11:53:33//SCHISTOSOMA MANS

ONI (BLOOD FLUKE).//044125
 F-HEMBA1005506
 F-HEMBA1005508
 F-HEMBA1005511//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.5e-30:92:73/
 /HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//2.0e-39
 :95:61//DROSOPHILA MELANOGASTER (FRUIT FLY).//002193
 F-HEMBA1005517//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.1e-06:56:44//MUS
 MUSCULUS (MOUSE).//P05142
 F-HEMBA1005518//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//5.8e-05:192:33//
 BOS TAURUS (BOVINE).//P02453
 F-HEMBA1005520//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.0e-18:87:57//
 HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1005526//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//5.1e-22:77:54
 //HOMO SAPIENS (HUMAN).//P39191
 F-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.2e-81:157:98//MUS MU
 SCULUS (MOUSE).//Q60809
 F-HEMBA1005530//POLLEN ALLERGEN AMB P 5-A PRECURSOR (AMB P V-A).//0.98:1
 9:47//AMBROSIA PSILOSTACHYA (WESTERN RAGWEED).//P43174
 F-HEMBA1005548//TRANSCRIPTION FACTOR MAF1.//1.4e-72:137:97//RATTUS NORVE
 GICUS (RAT).//P54842
 F-HEMBA1005552//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.7e-29:47:78/
 /HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1005558//HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGENIC RE
 GION.//1.6e-20:202:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04272
 F-HEMBA1005568
 F-HEMBA1005570//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3).//1.
 0:80:31//CAENORHABDITIS ELEGANS.//P24885
 F-HEMBA1005576//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//8.5e-58:152:75//HO

MO SAPIENS (HUMAN).//P51805
 F-HEMBA1005577//KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A.//0.98:57:36//O
 VIS ARIES (SHEEP).//P02438
 F-HEMBA1005581//SLIT PROTEIN PRECURSOR.//1.1e-62:254:41//DROSOPHILA MELA
 NOGASTER (FRUIT FLY).//P24014
 F-HEMBA1005582//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYP
 EPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.0091:189:29//RATTUS NORVEGIC
 US (RAT).//P28023
 F-HEMBA1005583//HYPOTHETICAL 41.2 KD PROTEIN IN CPS REGION (ORF7).//0.83
 :119:23//KLEBSIELLA PNEUMONIAE.//Q48453
 F-HEMBA1005588//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-17:108:53/
 /HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1005593//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.
 23:24:54//HOMO SAPIENS (HUMAN).//P22532
 F-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).//2.7e-39:257:39//D
 ICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34036
 F-HEMBA1005606
 F-HEMBA1005609//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.2e-20:27:96/
 /HOMO SAPIENS (HUMAN).//P39192
 F-HEMBA1005616//LATE CONTROL GENE B PROTEIN (GPB).//0.48:51:33//BACTERIO
 PHAGE 186.//P08711
 F-HEMBA1005621//MITOTIC MAD2 PROTEIN.//1.2e-06:137:32//SACCHAROMYCES CER
 EVISIAE (BAKER'S YEAST).//P40958
 F-HEMBA1005627//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3' REGION.//0.18:100
 :32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898
 F-HEMBA1005631
 F-HEMBA1005632//HYPOTHETICAL 7.4 KD PROTEIN.//0.32:59:32//VACCINIA VIRUS
 (STRAIN WR).//P04309
 F-HEMBA1005634//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-14:93:58//

HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005666//HYPOTHETICAL PROTEIN KIAA0129.//2.1e-05:126:25//HOMO SAPIENS (HUMAN).//Q14142

F-HEMBA1005670

F-HEMBA1005679//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.2e-08:40:72//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005680//SMALL PROLINE-RICH PROTEIN 2-1.//0.015:19:47//HOMO SAPIENS (HUMAN).//P35326

F-HEMBA1005685

F-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//4.2e-38:98:81//HOMO SAPIENS (HUMAN).//Q15768

F-HEMBA1005705//PROTEIN Q300.//0.11:23:56//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1005717

F-HEMBA1005732//BACTENECIN 7 PRECURSOR (BAC7).//0.22:55:41//OVIS ARIES (SHEEP).//P50415

F-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//4.5e-18:167:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25296

F-HEMBA1005746

F-HEMBA1005755//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.4e-30:69:65//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005765//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.8e-19:60:63//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005780//METALLOTHIONEIN-I (MT-1).//1.0:31:38//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786

F-HEMBA1005813

F-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//1.0e-23:200:31//G

ALLUS GALLUS (CHICKEN).//P00789
 F-HEMBA1005822//PROTEIN Q300.//0.0016:21:80//MUS MUSCULUS (MOUSE).//Q027
 22
 F-HEMBA1005829//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.6e-33:96:73/
 /HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1005834//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-22:103:46//N
 YCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-HEMBA1005852//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//8.8e-06:95:35//MU
 S MUSCULUS (MOUSE).//P05143
 F-HEMBA1005853//HYPOTHETICAL PROTEIN MJ0647.//0.39:28:39//METHANOCOCCUS
 JANNASCHII.//Q58063
 F-HEMBA1005884
 F-HEMBA1005891//HYPOTHETICAL PROTEIN MTH137.//0.95:51:27//METHANOBACTERI
 UM THERMOAUTOTROPHICUM.//026240
 F-HEMBA1005894//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-29:81:71/
 /HOMO SAPIENS (HUMAN).//P39195
 F-HEMBA1005909//HYPOTHETICAL 8.2 KD PROTEIN B0353.1 IN CHROMOSOME III.//
 0.98:19:52//CAENORHABDITIS ELEGANS.//Q10958
 F-HEMBA1005911//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-27:86:70//
 HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1005921//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-38:99:81/
 /HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.3e
 -17:76:51//HOMO SAPIENS (HUMAN).//P51522
 F-HEMBA1005934//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.024:54:40//H
 OMO SAPIENS (HUMAN).//P39189
 F-HEMBA1005962
 F-HEMBA1005963//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).
 //1.7e-32:89:79//BOS TAURUS (BOVINE).//P53620

F-HEMBA1005990//HYPOTHETICAL BHLF1 PROTEIN.//3.0e-09:180:36//EPSTEIN-BAR
R VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEMBA1005991//HYPOTHETICAL PROTEIN KIAA0032.//3.0e-17:107:43//HOMO SAP
PIENS (HUMAN).//Q15034

F-HEMBA1005999

F-HEMBA1006002

F-HEMBA1006005//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1
B).//0.0017:45:44//MUS MUSCULUS (MOUSE).//Q62267

F-HEMBA1006031//BASIC PROLINE-RICH PEPTIDE IB-1.//0.00016:84:39//HOMO SA
PIENS (HUMAN).//P04281

F-HEMBA1006035//DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70).//0.43:10
0:27//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q55154

F-HEMBA1006036//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.2e-64:150:74
//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1006042

F-HEMBA1006067//METALLOTHIONEIN A (MT-A).//0.86:34:41//THERMARCUS CERBER
US.//P52721

F-HEMBA1006081

F-HEMBA1006090//SODIUM/GLUCOSE COTRANSPORTER 3 (NA+)/GLUCOSE COTRANSPOR
TER 3) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.87:35:54//SUS SCR
OFA (PIG).//P31636

F-HEMBA1006091//EARLY NODULIN 20 PRECURSOR (N-20).//0.027:87:32//MEDICAG
O TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBA1006100//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.1e-09:58:60/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1006108//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC RE
GION.//5.6e-16:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867

F-HEMBA1006121//HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1).
//3.4e-05:106:37//HOMO SAPIENS (HUMAN).//P47902

F-HEMBA1006124//50S RIBOSOMAL PROTEIN L33.//1.0:12:83//BACILLUS STEAROTH
ERMOPHILUS.//P23375

F-HEMBA1006130//SEL-10 PROTEIN.//7.7e-05:129:28//CAENORHABDITIS ELEGANS.
//Q93794

F-HEMBA1006138//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.8e-13:41:73/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1006142//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.3e-39:101:77
//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1006155//GENE 33 POLYPEPTIDE.//0.21:70:31//RATTUS NORVEGICUS (RAT
).//P05432

F-HEMBA1006158

F-HEMBA1006173//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3
.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT).//
0.017:20:95//HOMO SAPIENS (HUMAN).//P54829

F-HEMBA1006182//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.37:31:61//HOM
O SAPIENS (HUMAN).//P39188

F-HEMBA1006198//HOMEBOX PROTEIN HOX-B3 (HOX-2.7) (MH-23).//0.85:61:29//
MUS MUSCULUS (MOUSE).//P09026

F-HEMBA1006235//50S RIBOSOMAL PROTEIN L33.//1.0:26:38//AQUIFEX AEOLICUS.
//067756

F-HEMBA1006248//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.0041:64:37//DROS
OPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-HEMBA1006252//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR DE-3.//1.0:22:40//
DOLICHOS AXILLARIS (MACROTYLOMA AXILLARE).//P01057

F-HEMBA1006253//DISINTEGRIN ERISTICOPHIN (PLATELET AGGREGATION ACTIVATIO
N INHIBITOR).//0.95:19:47//ERISTOCOPHIS MACMAHONI (LEAF-NOSED VIPER).//P
22826

F-HEMBA1006259

F-HEMBA1006268//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.0e-05:32:65/

/HOMO SAPIENS (HUMAN).//P39192
 F-HEMBA1006272//RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 2).//4.8e-11
 2:248:78//HOMO SAPIENS (HUMAN).//P10264
 F-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A
 DENYLYLTRANSFERASE) (FRAGMENT).//2.5e-71:164:75//HOMO SAPIENS (HUMAN).//
 P51003
 F-HEMBA1006283//50S RIBOSOMAL PROTEIN L32.//0.81:27:44//THERMUS AQUATICU
 S (SUBSP. THERMOPHILUS).//P80339
 F-HEMBA1006284//CUTICLE COLLAGEN 2.//0.36:42:40//CAENORHABDITIS ELEGANS.
 //P17656
 F-HEMBA1006291//HYPOTHETICAL 43.3 KD PROTEIN IN EVGS-GLK INTERGENIC REGI
 ON.//2.4e-37:143:31//ESCHERICHIA COLI.//P76518
 F-HEMBA1006293//MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.//0.20:134
 :29//RATTUS NORVEGICUS (RAT).//Q63345
 F-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REG
 ION.//2.1e-43:187:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821
 F-HEMBA1006310//SIGNAL TRANSDUCER CD24 PRECURSOR (HEAT STABLE ANTIGEN) (HSA)
 (NECTADRIN).//0.71:46:39//RATTUS NORVEGICUS (RAT).//Q07490
 F-HEMBA1006328//RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48) (NUCLEOCAPSID
 PHOSPHOPROTEIN).//0.44:141:24//HUMAN PARAINFLUENZA 1 VIRUS (STRAIN CI-5
 /73).//P32531
 F-HEMBA1006334//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//0.98:26:
 46//ARCHAEOGLOBUS FULGIDUS.//028646
 F-HEMBA1006344//EZRIN (P81) (CYTOVILLIN) (VILLIN-2).//8.8e-08:91:36//MUS
 MUSCULUS (MOUSE).//P26040
 F-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//9.1e-48
 :149:50//DROSOPHILA MELANOGASTER (FRUIT FLY).//002193
 F-HEMBA1006349//METALLOTHIONEIN-LIKE PROTEIN 1.//0.015:59:33//CASUARINA
 GLAUCA (SWAMP OAK).//Q39511

F-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//6.8e-96:261
:66//HOMO SAPIENS (HUMAN).//P28160

F-HEMBA1006364//PUTATIVE ENDONUCLEASE C1F12.06C (EC 3.1.-.-).//0.97:60:3
5//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10348

F-HEMBA1006377//EARLY NODULIN 20 PRECURSOR (N-20).//0.00023:110:35//MEDI
CAGO TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBA1006380

F-HEMBA1006381//METALLOTHIONEIN-II.//1.0:26:38//CANDIDA GLABRATA (YEAST)
(TORULOPSIS GLABRATA).//P15114

F-HEMBA1006398//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.3e-26:123:52//H
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1006416

F-HEMBA1006419//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-24:102:50
//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1006421//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.1e-21:101:57/
/HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006424//HYPOTHETICAL PROTEIN IORF1.//0.85:55:30//BOVINE CORONAVI
RUS (STRAIN MEBUS), AND BOVINE CORONAVIRUS (STRAIN QUEBEC).//P22053

F-HEMBA1006426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-36:78:74/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1006438//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//1.0:38:36//GUILLAR
DIA THETA (CRYPTOMONAS PHI).//078421

F-HEMBA1006445//RAS-LIKE PROTEIN 3.//1.9e-06:40:47//RHIZOMUCOR RACEMOSUS
(MUCOR CIRCINELLOIDES F. LUSITANICUS).//P22280

F-HEMBA1006446

F-HEMBA1006461//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//4.1e-18:68:67/
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1006467

F-HEMBA1006471

F-HEMBA1006474//40 KD PROTEIN.//1.1e-37:231:38//BORNA DISEASE VIRUS (BDV).//Q01552

F-HEMBA1006483//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//6.1e-38:77:74//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1006485//HYPOTHETICAL 9.3 KD PROTEIN IN NAD3-NAD7 INTERGENIC REGION (ORF 79).//0.91:30:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38465

F-HEMBA1006486//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-12:78:51//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1006489//FUN34 PROTEIN.//0.94:58:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32907

F-HEMBA1006492//NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MWFE) (CI-MWFE).//0.87:44:36//HOMO SAPIENS (HUMAN).//O15239

F-HEMBA1006494//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//0.11:46:26//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLII).//P42711

F-HEMBA1006497

F-HEMBA1006502//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.15:26:73//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006507//DIAPHANOUS PROTEIN.//0.0055:129:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608

F-HEMBA1006521//3-OXOACYL- [ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL- ACYL CARRIER PROTEIN REDUCTASE).//1.1e-32:177:41//ESCHERICHIA COLI.//P25716

F-HEMBA1006530//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.052:84:26//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583

F-HEMBA1006535//INHIBITOR OF APOPTOSIS PROTEIN 1 (MIAP1) (MIAP-1).//6.6e-05:53:39//MUS MUSCULUS (MOUSE).//O08863

F-HEMBA1006540//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97

) (DISCS, LARGE HOMOLOG 1).//2.1e-07:206:23//RATTUS NORVEGICUS (RAT).//Q
62696

F-HEMBA1006546//PROBABLE E5 PROTEIN.//0.11:70:32//HUMAN PAPILLOMAVIRUS T
YPE 51.//P26553

F-HEMBA1006559//SUPPRESSOR PROTEIN SRP40.//0.015:221:20//SACCHAROMYCES C
EREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1006562//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//
1.5e-07:122:33//HOMO SAPIENS (HUMAN).//P10163

F-HEMBA1006566//CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (CDC2 HOMOLO
G EG1 PROTEIN KINASE).//0.63:53:37//XENOPUS LAEVIS (AFRICAN CLAWED FROG)
.//P23437

F-HEMBA1006569//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//4.4e-06:88:39//BO
S TAURUS (BOVINE).//P02465

F-HEMBA1006579

F-HEMBA1006583//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.011:61:40//MUS M
USCULUS (MOUSE).//P05142

F-HEMBA1006595//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.6e-34:93:77/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1006597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.9e-26:75:74/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1006612//SUPPRESSOR PROTEIN SRP40.//0.026:221:22//SACCHAROMYCES C
EREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1006617//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.6e-20:73:63//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006624//HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REG
ION.//2.6e-31:209:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40506

F-HEMBA1006631//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC R
EGION.//1.5e-15:131:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5333

F-HEMBA1006635

F-HEMBA1006639//POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN
1) (PABP 1).//2.2e-11:48:75//MUS MUSCULUS (MOUSE).//P29341

F-HEMBA1006643//LONG NEUROTOXIN CR1 PRECURSOR (KAPPA NEUROTOXIN).//0.28:
48:27//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P15817

F-HEMBA1006648//ZINC FINGER PROTEIN 12 (ZINC FINGER PROTEIN KOX3) (FRAGM
ENT).//0.26:17:47//HOMO SAPIENS (HUMAN).//P17014

F-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.4e-44:206:47//MUS MUSCULUS
(MOUSE).//P14148

F-HEMBA1006653

F-HEMBA1006659

F-HEMBA1006665//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.018:43:58//HOMO
SAPIENS (HUMAN).//P08547

F-HEMBA1006674//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA
FII-135) (TAFII135) (TAFII-130) (TAFII130).//2.9e-05:154:33//HOMO SAPIEN
S (HUMAN).//000268

F-HEMBA1006676//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//3.6e-09:5
2:51//OWENIA FUSIFORMIS.//P21260

F-HEMBA1006682

F-HEMBA1006695//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-06:35:65//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006696

F-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN
IN PMC1-TFG2 INTERGENIC REGION.//3.4e-19:104:45//SACCHAROMYCES CEREVISIA
E (BAKER'S YEAST).//P53196

F-HEMBA1006709//RETINOIC ACID RECEPTOR RXR-BETA.//0.24:111:36//HOMO SAPI
ENS (HUMAN).//P28702

F-HEMBA1006717

F-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHR

O1D) (FRAGMENT).//5.8e-09:111:40//HOMO SAPIENS (HUMAN).//Q01485
 F-HEMBA1006744//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.8e-32:84:78
 //HOMO SAPIENS (HUMAN).//P39191
 F-HEMBA1006754//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-75:220:62//H
 OMO SAPIENS (HUMAN).//P08547
 F-HEMBA1006758//VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (C
 ADHERIN-5) (7B4 ANTIGEN) (CD144 ANTIGEN).//0.024:110:29//HOMO SAPIENS (H
 UMAN).//P33151
 F-HEMBA1006767
 F-HEMBA1006779//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.67:19:42//LEISHM
 ANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940
 F-HEMBA1006780
 F-HEMBA1006789//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.056:98:30//MUS
 MUSCULUS (MOUSE).//P05143
 F-HEMBA1006795//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.9e-11:143:30//N
 YCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-HEMBA1006796//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.16:3
 8:42//MUS MUSCULUS (MOUSE).//P70315
 F-HEMBA1006807//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III.
 //4.4e-75:184:77//CAENORHABDITIS ELEGANS.//P34568
 F-HEMBA1006821//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.011:20:85//H
 OMO SAPIENS (HUMAN).//P39194
 F-HEMBA1006824//PROTEIN B11.//0.44:27:44//VACCINIA VIRUS (STRAIN WR).//Q
 01229
 F-HEMBA1006832//HYPOTHETICAL 34.6 KD PROTEIN C13G5.2 IN CHROMOSOME III./
 /1.0:46:36//CAENORHABDITIS ELEGANS.//P34327
 F-HEMBA1006849
 F-HEMBA1006865//ACROSIN INHIBITORS IIA AND IIB (BUSI-II).//1.0:41:31//BO
 S TAURUS (BOVINE).//P01001

F-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//3.7e-26:239:36//ORYCTOLAGUS
CUNICULUS (RABBIT).//P16258

F-HEMBA1006885//HYPOTHETICAL 27.2 KD PROTEIN F09E5.8 IN CHROMOSOME II.//
4.5e-38:185:43//CAENORHABDITIS ELEGANS.//P52057

F-HEMBA1006900

F-HEMBA1006914//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACT
ING PROTEIN 2).//5.2e-27:269:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST
) .//P52488

F-HEMBA1006921//CYTOTOXIN 3 (COMPONENT 3.20).//0.99:32:37//NAJA MELANOLE
UCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01473

F-HEMBA1006926//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN
) .//0.0024:148:33//RATTUS NORVEGICUS (RAT).//P54258

F-HEMBA1006929//HYPOTHETICAL PROTEIN MJ0525.//0.95:35:20//METHANOCOCCUS
JANNASCHII.//Q57945

F-HEMBA1006936//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSO
R (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C
) [CONTAINS: PEPTIDE P-C].//0.074:116:31//HOMO SAPIENS (HUMAN).//P02810

F-HEMBA1006938

F-HEMBA1006941//THIOREDOXIN H-TYPE 1 (TRX-H1).//2.1e-13:90:33//NICOTIANA
TABACUM (COMMON TOBACCO).//P29449

F-HEMBA1006949

F-HEMBA1006973//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.75:29:55//BO
S TAURUS (BOVINE).//P25508

F-HEMBA1006976//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIA
LYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERA
SE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4
) .//3.9e-108:117:95//HOMO SAPIENS (HUMAN).//Q11206

F-HEMBA1006993

F-HEMBA1006996//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC RE

GION (ORF70).//0.12:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
 F-HEMBA1007002//PLATELET GLYCOPROTEIN IX PRECURSOR (GPIX) (CD42A).//0.00
 096:60:33//HOMO SAPIENS (HUMAN).//P14770
 F-HEMBA1007017//HYPOTHETICAL 7.2 KD PROTEIN IN CYAY-DAPF INTERGENIC REGI
 ON.//1.0:25:56//ESCHERICHIA COLI.//P39166
 F-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59)
 (DYNEIN LIGHT CHAIN A) (DLC-A).//8.5e-120:278:80//GALLUS GALLUS (CHICKEN
).//Q90828
 F-HEMBA1007045//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.
 1e-12:158:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-HEMBA1007051
 F-HEMBA1007052//60S RIBOSOMAL PROTEIN L37-B (L35) (YP55).//0.94:37:35//S
 ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P51402
 F-HEMBA1007062//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:55:29/
 /RHINOCEROS UNICORNIS (GREATER INDIAN RHINOCEROS).//Q96063
 F-HEMBA1007066//ECLOSION HORMONE PRECURSOR (ECDYSIS ACTIVATOR) (EH).//0.
 58:49:38//BOMBYX MORI (SILK MOTH).//P25331
 F-HEMBA1007073//PUTATIVE SMALL MEMBRANE PROTEIN (ORF 4).//0.86:46:34//CA
 NINE ENTERIC CORONAVIRUS (STRAIN INSAVC-1) (CCV).//P36696
 F-HEMBA1007078//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.6e-29:56:67/
 /HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1007080//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.
 028:122:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-HEMBA1007085//RTOA PROTEIN (RATIO-A).//7.4e-11:221:31//DICTYOSTELIUM D
 ISCOIDEUM (SLIME MOLD).//P54681
 F-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//3.3e-29:173:36//METHANOCOC
 CUS JANNASCHII.//Q57626
 F-HEMBA1007112
 F-HEMBA1007113

F-HEMBA1007121//INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1.3.57) (IPP)
 ./5.4e-07:90:28//HOMO SAPIENS (HUMAN).//P49441

F-HEMBA1007129//HIRUSTASIN.//0.88:37:32//HIRUDO MEDICINALIS (MEDICINAL L
 EECH).//P80302

F-HEMBA1007147//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REG
 ION.//0.92:23:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182

F-HEMBA1007149//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.0078:17:7
 0//ESCHERICHIA COLI.//P05834

F-HEMBA1007151//WDNM1 PROTEIN PRECURSOR.//0.25:45:37//MUS MUSCULUS (MOUS
 E).//Q62477

F-HEMBA1007174//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REG
 ION.//6.9e-18:97:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-HEMBA1007178//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.8e-06:38:65/
 /HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1007194//GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFOR
 M PRECURSOR (EC 1.1.1.49) (G6PD).//1.0:80:32//NICOTIANA TABACUM (COMMON
 TOBACCO).//Q43793

F-HEMBA1007203//PROTEIN A22.//1.0:115:26//VARIOLA VIRUS.//P33845

F-HEMBA1007206

F-HEMBA1007224//HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II.//
 2.4e-05:92:30//CAENORHABDITIS ELEGANS.//Q09275

F-HEMBA1007243//HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2
 .8) (HGPRT) (HGPRTASE) (HPRT B).//3.1e-74:205:67//MUS MUSCULUS (MOUSE)./
 /P00493

F-HEMBA1007251//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-
 4) (PROTEIN SV23).//0.52:108:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P
 13238

F-HEMBA1007256

F-HEMBA1007267//CALICIN (FRAGMENT).//0.060:88:31//HOMO SAPIENS (HUMAN)./

/Q13939

F-HEMBA1007273//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//0.95:40:37//GUILLARDIA THETA (CRYPTOMONAS PHI).//078421

F-HEMBA1007279//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.6e-24:98:64//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1007281

F-HEMBA1007288//HYPOTHETICAL 13.5 KD PROTEIN IN ZMS1-MNS1 INTERGENIC REGION.//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47162

F-HEMBA1007300//CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) (CGB-PDE).//2.7e-43:220:41//BOS TAURUS (BOVINE).//Q28156

F-HEMBA1007301//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//3.3e-22:115:33//HOMO SAPIENS (HUMAN).//P02461

F-HEMBA1007319

F-HEMBA1007320//HYPOTHETICAL 28.0 KD PROTEIN IN GLOB-RNHA INTERGENIC REGION.//1.0:48:37//ESCHERICHIA COLI.//P75672

F-HEMBA1007322//THREONINE DEHYDRATASE OPERON ACTIVATOR PROTEIN.//1.0:59:33//ESCHERICHIA COLI.//P11866

F-HEMBA1007327

F-HEMBA1007341//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.1e-12:37:62//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1007342//PROBABLE E5 PROTEIN.//0.89:96:29//PYGMY CHIMPANZEE PAPILOMAVIRUS TYPE 1.//Q02268

F-HEMBA1007347//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2).//0.92:62:43//OVIS ARIES (SHEEP).//Q29400

F-HEMBA1000005//WEAK NEUROTOXIN 5.//0.98:30:33//NAJA NAJA (INDIAN COBRA).//P29179

F-HEMBA1000008//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.7e-35:73:84//HOMO SAPIENS (HUMAN).//P39195

F-HEM BB1000018//HYPOTHETICAL BHLF1 PROTEIN.//0.39:90:37//EPSTEIN-BARR VI
RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEM BB1000024//VIRE LOCUS 9 KD VIRULENCE PROTEIN.//0.66:36:41//AGROBACT
ERIUM TUMEFACIENS.//P08061

F-HEM BB1000025//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//0.46:32:40//DENDROAS
PIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494

F-HEM BB1000030//SUPPRESSOR PROTEIN SRP40.//6.7e-07:50:52//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32583

F-HEM BB1000036//HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III.
//2.5e-07:120:29//CAENORHABDITIS ELEGANS.//P46576

F-HEM BB1000037//HYPOTHETICAL 59.9 KD PROTEIN IN SGA1-KTR7 INTERGENIC REG
ION.//1.7e-05:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40492

F-HEM BB1000039//VERY HYPOTHETICAL 11.9 KD PROTEIN C4H3.12C IN CHROMOSOME
I.//1.0:61:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10219

F-HEM BB1000044

F-HEM BB1000048//HYPOTHETICAL 15.7 KD PROTEIN IN IDH-DEOR INTERGENIC REGI
ON.//1.0:63:31//BACILLUS SUBTILIS.//P54942

F-HEM BB1000050//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-14:34:79/
/HOMO SAPIENS (HUMAN).//P39194

F-HEM BB1000054//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.9e-31:45:73/
/HOMO SAPIENS (HUMAN).//P39193

F-HEM BB1000055//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//1.0:14:57//DENDROASP
IS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494

F-HEM BB1000059//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.0e-21:82:59/
/HOMO SAPIENS (HUMAN).//P39195

F-HEM BB1000083//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN;
BETA-GRANIN; WE-14].//0.87:172:28//RATTUS NORVEGICUS (RAT).//P10354

F-HEM BB1000089//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGI
ON (F83).//1.0:42:33//ESCHERICHIA COLI.//P46879

F-HEMBB1000099//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/7.7e-08:31:87/
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1000103//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-38:136:58//H
OMO SAPIENS (HUMAN).//P08547

F-HEMBB1000113//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.9e-13:57:64//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000119//MAF PROTEIN.//3.6e-32:195:43//BACILLUS SUBTILIS.//Q02169

F-HEMBB1000136//HYPOTHETICAL 12.7 KD PROTEIN IN PCS60-ABD1 INTERGENIC RE
GION.//0.65:71:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38327

F-HEMBB1000141//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00014:34
:64//HOMO SAPIENS (HUMAN).//P20931

F-HEMBB1000144//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.0e-26:81:69
//HOMO SAPIENS (HUMAN).//P39191

F-HEMBB1000173//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.2e-29:91:71//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000175//ANTIMICROBIAL PEPTIDE ENAP-1 (FRAGMENT).//0.97:41:36//EQ
UUS CABALLUS (HORSE).//P80930

F-HEMBB1000198//HYPOTHETICAL 7.7 KD PROTEIN YCF33 (ORF67).//0.91:21:52//
PORPHYRA PURPUREA.//P51329

F-HEMBB1000215//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:39:76/
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1000217//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//2.9
e-32:174:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624

F-HEMBB1000218//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.73:31:38/
/MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P24949

F-HEMBB1000226//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//
6.5e-26:191:34//CAENORHABDITIS ELEGANS.//Q09217

F-HEMBB1000240

F-HEMBB1000244//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-05:44:61//

HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000250

F-HEMBB1000258

F-HEMBB1000264//CUTICLE COLLAGEN SQT-1.//0.15:89:33//CAENORHABDITIS ELEGANS.//P12114

F-HEMBB1000266//TRANSLATION INITIATION FACTOR IF-2.//2.7e-06:167:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730

F-HEMBB1000272//CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED).//0.75:30:43//BOS TAURUS (BOVINE).//P00429

F-HEMBB1000274//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//1.0:38:36//SUS SCROFA (PIG).//P35323

F-HEMBB1000284//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//1.0:56:30//MUS MUSCULUS (MOUSE).//Q09098

F-HEMBB1000307

F-HEMBB1000312

F-HEMBB1000317//THROMBOSPONDIN 1 PRECURSOR.//3.2e-32:135:43//HOMO SAPIENS (HUMAN).//P07996

F-HEMBB1000318//PUTATIVE SMALL MEMBRANE PROTEIN (NONSTRUCTURAL PROTEIN NS3) (NONSTRUCTURAL 9.5 KD PROTEIN).//0.41:51:31//HUMAN CORONAVIRUS (STRAIN OC43).//Q04854

F-HEMBB1000335//ZINC FINGER PROTEIN 13 (ZFP-13) (KROX-8 PROTEIN) (FRAGMENT).//0.82:33:45//MUS MUSCULUS (MOUSE).//P10754

F-HEMBB1000336//ALDEHYDE OXIDASE (EC 1.2.3.1) (FRAGMENTS).//0.80:44:40//ORYZCTOLAGUS CUNICULUS (RABBIT).//P80456

F-HEMBB1000337//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//0.94:118:22//HOMO SAPIENS (HUMAN).//Q08170

F-HEMBB1000338//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.042:33:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642

F-HEMBB1000339//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-14:54:55//
HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000341//GENE 74 PROTEIN (GP74).//1.0:39:33//MYCOBACTERIOPHAGE L5
.//Q05289
F-HEMBB1000343
F-HEMBB1000354//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-15:83:56//
HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000369//PROTEIN Q300.//0.99:27:40//MUS MUSCULUS (MOUSE).//Q02722
F-HEMBB1000374//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.7e-34:56:78/
/HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1000376
F-HEMBB1000391//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:79:35//
BOS TAURUS (BOVINE).//P25508
F-HEMBB1000399//CHECKPOINT PROTEIN RAD17.//2.8e-15:187:31//SCHIZOSACCHAR
OMYCES POMBE (FISSION YEAST).//P50531
F-HEMBB1000402//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRA
GMENT).//0.027:60:38//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)
.//P15583
F-HEMBB1000404//CYANELLE 50S RIBOSOMAL PROTEIN L28.//0.94:29:27//CYANOPH
ORA PARADOXA.//P48129
F-HEMBB1000420//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.
023:97:35//HOMO SAPIENS (HUMAN).//Q15427
F-HEMBB1000434//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.8e-20:111:54
//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1000438//HYPOTHETICAL 7.9 KD PROTEIN IN GP55-NRDG INTERGENIC REGI
ON.//0.93:24:50//BACTERIOPHAGE T4.//P07076
F-HEMBB1000441//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-23:85:70//
HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000449//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.88:27:51//HO

MO SAPIENS (HUMAN).//P39195

F-HEMBB1000455

F-HEMBB1000472

F-HEMBB1000480//PROTEIN STBC.//1.0:52:30//ESCHERICHIA COLI.//P11905

F-HEMBB1000487//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA) (NEUROTOXIN II).//

0.93:29:34//NAJA OXIANA (CENTRAL ASIAN COBRA) (OXUS COBRA).//P01427

F-HEMBB1000490//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.3e-16:50:80/

/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1000491

F-HEMBB1000493//3A PROTEIN.//1.0:51:35//AVIAN INFECTIOUS BRONCHITIS VIRU

S (STRAIN BEAUDETTE) (IBV).//P30237

F-HEMBB1000510//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:132:45//H

OMO SAPIENS (HUMAN).//P08547

F-HEMBB1000518//CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).//0.02

1:47:40//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P14546

F-HEMBB1000523

F-HEMBB1000530//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//9.8e-1

4:43:83//GALLUS GALLUS (CHICKEN).//P32018

F-HEMBB1000550//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.

19:97:30//TRYPANOSOMA BRUCEI BRUCEI.//P04540

F-HEMBB1000554//MATERNAL B9.10 PROTEIN (P30 B9.10).//0.94:82:25//XENOPUS

LAEVIS (AFRICAN CLAWED FROG).//P40744

F-HEMBB1000556//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA

FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.043:201:29//HOMO SAPIENS

(HUMAN).//000268

F-HEMBB1000564//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:52:34//

METRIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//047493

F-HEMBB1000573//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//2.3e-10:52:73

//HOMO SAPIENS (HUMAN).//P39191

F-HEMBB1000575//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.8e-26:76:76/
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1000586//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3)
(EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ).//0.74:23:52//HOMO SAPIENS (HU
MAN).//000483

F-HEMBB1000589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.9e-25:61:75/
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBB1000591//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:34:35//
PETROMYZON MARINUS (SEA LAMPREY).//Q35537

F-HEMBB1000592//SMALL PROLINE-RICH PROTEIN 2-1.//0.0016:49:42//HOMO SAPI
ENS (HUMAN).//P35326

F-HEMBB1000593//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.0070:189:32/
/GALLUS GALLUS (CHICKEN).//P12105

F-HEMBB1000598//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.7e-10:110:41//N
YCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1000623//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III./
/0.0022:98:28//CAENORHABDITIS ELEGANS.//P34284

F-HEMBB1000630

F-HEMBB1000631//ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR)
(SUBTYPE C4).//8.8e-06:59:40//HOMO SAPIENS (HUMAN).//P18825

F-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//7.3e-13:17
3:28//MUS MUSCULUS (MOUSE).//P27671

F-HEMBB1000637//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.6e-41:94:82/
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBB1000638//INVOLUCRIN.//1.9e-06:144:29//HOMO SAPIENS (HUMAN).//P074
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F-HEMBB1000643//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.3e-30:77:76/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1000649//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.5e-37:58:81/

/HOMO SAPIENS (HUMAN).//P39189
 F-HEMBB1000652//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.2e-37:61:77/
 /HOMO SAPIENS (HUMAN).//P39193
 F-HEMBB1000665//HYPOTHETICAL PROTEIN BBD24.//0.83:38:36//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//P70845
 F-HEMBB1000671//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-51:74:71//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBB1000673//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H).//0.012:37:37//ESCHERICHIA COLI.//P07965
 F-HEMBB1000684//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.1e-21:66:72/
 /HOMO SAPIENS (HUMAN).//P39193
 F-HEMBB1000693//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1).//5.2e-26:121:49/
 /RATTUS NORVEGICUS (RAT).//P54256
 F-HEMBB1000705
 F-HEMBB1000706
 F-HEMBB1000709//HYPOTHETICAL 5.8 KD PROTEIN.//1.0:29:44//CLOVER YELLOW MOSAIC VIRUS (CYMV).//P16485
 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8B.//7.4e-105:205:98//RATTUS NORVEGICUS (RAT).//P70550
 F-HEMBB1000726//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.4e-25:85:70/
 /HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1000738//50S RIBOSOMAL PROTEIN L33.//1.0:41:31//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P35871
 F-HEMBB1000749//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-29:42:85/
 /HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1000763//NIFU PROTEIN.//0.089:63:36//FRANKIA ALNI.//P46045
 F-HEMBB1000770//CALTRIN-LIKE PROTEIN II.//0.98:13:69//CAVIA PORCELLUS (GUINEA PIG).//P22075
 F-HEMBB1000774//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.029:53:32//MUS MUS

CULUS (MOUSE).//P17095

F-HEMBB1000781//MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEK KINASE 2).//3.5e-75:144:98//MUS MUSCULUS (MOUSE).//Q61083

F-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//2.6e-49:232:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39956

F-HEMBB1000790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:93:51//HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000794

F-HEMBB1000807//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0.54:111:27//GALLUS GALLUS (CHICKEN).//P49578

F-HEMBB1000810

F-HEMBB1000821

F-HEMBB1000822//HYPOTHETICAL 10 KD PROTEIN (ORF 6).//0.10:50:34//NARCISSUS MOSAIC VIRUS (NMV).//P15099

F-HEMBB1000826//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00025:73:39//HOMO SAPIENS (HUMAN).//P20931

F-HEMBB1000827//HYPOTHETICAL 7.4 KD PROTEIN.//0.89:23:52//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302

F-HEMBB1000831//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:35:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-HEMBB1000835//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.8e-31:96:46//HOMO SAPIENS (HUMAN).//P08547

F-HEMBB1000840//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00012:102:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1000848//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-97:239:70//HOMO SAPIENS (HUMAN).//P08547

F-HEMBB1000852

F-HEMBB1000870

F-HEMBB1000876//METALLOTHIONEIN (MT).//0.99:14:64//PERCA FLUVIATILIS (PERCH).//P52725

F-HEMBB1000883//HYPOTHETICAL 7.8 KD PROTEIN (ORF62).//0.34:60:33//GUILLARDIA THETA (CRYPTOMONAS PHI).//078459

F-HEMBB1000887//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//1.0:26:42//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

F-HEMBB1000888

F-HEMBB1000890

F-HEMBB1000893

F-HEMBB1000908//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0074:45:51//HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000910//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552

F-HEMBB1000913//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.29:56:46//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1000915//CYTOCHROME B (EC 1.10.2.2).//2.5e-24:62:90//HOMO SAPIENS (HUMAN).//P00156

F-HEMBB1000917//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.9e-26:53:66//HOMO SAPIENS (HUMAN).//P39193

F-HEMBB1000927//NEURONAL CALCIUM SENSOR 1 (NCS-1) (FREQUENIN).//3.9e-44:182:45//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91614

F-HEMBB1000947//SMALL PROLINE-RICH PROTEIN 2-1.//0.24:69:27//HOMO SAPIENS (HUMAN).//P35326

F-HEMBB1000959//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.0e-31:89:68//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1000973//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.96:66:36//BOS TAURUS (BOVINE).//O18739

F-HEMBB1000975//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG).//0.00042:77:41//HOMO SAPIENS (HUMAN).//P0419

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F-HEMBB1000981

F-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//1.0e-18:178:30//MUS MUSCULUS (MOUSE).//P28575

F-HEMBB1000991

F-HEMBB1000996//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.58:34:35//ESCHERICHIA COLI.//P33669

F-HEMBB1001004//PROBABLE E4 PROTEIN.//0.24:110:35//HUMAN PAPILLOMAVIRUS TYPE 5B.//P26550

F-HEMBB1001008

F-HEMBB1001011//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16).//3.2e-17:104:47//HOMO SAPIENS (HUMAN).//P17097

F-HEMBB1001014//EOTAXIN PRECURSOR (EOSINOPHIL CHEMOTACTIC PROTEIN).//1.0:58:39//RATTUS NORVEGICUS (RAT).//P97545

F-HEMBB1001020//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.4e-07:36:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1001024

F-HEMBB1001037//FERREDOXIN.//1.0:52:25//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203

F-HEMBB1001047

F-HEMBB1001051//PROTEIN FAN (FACTOR ASSOCIATED WITH N-SMASE ACTIVATION).//3.4e-21:50:100//HOMO SAPIENS (HUMAN).//Q92636

F-HEMBB1001056//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0099:115:35//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341

F-HEMBB1001058//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-33:95:76//HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1001060//HYPOTHETICAL 8.2 KD PROTEIN ZC21.7 IN CHROMOSOME III.//1.0:38:36//CAENORHABDITIS ELEGANS.//P34591

F-HEMBB1001063

F-HEMBB1001068

F-HEMBB1001096//NOXIUSTOXIN (NTX) (TOXIN II.11).//0.99:36:38//CENTRUROID
ES NOXIUS (MEXICAN SCORPION).//P08815

F-HEMBB1001102//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1
.1e-27:115:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-HEMBB1001105//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECU
RSOR.//0.80:70:40//HOMO SAPIENS (HUMAN).//P28067

F-HEMBB1001112//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.1e-126
:287:85//RATTUS NORVEGICUS (RAT).//P38378

F-HEMBB1001114//HYPOTHETICAL 9.6 KD PROTEIN (ORF2).//0.84:62:27//BACTERI
OPHAGE L2.//P42537

F-HEMBB1001117

F-HEMBB1001119//COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR.//1.6e-21:50:98//H
OMO SAPIENS (HUMAN).//Q99715

F-HEMBB1001126//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//
1.7e-50:184:53//CAENORHABDITIS ELEGANS.//Q09296

F-HEMBB1001133//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.4e-09:53:62/
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1001137//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7
.6) (RPB1) (FRAGMENT).//2.0e-05:206:27//CRICETULUS GRISEUS (CHINESE HAMS
TER).//P11414

F-HEMBB1001142//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.1e-05:46:56/
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBB1001151//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//
2.3e-23:109:44//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-HEMBB1001153//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.75:76:34//AS
CARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P27393

F-HEMBB1001169//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-16:71:59/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1001175//ANKYRIN.//3.2e-12:169:31//MUS MUSCULUS (MOUSE).//Q02357
 F-HEMBB1001177//PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.//9.4e-07:148:27//
 HOMO SAPIENS (HUMAN).//Q15269
 F-HEMBB1001182//HYPOTHETICAL 36.0 KD PROTEIN.//1.3e-09:110:31//SACCHAROM
 YCES CEREVISIAE (BAKER'S YEAST).//P54858
 F-HEMBB1001199
 F-HEMBB1001208//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.053:23:47//MUS MUSCU
 LUS (MOUSE).//P15974
 F-HEMBB1001209
 F-HEMBB1001210//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.14:40:37//MUS MUSCUL
 US (MOUSE).//P15974
 F-HEMBB1001218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.4e-19:49:67/
 /HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1001221//CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR (E
 C 1.9.3.1).//0.11:44:38//HOMO SAPIENS (HUMAN).//P14406
 F-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//2.0e-45:192:53//M
 US MUSCULUS (MOUSE).//P46938
 F-HEMBB1001242//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN
 C12G12.13C IN CHROMOSOME I.//5.5e-37:226:41//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST).//Q09876
 F-HEMBB1001249//OXALOACETATE DECARBOXYLASE GAMMA CHAIN (EC 4.1.1.3).//1.
 0:23:43//KLEBSIELLA PNEUMONIAE.//P13155
 F-HEMBB1001253//METALLOTHIONEIN-IH (MT-1H) (METALLOTHIONEIN-0) (MT-0).//
 0.14:16:43//HOMO SAPIENS (HUMAN).//P80294
 F-HEMBB1001254//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-12:40:75/
 /HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1001267//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-12:33:78/
 /HOMO SAPIENS (HUMAN).//P39193
 F-HEMBB1001271//HYPOTHETICAL 25.1 KD PROTEIN B0302.5 IN CHROMOSOME X.//1

.0:58:37//CAENORHABDITIS ELEGANS.//Q10928
 F-HEMBB1001282//ANKYRIN HOMOLOG PRECURSOR.//9.5e-13:206:31//CHROMATIUM V
 INOSUM.//Q06527
 F-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//4.6e-42:163:51//ESCHER
 ICHIA COLI.//P46719
 F-HEMBB1001289//HYPOTHETICAL PROTEIN ORF-1137.//1.0e-05:106:26//MUS MUSC
 ULUS (MOUSE).//P11260
 F-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.3e-34:58:94//HOMO SAPIENS (
 HUMAN).//P17081
 F-HEMBB1001302//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2)
 (CDX-3).//0.24:49:46//HOMO SAPIENS (HUMAN).//Q99626
 F-HEMBB1001304//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1)
 (FRAGMENT).//1.0:17:70//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157
 F-HEMBB1001314//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.21:104:27//DRO
 SOPHILA ERECTA (FRUIT FLY).//P13730
 F-HEMBB1001315//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-24:53:71/
 /HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1001317//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//
 0.24:90:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09782
 F-HEMBB1001326//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.36:26:50//MUS MUSCUL
 US (MOUSE).//P15974
 F-HEMBB1001331//HYPOTHETICAL BHLF1 PROTEIN.//1.0:127:33//EPSTEIN-BARR VI
 RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-HEMBB1001335//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT).//0.85:44:29//
 SCIARA COPROPHILA (FUNGUS GNAT).//Q01799
 F-HEMBB1001337//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.2e-20:62:62/
 /HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1001339//HYPOTHETICAL 17.3 KD PROTEIN CY1A11.16C.//8.2e-07:123:34
 //MYCOBACTERIUM TUBERCULOSIS.//Q50606

F-HEMBB1001346//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-14:60:45//HO
MO SAPIENS (HUMAN).//P08547
F-HEMBB1001348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-14:61:62//
HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1001356
F-HEMBB1001364
F-HEMBB1001366//HISTIDINE-RICH PROTEIN.//0.87:26:42//PLASMODIUM FALCIPAR
UM (ISOLATE FCM17 / SENEGAL).//P14586
F-HEMBB1001367//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//8.6e-40:146:61
//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1001369
F-HEMBB1001380//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.9e-25:49:83/
/HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1001384//BH3 INTERACTING DOMAIN DEATH AGONIST (BID).//0.80:95:29/
/MUS MUSCULUS (MOUSE).//P70444
F-HEMBB1001387//PEA2 PROTEIN (PPF2 PROTEIN).//0.022:117:34//SACCHAROMYCE
S CEREVISIAE (BAKER'S YEAST).//P40091
F-HEMBB1001394//ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALP
HA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADA
PTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT).//0.38:85:31//MUS MUSCULUS (MOUSE)
./P17426
F-HEMBB1001410
F-HEMBB1001424//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//
0.99:37:21//ORYZA SATIVA (RICE).//P12162
F-HEMBB1001426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0035:40:60//
HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1001429//CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTI
DASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (EC 3.4.11.
5) (PROLYL AMINOPEPTIDASE).//1.1e-99:219:86//BOS TAURUS (BOVINE).//P0072

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F-HEMBB1001436//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-30:57:78/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1001443//[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE PRECURS
OR (PDP) (EC 3.1.3.43) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SU
BUNIT) (PDPC).//2.5e-79:155:97//BOS TAURUS (BOVINE).//P35816

F-HEMBB1001449

F-HEMBB1001454//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: P
EPTIDE P-D] (FRAGMENT).//1.1e-05:196:31//HOMO SAPIENS (HUMAN).//P10161

F-HEMBB1001458//24 KD ANTIGEN (FRAGMENT).//0.94:18:50//PLASMODIUM CHABAU
DI.//P14592

F-HEMBB1001463

F-HEMBB1001464//PPF2L ANTIGEN (FRAGMENT).//1.0:45:28//PLASMODIUM FALCIPA
RUM (ISOLATE PALO ALTO / UGANDA).//P07765

F-HEMBB1001482//GASTRULA ZINC FINGER PROTEIN XLCGF16.1 (FRAGMENT).//4.2e
-10:37:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18712

F-HEMBB1001500

F-HEMBB1001521//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-39:59:72//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1001527//HOMEBOX PROTEIN HOX-B5 (XLHBOX-4) (XHOX-1B) (FRAGMENT).
//0.21:131:25//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09019

F-HEMBB1001531//GENE 32 PROTEIN (GP32).//0.88:95:30//MYCOBACTERIOPHAGE L
5.//Q05241

F-HEMBB1001535//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:31:38//
LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-HEMBB1001536

F-HEMBB1001537//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//0.0063:52:50/
/HOMO SAPIENS (HUMAN).//P39191

F-HEMBB1001555//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.9e-23:69:63//

HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1001562//RABPHILIN-3A.//0.087:147:27//RATTUS NORVEGICUS (RAT).//P
 47709
 F-HEMBB1001564//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.9e-27:107:54//H
 OMO SAPIENS (HUMAN).//P08547
 F-HEMBB1001565//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.9e-12:51:54/
 /HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1001585
 F-HEMBB1001586
 F-HEMBB1001588//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REG
 ION.//0.0031:31:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140
 F-HEMBB1001603
 F-HEMBB1001618//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR
 ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//0.00076:47:44//MUS MUSCULUS (
 MOUSE).//P11369
 F-HEMBB1001619//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//1.0
 :52:32//HOMO SAPIENS (HUMAN).//P22531
 F-HEMBB1001630
 F-HEMBB1001635//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 A.//1.0:27:44//LYCOP
 ERSICON ESCULENTUM (TOMATO).//Q40157
 F-HEMBB1001637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0042:26:73//H
 OMO SAPIENS (HUMAN).//P39188
 F-HEMBB1001641
 F-HEMBB1001653//SURVIVAL MOTOR NEURON PROTEIN 1.//0.51:36:47//CANIS FAMI
 LIARIS (DOG).//002771
 F-HEMBB1001665//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1).//0.0030:135:34//
 HOMO SAPIENS (HUMAN).//Q05925
 F-HEMBB1001668//PROBABLE 60S RIBOSOMAL PROTEIN L39.//0.99:25:44//CAENORH
 ABDITIS ELEGANS.//P52814

F-HEMBB1001673//HYPOTHETICAL 46.1 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//0.0054:128:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38823

F-HEMBB1001684//SUPPRESSOR PROTEIN SRP40.//0.56:81:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-HEMBB1001685//CYTOCHROME C OXIDASE POLYPEPTIDE VIII-HEART PRECURSOR (EC 1.9.3.1) (VIIIB) (IX).//1.0:21:47//BOS TAURUS (BOVINE).//P10175

F-HEMBB1001695//MYOSIN IC HEAVY CHAIN.//8.9e-05:86:40//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-HEMBB1001704//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.0e-08:35:71//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1001706//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.91:39:41//SUS SCROFA (PIG).//P35323

F-HEMBB1001707//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//1.0:43:23//BRADYRHIZOBIUM JAPONICUM.//P27394

F-HEMBB1001717//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT).//1.0:71:25//LEMUR CATTAL (RING-TAILED LEMUR).//Q34878

F-HEMBB1001735//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-35:97:74//HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3 P116) (EIF3 P110).//0.00069:180:28//HOMO SAPIENS (HUMAN).//P55884

F-HEMBB1001747

F-HEMBB1001749//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-43:75:70//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1001753//PROTEIN Q300.//0.00091:16:81//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBB1001756//CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (XE-P9).//0.94:35:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91879

F-HEMBB1001760

F-HEMBB1001762//GENE 35 PROTEIN (GP35).//0.76:21:47//MYCOBACTERIOPHAGE L
5.//Q05245

F-HEMBB1001785

F-HEMBB1001797//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35.//0.99:41:31//PORP
HYRA PURPUREA.//P51270

F-HEMBB1001802

F-HEMBB1001812//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.2e-39:54:77/
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBB1001816//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.1e-19:97:57/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1001831//HYPOTHETICAL 45.6 KD PROTEIN IN COX5A-ALG11 INTERGENIC R
EGION.//0.62:204:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53951

F-HEMBB1001834//GLYCINE-RICH RNA-BINDING PROTEIN 1 (FRAGMENT).//0.0014:4
0:45//SORGHUM VULGARE (SORGHUM).//Q99069

F-HEMBB1001836//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//7.1e-14:85:61
//HOMO SAPIENS (HUMAN).//P39191

F-HEMBB1001839//PROBABLE E4 PROTEIN.//0.61:49:34//HUMAN PAPILLOMAVIRUS T
YPE 6C.//P20969

F-HEMBB1001850

F-HEMBB1001863//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-30:57:68/
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1001867

F-HEMBB1001868//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOP
ROTEIN).//0.00036:47:53//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-HEMBB1001869//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.0e-11:95:45//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1001872//HYPOTHETICAL 8.2 KD PROTEIN IN LEF8-FP INTERGENIC REGION
.//1.0:34:38//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV)

.//P41459
 F-HEMBB1001874
 F-HEMBB1001875
 F-HEMBB1001880
 F-HEMBB1001899//GENE 11 PROTEIN.//1.0:45:31//SPIROPLASMA VIRUS SPV1-R8A2
 B.//P15902
 F-HEMBB1001905//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REG
 ION.//8.8e-54:216:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234
 F-HEMBB1001906
 F-HEMBB1001908//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//6.3e-51:138:80/
 /HOMO SAPIENS (HUMAN).//Q92794
 F-HEMBB1001910
 F-HEMBB1001911
 F-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15)
 (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64
 E) (DEUBIQUITINATING ENZYME 64E).//2.3e-27:71:70//DROSOPHILA MELANOGASTE
 R (FRUIT FLY).//Q24574
 F-HEMBB1001921//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8e-13:75:53//HO
 MO SAPIENS (HUMAN).//P08547
 F-HEMBB1001922
 F-HEMBB1001925//EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED
 MEMBRANE PROTEIN).//1.0:55:30//MUS MUSCULUS (MOUSE).//P47801
 F-HEMBB1001930//HYPOTHETICAL 9.6 KD PROTEIN K10D2.7 IN CHROMOSOME III.//
 0.43:49:26//CAENORHABDITIS ELEGANS.//Q09412
 F-HEMBB1001944//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.1e-34:63:85/
 /HOMO SAPIENS (HUMAN).//P39189
 F-HEMBB1001945//NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (PHOSPHOLIPID T
 RANSFER PROTEIN) (PLTP).//0.28:45:40//AMARANTHUS CAUDATUS (LOVE-LIES-BLE
 EDING) (INCA-WHEAT).//P80450

F-HEMBB1001947//PROTEIN UL24.//0.48:42:47//HERPES SIMPLEX VIRUS (TYPE 1
/ STRAIN 17).//P10208

F-HEMBB1001950//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REG
ION (0378).//1.6e-24:162:36//ESCHERICHIA COLI.//P52062

F-HEMBB1001952

F-HEMBB1001953

F-HEMBB1001957//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.7e-11:51:60//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1001962//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.6e-24:163:42/
/HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1001967//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.1e-35:55:80/
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1001973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-37:108:75
//HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1001983//LYSIS PROTEIN (E PROTEIN) (GPE).//0.84:45:37//BACTERIOPH
AGE ALPHA-3.//P31280

F-HEMBB1001988

F-HEMBB1001990

F-HEMBB1001996//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-14:98:40//HO
MO SAPIENS (HUMAN).//P08547

F-HEMBB1001997//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.1e-19:38:73//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1002002//CYTOCHROME C BIOGENESIS PROTEIN CCSA.//1.0:150:25//PORPH
YRA PURPUREA.//P51369

F-HEMBB1002005//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.6e-12:94:40/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1002009

F-HEMBB1002015//HYPOTHETICAL 7.7 KD PROTEIN IN MRR-TSR INTERGENIC REGION
(F67).//1.0:17:47//ESCHERICHIA COLI.//P39395

F-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.4e-50:1
 39:55//BLABERUS DISCOIDALIS (TROPICAL COCKROACH).//P29981
 F-HEMBB1002043//HYPOTHETICAL 9.5 KD PROTEIN IN DHFR 3' REGION (ORF3).//0.
 052:40:42//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488).//P22577
 F-HEMBB1002044//CELLULOSE COMPLEMENTING PROTEIN.//0.45:87:33//ACETOBACTE
 R XYLINUM (ACETOBACTER PASTEURIANUS).//P37697
 F-HEMBB1002045//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.78:18:55/
 /HOMO SAPIENS (HUMAN).//P03928
 F-HEMBB1002049
 F-HEMBB1002050//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CON
 TAINS: BASIC PEPTIDE P-F] (FRAGMENT).//1.0e-06:188:27//HOMO SAPIENS (HUM
 AN).//P02812
 F-HEMBB1002068//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0023:56:44//GALLU
 S GALLUS (CHICKEN).//P17277
 F-HEMBB1002069//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOP
 ROTEIN).//0.0074:134:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
 F-HEMBB1002092//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS:
 OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].//2.4e-07:75:40
 //BABOON ENDOGENOUS VIRUS (STRAIN M7).//P10269
 F-HEMBB1002094//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.9e-24:63:82
 //HOMO SAPIENS (HUMAN).//P39191
 F-HEMBB1002115//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.9
 4:26:42//ZEA MAYS (MAIZE).//P43401
 F-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//4.6e-57:176:67//RATTUS NO
 RVEGICUS (RAT).//P56163
 F-HEMBB1002139//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35.//1.0:17:52//PORPH
 YRA PURPUREA.//P51270
 F-HEMBB1002142//EARLY NODULIN 20 PRECURSOR (N-20).//0.087:52:36//MEDICAG
 O TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBB1002152//HYPOTHETICAL 12.3 KD PROTEIN IN RPL3-RPL33 INTERGENIC REGION (ORF102).//5.8e-05:61:37//CYANOPHORA PARADOXA.//P15811

F-HEMBB1002189//HYPOTHETICAL PROTEIN UL125.//1.0:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16835

F-HEMBB1002190

F-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK).//1.2e-27:59:100//HOMO SAPIENS (HUMAN).//Q06418

F-HEMBB1002217//ZINC FINGER PROTEIN 184 (FRAGMENT).//6.6e-22:106:50//HOMO SAPIENS (HUMAN).//Q99676

F-HEMBB1002218//PROTEIN Q300.//0.85:19:52//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBB1002232//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.6e-21:56:71//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1002247

F-HEMBB1002249//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.2e-29:93:69//HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1002254//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-29:101:67//HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1002255//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.0:73:28//PARAMECIUM TETRAURELIA.//P15579

F-HEMBB1002266//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0079:151:26//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816

F-HEMBB1002280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.2e-15:182:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1002300

F-HEMBB1002306//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.00011:26:84//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1002327//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.1e-11:41:85//HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1002329//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//9.9e-17:232:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
F-HEMBB1002340

F-HEMBB1002342//HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REGION.//3.6e-40:102:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03835

F-HEMBB1002358//THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE).//6.1e-30:63:96//HOMO SAPIENS (HUMAN).//P23919

F-HEMBB1002359//HYPOTHETICAL 7.1 KD PROTEIN C6G9.01C IN CHROMOSOME I.//0.97:28:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q92346

F-HEMBB1002364//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.47:119:25//HOMO SAPIENS (HUMAN).//P12895

F-HEMBB1002371//HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME I PRECURSOR.//3.0e-05:111:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09703

F-HEMBB1002381//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.34:105:34//CAENORHABDITIS ELEGANS.//Q09455

F-HEMBB1002383//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.049:103:32//AQUIFEX AEOLICUS.//066566

F-HEMBB1002387//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 11).//0.18:75:28//RICKETTSIA TSUTSUGAMUSHI.//P16626

F-HEMBB1002409//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.014:61:36//MUS MUSCULUS (MOUSE).//P17095

F-HEMBB1002415

F-HEMBB1002425//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-18:55:70//HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1002442//LIN-10 PROTEIN.//5.1e-15:121:31//CAENORHABDITIS ELEGANS.//P34692

F-HEMBB1002453//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:54:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1002457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-07:31:64//
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1002458//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.92:28:53//DROSOP
HILA MELANOGASTER (FRUIT FLY).//Q01642

F-HEMBB1002477//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7
.6) (RPB1) (FRAGMENT).//0.0066:198:27//CRICETULUS GRISEUS (CHINESE HAMST
ER).//P11414

F-HEMBB1002489//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.
030:182:28//HOMO SAPIENS (HUMAN).//Q15427

F-HEMBB1002492

F-HEMBB1002495//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-08:41:75/
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1002502//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00030:
31:77//HOMO SAPIENS (HUMAN).//P12895

F-HEMBB1002509

F-HEMBB1002510

F-HEMBB1002520//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-36:162:50//N
YCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1002522//7 KD PROTEIN (ORF 4).//0.77:32:40//CHRYSANTHEMUM VIRUS B
(CVB).//P37990

F-HEMBB1002531

F-HEMBB1002534//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.1e-36:80:73/
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1002545

F-HEMBB1002550//HOMEBOX PROTEIN HOX-D11 (HOX-4.6) (HOX-5.5).//3.8e-05:8
3:34//MUS MUSCULUS (MOUSE).//P23813

F-HEMBB1002556

F-HEMBB1002579//SPLICING FACTOR U2AF 35 KD SUBUNIT (U2 AUXILIARY FACTOR
35 KD SUBUNIT) (U2 SNRNP AUXILIARY FACTOR SMALL SUBUNIT) (FRAGMENT).//5.

0e-06:27:77//SUS SCROFA (PIG).//Q29350
 F-HEMBB1002582//PROTEINASE INHIBITOR.//1.0:27:40//SOLANUM MELONGENA (EGG
 PLANT) (AUBERGINE).//P01078
 F-HEMBB1002590//HYPOTHETICAL PROTEIN IN MMSB 3' REGION (ORF1) (FRAGMENT).
 //1.9e-20:90:54//PSEUDOMONAS AERUGINOSA.//P28812
 F-HEMBB1002596
 F-HEMBB1002600//NOVEL ANTIGEN 2 (NAG-2).//1.9e-60:187:59//HOMO SAPIENS (HUMAN).//014817
 F-HEMBB1002601//M PROTEIN, SEROTYPE 6 PRECURSOR.//1.0:71:35//STREPTOCOCCUS PYOGENES.//P08089
 F-HEMBB1002603
 F-HEMBB1002607//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0032:142:33//HOMO SAPIENS (HUMAN).//P10162
 F-HEMBB1002610//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:79:49//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBB1002613//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-08:41:60//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1002614//HYPOTHETICAL 9.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20553
 F-HEMBB1002617//INSECT TOXIN 1 (BOT IT1).//1.0:44:29//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION).//P55902
 F-HEMBB1002623//HYPOTHETICAL 9.7 KD PROTEIN (ORF88) (PUTATIVE DNA-BINDING PROTEIN).//0.42:31:54//BACTERIOPHAGE P4.//P12552
 F-HEMBB1002635//STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 3) (MAP KINASE P49 3F12).//6.2e-17:44:95//HOMO SAPIENS (HUMAN).//P53779
 F-HEMBB1002664//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEIN B (SM-B) (SNRNP-B) (SM11) (FRAGMENT).//1.0:57:36//RATTUS NORVEGICUS (RAT).//P17136

F-HEMBB1002677//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.9e-06:194:34//N
YCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1002683//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRA
GMENT).//0.96:56:35//LEMUR CATTAL (RING-TAILED LEMUR).//Q34879

F-HEMBB1002684//SILLUCIN.//1.0:16:50//RHIZOMUCOR PUSILLUS.//P02885

F-HEMBB1002686

F-HEMBB1002692

F-HEMBB1002697//HELIX-DESTABILIZING PROTEIN (SINGLE-STRANDED DNA BINDING
PROTEIN) (GPV).//0.57:36:38//BACTERIOPHAGE FD, BACTERIOPHAGE F1, AND BA
CTERIOPHAGE M13.//P03669

F-HEMBB1002699

F-HEMBB1002702

F-HEMBB1002705//HYPOTHETICAL 34.8 KD PROTEIN C4H3.04C IN CHROMOSOME I.//
3.6e-40:180:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10212

F-HEMBB1002712

F-MAMMA1000009//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:95:75/
/HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000019

F-MAMMA1000020//DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 5 (EC 1.
14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLAN
ILINE OXIDASE 5).//5.2e-12:24:100//HOMO SAPIENS (HUMAN).//P49326

F-MAMMA1000025//BETA-2-MICROGLOBULIN PRECURSOR.//1.0:73:26//BRACHYDANIO
RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q04475

F-MAMMA1000043//HYPOTHETICAL PXBL-I PROTEIN (FRAGMENT).//0.057:130:31//B
OVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1) (BLV).//P03412

F-MAMMA1000045

F-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//7.5e-44:13
8:55//MUS MUSCULUS (MOUSE).//P47226

F-MAMMA1000057//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-39:92:69/

/HOMO SAPIENS (HUMAN).//P39194
 F-MAMMA1000069//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0044:96:34//ORG
 YIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341
 F-MAMMA1000084//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.4e-28:94:73/
 /HOMO SAPIENS (HUMAN).//P39195
 F-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.1
 6) (CYSTEINE-- TRNA LIGASE) (CYSRS).//6.6e-38:90:51//SCHIZOSACCHAROMYCES
 POMBE (FISSION YEAST).//Q09860
 F-MAMMA1000092//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.4e-30:43:86/
 /HOMO SAPIENS (HUMAN).//P39192
 F-MAMMA1000103//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0
 38:17:52//HOMO SAPIENS (HUMAN).//P22531
 F-MAMMA1000117//50S RIBOSOMAL PROTEIN L24E (HL21/HL22).//0.90:25:48//HAL
 OARCULA MARISMORTUI (HALOBACTERIUM MARISMORTUI).//P14116
 F-MAMMA1000129//HYPOTHETICAL BHLF1 PROTEIN.//0.0016:75:40//EPSTEIN-BARR
 VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-MAMMA1000133
 F-MAMMA1000134//HYPOTHETICAL PROTEIN MJ0647.//1.0:41:41//METHANOCOCCUS J
 ANNASCHII.//Q58063
 F-MAMMA1000139//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-
 3 SUBUNIT.//0.99:69:28//BOS TAURUS (BOVINE), AND MUS MUSCULUS (MOUSE).//
 P29798
 F-MAMMA1000143//CALPAIN INHIBITOR (CALPASTATIN) (FRAGMENT).//0.023:111:2
 7//MUS MUSCULUS (MOUSE).//P51125
 F-MAMMA1000155//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.018:125:34//CAENOR
 HABDITIS ELEGANS.//Q09456
 F-MAMMA1000163//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURS
 OR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN)
 .//0.11:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q544

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F-MAMMA1000171

F-MAMMA1000173//DREBRIN E.//7.6e-41:197:43//HOMO SAPIENS (HUMAN).//Q1664

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F-MAMMA1000175//GAMMA-THIONIN HOMOLOG PPT PRECURSOR.//0.92:39:38//PETUNIA
A INTEGRIFOLIA (VIOLET-FLOWERED PETUNIA) (PETUNIA INFLATA).//Q40901

F-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4e
-106:249:61//HOMO SAPIENS (HUMAN).//P51523

F-MAMMA1000198//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0014:35:42//DROS
OPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-MAMMA1000221

F-MAMMA1000227//6.8 KD MITOCHONDRIAL PROTEOLIPID.//1.0:30:40//MUS MUSCUL
US (MOUSE).//P56379

F-MAMMA1000241//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//1.0:40
:37//PORPHYRA PURPUREA.//P51370

F-MAMMA1000251//HYPOTHETICAL 6.8 KD PROTEIN IN FIC-PPIA INTERGENIC REGIO
N.//0.99:29:48//SALMONELLA TYPHIMURIUM.//P37771

F-MAMMA1000254//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5' REGION.//1.0:20:5
0//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

F-MAMMA1000257//HYPOTHETICAL 50.0 KD PROTEIN IN HEML 3' REGION (ORF2).//0
.22:50:44//PSEUDOMONAS AERUGINOSA.//Q51470

F-MAMMA1000264//GASTRIN-RELEASING PEPTIDE RECEPTOR (GRP-R) (GRP-PREFERRI
NG BOMBESIN RECEPTOR).//0.80:39:43//HOMO SAPIENS (HUMAN).//P30550

F-MAMMA1000266

F-MAMMA1000270//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.5e-42:95:84/
/HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000277//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHOND
ROCALCIN].//0.0062:90:34//MUS MUSCULUS (MOUSE).//P28481

F-MAMMA1000278//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.00096:59:33//

HORDEUM VULGARE (BARLEY).//P17991
 F-MAMMA1000279//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.4e-17:56:76/
 /HOMO SAPIENS (HUMAN).//P39195
 F-MAMMA1000284//ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT P
 ROTEIN 2).//0.017:146:30//MUS MUSCULUS (MOUSE).//Q61324
 F-MAMMA1000287//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.5e-32:84:58/
 /HOMO SAPIENS (HUMAN).//P39189
 F-MAMMA1000302//C-HORDEIN (CLONE PC-919) (FRAGMENT).//1.0:42:33//HORDEUM
 VULGARE (BARLEY).//P17992
 F-MAMMA1000307//PROBABLE E4 PROTEIN.//0.21:71:30//RHESUS PAPILLOMAVIRUS
 TYPE 1 (RHPV 1).//P24832
 F-MAMMA1000309//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLL
 AGEN).//0.0026:141:36//HOMO SAPIENS (HUMAN).//P27658
 F-MAMMA1000312
 F-MAMMA1000313//DNA REPAIR PROTEIN RAD51 HOMOLOG (25 KD PROTEIN) (FRAGMEN
 T).//0.76:52:32//STAPHYLOCOCCUS AUREUS.//P31337
 F-MAMMA1000331
 F-MAMMA1000339//50S RIBOSOMAL PROTEIN L29P.//0.78:32:46//METHANOBACTERIU
 M THERMOAUTOTROPHICUM.//026117
 F-MAMMA1000340//HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REG
 ION.//1.0:29:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36039
 F-MAMMA1000348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.5e-09:63:60//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1000356//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.3e-05:42:52//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1000360
 F-MAMMA1000361//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.4e-33:84:72/
 /HOMO SAPIENS (HUMAN).//P39189
 F-MAMMA1000372//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.6e-21:53:71/

/HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000385

F-MAMMA1000388//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPT
IONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//0.40:72:36/
/HOMO SAPIENS (HUMAN).//P43489

F-MAMMA1000395//RABPHILIN-3A (FRAGMENT).//0.032:125:25//MUS MUSCULUS (MO
USE).//P47708

F-MAMMA1000402//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-28:266:40//H
OMO SAPIENS (HUMAN).//P08547

F-MAMMA1000410//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (EC 1.6.5
.3) (EC 1.6.99.3) (COMPLEX I-13KD-B) (CI-13KD-B) (B13).//5.9e-06:32:68//
HOMO SAPIENS (HUMAN).//Q16718

F-MAMMA1000413//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR
ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.7e-05:93:31//MUS MUSCULUS (
MOUSE).//P11369

F-MAMMA1000414

F-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./
/4.1e-28:119:53//CAENORHABDITIS ELEGANS.//Q09232

F-MAMMA1000421//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-23:68:76/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000422//METALLOTHIONEIN (MT).//0.037:42:42//GADUS MORHUA (ATLANT
IC COD).//P51902

F-MAMMA1000423

F-MAMMA1000424//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.048:23:73//H
OMO SAPIENS (HUMAN).//P39189

F-MAMMA1000429//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//2.7e-
05:110:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

F-MAMMA1000431//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.4e-15:85:58/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000444//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.3e-25:65:76/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000446//ZYXIN.//0.79:155:29//GALLUS GALLUS (CHICKEN).//Q04584

F-MAMMA1000458//HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME 1./
/0.0048:46:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09713

F-MAMMA1000468//PERIOD CLOCK PROTEIN (FRAGMENT).//0.50:20:55//DROSOPHILA
ROBUSTA (FRUIT FLY).//Q03296

F-MAMMA1000472//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-17:106:55/
/HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000478//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.9e-35:80:68/
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000483//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.8e-24:74:77/
/HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000490//TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (
RESTING LYMPHOCYTE KINASE).//0.43:21:57//MUS MUSCULUS (MOUSE).//P42682

F-MAMMA1000500//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.61:
33:54//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).
//P12506

F-MAMMA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-32:43:83/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000516

F-MAMMA1000522//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0015:113:32//HO
MO SAPIENS (HUMAN).//P08547

F-MAMMA1000524//HYPOTHETICAL HOST RANGE 8.5 KD PROTEIN.//1.0:63:31//VACC
INIA VIRUS (STRAIN WR).//P17359

F-MAMMA1000559//METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA).//0.31:16:50//CAL
LINECTES SAPIDUS (BLUE CRAB).//P55949

F-MAMMA1000565//FERREDOXIN-TYPE PROTEIN NAPF.//0.98:37:35//ESCHERICHIA C
OLI.//P33939

F-MAMMA1000567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.5e-37:95:76/
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000576//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.1e-07:34:64
//HOMO SAPIENS (HUMAN).//P39191

F-MAMMA1000583

F-MAMMA1000585//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-28:89:75/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000594//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-24:38:71/
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.1e-25:74:77/
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000605//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-18:83:50/
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000612//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN
IN SIS1-MRPL2 INTERGENIC REGION.//4.0e-42:166:48//SACCHAROMYCES CEREVISI
AE (BAKER'S YEAST).//P41318

F-MAMMA1000616

F-MAMMA1000621

F-MAMMA1000623//METALLOTHIONEIN-1K (MT-1K).//0.0045:25:48//HOMO SAPIENS
(HUMAN).//P80296

F-MAMMA1000625//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.00078:79:35//MU
S MUSCULUS (MOUSE).//P05143

F-MAMMA1000643//HYPOTHETICAL 9.3 KD PROTEIN.//1.0:25:28//MAGUARI VIRUS./
/P16607

F-MAMMA1000664

F-MAMMA1000669//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-05:186:30//H
OMO SAPIENS (HUMAN).//P08547

F-MAMMA1000670//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.6e-06:195:30//M
US MUSCULUS (MOUSE).//P05143

F-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-)//
 3.8e-28:184:35//AEDES AEGYPTI (YELLOWFEVER MOSQUITO)//P42660
 F-MAMMA1000684//DNA-BINDING PROTEIN (VMW21)//1.1e-07:55:56//HERPES SIMP
 LEX VIRUS (TYPE 1 / STRAIN 17)//P04487
 F-MAMMA1000696//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-31:97:74/
 /HOMO SAPIENS (HUMAN)//P39194
 F-MAMMA1000707//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA)//0.31:19:42/
 /CALLINECTES SAPIDUS (BLUE CRAB)//P55950
 F-MAMMA1000713//XYLULOSE KINASE (EC 2.7.1.17) (XYLUKINASE)//1.6e-05:8
 8:35//LACTOBACILLUS PENTOSUS//P21939
 F-MAMMA1000714//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL
 OXIDASE)//0.44:126:30//RATTUS NORVEGICUS (RAT)//P16636
 F-MAMMA1000718//METALLOTHIONEIN-IIIE (MT-2E)//1.0:51:31//ORYCTOLAGUS CUN
 ICULUS (RABBIT)//P80292
 F-MAMMA1000720//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.3e-28:60:71/
 /HOMO SAPIENS (HUMAN)//P39193
 F-MAMMA1000723//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.7e-14:63:53//HO
 MO SAPIENS (HUMAN)//P08547
 F-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)//1.
 8e-43:258:43//HOMO SAPIENS (HUMAN)//014647
 F-MAMMA1000732//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.9e-12:76:55//
 HOMO SAPIENS (HUMAN)//P39188
 F-MAMMA1000733
 F-MAMMA1000734//NPL1 PROTEIN (SEC63 PROTEIN)//2.5e-18:181:39//SACCHAROM
 YCES CEREVISIAE (BAKER'S YEAST)//P14906
 F-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.
 //5.4e-52:196:58//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P87115
 F-MAMMA1000744//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//6.3e-36:144:4
 7//HOMO SAPIENS (HUMAN)//P39190

F-MAMMA1000746

F-MAMMA1000752

F-MAMMA1000760//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//6.6e-29:75:72/
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000761//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-09:59:64/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000775

F-MAMMA1000776//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.3e-35:99:74/
/HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000778//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.1e-19:65:70/
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000782

F-MAMMA1000798//HYPOTHETICAL PROTEIN ORF-1137.//0.015:59:37//MUS MUSCULU
S (MOUSE).//P11260

F-MAMMA1000802//MYOSIN IC HEAVY CHAIN.//0.35:94:41//ACANTHAMOEBA CASTELL
ANII (AMOEBA).//P10569

F-MAMMA1000824//ACTIN 1.//0.046:60:31//ZEA MAYS (MAIZE).//P02582

F-MAMMA1000831//PROBABLE NI/FE-HYDROGENASE 1 B-TYPE CYTOCHROME SUBUNIT./
/1.0:30:46//ESCHERICHIA COLI.//P19929

F-MAMMA1000839//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-28:80:58//
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//1.5e-39:130:36//METHANOB
ACTERIUM THERMOAUTOTROPHICUM.//027540

F-MAMMA1000842//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.064:43:41//HORDE
UM VULGARE (BARLEY).//P17992

F-MAMMA1000843

F-MAMMA1000845//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//0.
43:58:34//DROSOPHILA YAKUBA (FRUIT FLY).//P03895

F-MAMMA1000851//CUTICLE COLLAGEN 34.//0.019:107:29//CAENORHABDITIS ELEGA

NS.//P34687

F-MAMMA1000855//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.

00098:149:32//HOMO SAPIENS (HUMAN).//Q15428

F-MAMMA1000856//METALLOTHIONEIN (MT).//0.63:39:41//POTAMON POTAMIOS.//P5
5952

F-MAMMA1000859//GLYCOPROTEIN X PRECURSOR.//0.014:192:28//EQUINE HERPESVI
RUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28968

F-MAMMA1000862//DISINTEGRIN KISTRIN (PLATELET AGGREGATION ACTIVATION INH
IBITOR).//1.0:66:27//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSE
LASMA RHODOSTOMA).//P17494

F-MAMMA1000863//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.4e-16:41:68//
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000865//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.030:10
0:32//HOMO SAPIENS (HUMAN).//P81489

F-MAMMA1000867//APTOTOXIN IX (PARALYTIC PEPTIDE IX) (PP IX).//0.98:43:32
//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49272

F-MAMMA1000875//PROLINE-RICH PEPTIDE P-B.//0.18:21:47//HOMO SAPIENS (HUM
AN).//P02814

F-MAMMA1000876//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.5e-22:85:71/
/HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000877//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.2e-38:62:74//
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000880//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.49:79:32//BO
S TAURUS (BOVINE).//P25508

F-MAMMA1000883//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0
.87:15:60//CAENORHABDITIS ELEGANS.//Q11116

F-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (IT
ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RE
LATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120)./

/5.3e-17:130:40//HOMO SAPIENS (HUMAN).//Q14624
 F-MAMMA1000905
 F-MAMMA1000906
 F-MAMMA1000908//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.0e-17:70:62//HOMO SAPIENS (HUMAN).//P08547
 F-MAMMA1000914//HYPOTHETICAL 6.2 KD PROTEIN.//0.97:36:36//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19299
 F-MAMMA1000921
 F-MAMMA1000931//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-10:49:65//HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1000940//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32.//0.42:22:54//RE CLINOMONAS AMERICANA.//021281
 F-MAMMA1000941//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-25:55:69//HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1000942//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-08:36:75//HOMO SAPIENS (HUMAN).//P39194
 F-MAMMA1000943
 F-MAMMA1000956//SMALL HISTIDINE-ALANINE-RICH PROTEIN PRECURSOR (SHARP) (ANTIGEN 57).//0.041:122:25//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P04930
 F-MAMMA1000957//HEAT-STABLE ENTEROTOXIN A2 PRECURSOR (STA2).//0.024:37:37//ESCHERICHIA COLI.//Q47185
 F-MAMMA1000962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//6.0e-39:61:78//HOMO SAPIENS (HUMAN).//P39189
 F-MAMMA1000968//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0054:29:72//HOMO SAPIENS (HUMAN).//P39194
 F-MAMMA1000975//CUTICLE COLLAGEN DPY-2 PRECURSOR.//1.0:93:30//CAENORHABDITIS ELEGANS.//P35799
 F-MAMMA1000979//PROLINE-RICH PEPTIDE P-B.//0.012:12:66//HOMO SAPIENS (HU

MAN).//P02814

F-MAMMA1000987//HYPOTHETICAL PROTEIN LAMBDA-SP34.//1.0:47:40//MUS MUSCULUS (MOUSE).//P15973

F-MAMMA1000998

F-MAMMA1001003//PROBABLE E5 PROTEIN.//1.0:52:42//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426

F-MAMMA1001008//PROGASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C) (FRAGMENT).//3.2e-14:131:35//MACACA FUSCATA FUSCATA (JAPANESE MACAQUE).//P03955

F-MAMMA1001021//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.016:61:42//STREPTOMYCES FRADIAE.//P20186

F-MAMMA1001024

F-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//2.4e-20:234:29//GALLUS GALLUS (CHICKEN).//Q90674

F-MAMMA1001035//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.7e-15:52:78//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1001038//NEUROTOXIN II (TOXIN RP-II) (SODIUM CHANNEL TOXIN II).//0.53:25:48//RADIANTHUS PAUMOTENSIS (SEA ANEMONE) (HETERACTIS PAUMOTENSIS).//P01534

F-MAMMA1001041//SPECTRIN BETA CHAIN, ERYTHROCYTE.//6.3e-18:112:43//MUS MUSCULUS (MOUSE).//P15508

F-MAMMA1001050

F-MAMMA1001059//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//1.3e-34:187:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747

F-MAMMA1001067//PROTEIN Q300.//0.36:12:75//MUS MUSCULUS (MOUSE).//Q02722

F-MAMMA1001073//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 (HFH-1).//1.0:70:37//RATTUS NORVEGICUS (RAT).//Q63244

F-MAMMA1001074//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00067:163:32//H

OMO SAPIENS (HUMAN).//P08547
 F-MAMMA1001075//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//0.53:72:34//
 HOMO SAPIENS (HUMAN).//P29374
 F-MAMMA1001078//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-79:184:73//H
 OMO SAPIENS (HUMAN).//P08547
 F-MAMMA1001080//IG HEAVY CHAIN PRECURSOR V-III REGION (VH26).//1.7e-27:8
 2:71//HOMO SAPIENS (HUMAN).//P01764
 F-MAMMA1001082
 F-MAMMA1001091//HYPOTHETICAL BHLF1 PROTEIN.//3.1e-05:198:32//EPSTEIN-BAR
 R VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-MAMMA1001092//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.1e-21:65:72//HO
 MO SAPIENS (HUMAN).//P08547
 F-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//1.0e-18:68:48//DROSO
 PHILA MELANOGASTER (FRUIT FLY).//P51521
 F-MAMMA1001110//PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.//0.080:108:37//
 MUS MUSCULUS (MOUSE).//P02463
 F-MAMMA1001126//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.3e-07:66:45/
 /HOMO SAPIENS (HUMAN).//P39189
 F-MAMMA1001133//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC RE
 GION.//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47174
 F-MAMMA1001139//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.
 4e-42:81:62//CAENORHABDITIS ELEGANS.//Q09201
 F-MAMMA1001143//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00014:36:66//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1001145
 F-MAMMA1001154//CSBA PROTEIN.//1.0:39:38//BACILLUS SUBTILIS.//P37953
 F-MAMMA1001161//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.2e-23:53:64//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1001162//CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27

).//0.69:86:31//MUS MUSCULUS (MOUSE).//P41272
 F-MAMMA1001181//HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III.
 //0.00010:74:47//CAENORHABDITIS ELEGANS.//Q18486
 F-MAMMA1001186//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-32:44:86/
 /HOMO SAPIENS (HUMAN).//P39194
 F-MAMMA1001191//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (
 FRAGMENT).//0.096:40:40//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466
 F-MAMMA1001198//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15
 (PROTEIN EPS15) (AF-1P PROTEIN).//2.5e-75:204:70//HOMO SAPIENS (HUMAN)./
 /P42566
 F-MAMMA1001202//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).//0.52:46:32/
 /CALLINECTES SAPIDUS (BLUE CRAB).//P55950
 F-MAMMA1001203//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.3e-11:82:58/
 /HOMO SAPIENS (HUMAN).//P39192
 F-MAMMA1001206//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-17:67:71//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1001215//9 KD PROTEIN.//1.0:51:33//HOMO SAPIENS (HUMAN).//P13994
 F-MAMMA1001220//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.4e-37:55:87/
 /HOMO SAPIENS (HUMAN).//P39189
 F-MAMMA1001222//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//3.7e-06:168:38//M
 YCOBACTERIUM TUBERCULOSIS.//Q10690
 F-MAMMA1001243
 F-MAMMA1001244//TRP OPERON LEADER PEPTIDE.//1.0:18:55//SERRATIA MARCESCE
 NS.//P03055
 F-MAMMA1001249//HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3' REGION (ORF57).//0
 .57:23:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34774
 F-MAMMA1001256//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-07:79:44//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1001259//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//0.046:86

:32//MYCOPLASMA GENITALIUM.//P47486
 F-MAMMA1001260//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE.//2.7e-05:
 219:27//HOMO SAPIENS (HUMAN).//P13535
 F-MAMMA1001268//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:89:67//HO
 MO SAPIENS (HUMAN).//P08547
 F-MAMMA1001271//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN
).//4.0e-06:126:38//HOMO SAPIENS (HUMAN).//P54259
 F-MAMMA1001274//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-29:57:66/
 /HOMO SAPIENS (HUMAN).//P39194
 F-MAMMA1001280//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.27:24:54/
 /ESCHERICHIA COLI.//P05834
 F-MAMMA1001292//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-73:208:6
 9//HOMO SAPIENS (HUMAN).//Q14681
 F-MAMMA1001296//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.9e-22:41:80/
 /HOMO SAPIENS (HUMAN).//P39193
 F-MAMMA1001298//HYPOTHETICAL PROTEIN HI0371.//0.99:29:37//HAEMOPHILUS IN
 FLUENZAE.//P44668
 F-MAMMA1001305//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPA
 SE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//9
 .9e-62:222:54//HOMO SAPIENS (HUMAN).//Q07960
 F-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//2.1e-09:46
 :60//HOMO SAPIENS (HUMAN).//P20931
 F-MAMMA1001324//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVER
 SE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].//2.5e-43:
 128:50//FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211) (F-MULV).//P26808
 F-MAMMA1001330//HEMOGLOBIN ZETA CHAIN (FRAGMENTS).//0.30:51:37//MACROPUS
 EUGENII (TAMMAR WALLABY).//P81044
 F-MAMMA1001341//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH
 FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475).//0.024:89:39//HOMO SAPIENS (

HUMAN).//P26651

F-MAMMA1001343//PROBABLE E5 PROTEIN.//0.60:64:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927

F-MAMMA1001346//PROTEINASE INHIBITOR IIB (FRAGMENTS).//0.97:33:45//SOLANUM TUBEROSUM (POTATO).//P01082

F-MAMMA1001383//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-30:86:77//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//9.2e-91:195:92//HOMO SAPIENS (HUMAN).//P02750

F-MAMMA1001397//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.5e-19:55:69//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001408//SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.//0.60:45:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P02841

F-MAMMA1001411//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.8e-06:153:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-MAMMA1001419//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.3e-16:99:51//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001420//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//0.0018:23:65//HOMO SAPIENS (HUMAN).//P39190

F-MAMMA1001435//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.7e-22:60:58//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001442

F-MAMMA1001446//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-23:48:75//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001452//GENE 35 PROTEIN (GP35).//0.61:31:45//MYCOBACTERIOPHAGE L5.//Q05245

F-MAMMA1001465//HYPOTHETICAL PROTEIN E-115.//0.0026:68:38//HUMAN ADENOVIRUS TYPE 2.//P03290

F-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE)
 (FRAGMENT).//3.7e-94:201:92//MUS MUSCULUS (MOUSE).//P52623

F-MAMMA1001487//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.6e-16:89:41//NY
 CTICEBUS COUCANG (SLOW LORIS).//P08548

F-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CAL
 CIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//6.2e-59:86:97//HOM
 O SAPIENS (HUMAN).//P07384

F-MAMMA1001502//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.21:79:30//STREPT
 OMYCES FRADIAE.//P26800

F-MAMMA1001510

F-MAMMA1001522//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.67
 :98:31//STREPTOMYCES FRADIAE.//P20186

F-MAMMA1001547//PROBABLE MOLYBDENUM-PTERIN BINDING PROTEIN.//0.97:35:42/
 /HAEMOPHILUS INFLUENZAE.//P45183

F-MAMMA1001551//HYPOTHETICAL PROTEIN MJ0458.1.//0.038:31:41//METHANOCOCC
 US JANNASCHII.//P81308

F-MAMMA1001575

F-MAMMA1001576//TUBULIN GAMMA CHAIN.//1.6e-86:162:99//XENOPUS LAEVIS (AF
 RICAN CLAWED FROG).//P23330

F-MAMMA1001590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.0035:38:55//
 HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001600//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.85:53:33//
 HOMO SAPIENS (HUMAN).//P29279

F-MAMMA1001604//HYPOTHETICAL 11.1 KD PROTEIN C30D11.02C IN CHROMOSOME I.
 //0.14:82:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09902

F-MAMMA1001606//HIGH MOBILITY GROUP PROTEIN HMGI-C.//8.2e-05:77:37//HOMO
 SAPIENS (HUMAN).//P52926

F-MAMMA1001620//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.5e-05:24:66/
 /HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001627//CUTICLE COLLAGEN 40.//0.82:131:31//CAENORHABDITIS ELEGAN
S.//P34804

F-MAMMA1001630//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.6e-26:57:78/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.9e-38:160:55//HOMO SAPIENS (
HUMAN).//P49910

F-MAMMA1001635

F-MAMMA1001649//SPERM PROTAMINE P1.//0.39:31:41//TACHYGLOSSUS ACULEATUS
ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

F-MAMMA1001654//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112
) (TYROSINE- PROTEIN KINASE 1).//5.6e-06:99:28//DICTYOSTELIUM DISCOIDEUM
(SLIME MOLD).//P18160

F-MAMMA1001663//VERY HYPOTHETICAL XYLU PROTEIN.//0.99:27:37//ESCHERICHIA
COLI.//P05056

F-MAMMA1001670//CUTICLE COLLAGEN 1.//0.033:97:37//CAENORHABDITIS ELEGANS
.//P08124

F-MAMMA1001671

F-MAMMA1001679//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.92:32:50//HO
MO SAPIENS (HUMAN).//P08572

F-MAMMA1001683//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00
026:147:34//STREPTOMYCES FRADIAE.//P20186

F-MAMMA1001686

F-MAMMA1001692//SMALL HYDROPHOBIC PROTEIN (SMALL PROTEIN 1A).//1.0:34:26
//BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A51908) (BRS).//P24616

F-MAMMA1001711//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.1e-28:56:69/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001715//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-08:39:71//
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001730//METALLOTHIONEIN-B (MTB).//1.0:17:64//STRONGYLOCENTROTUS

PURPURATUS (PURPLE SEA URCHIN).//Q27287
 F-MAMMA1001735//TUBULIN BETA-5 CHAIN (CLASS-V).//5.1e-121:213:97//GALLUS
 GALLUS (CHICKEN).//P09653
 F-MAMMA1001740
 F-MAMMA1001743//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-09:100:42
 //HOMO SAPIENS (HUMAN).//P39195
 F-MAMMA1001744//POU DOMAIN PROTEIN 2.//0.97:59:38//BRACHYDANIO RERIO (ZE
 BRA FISH) (ZEBRA DANIO).//Q90270
 F-MAMMA1001745//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-43:199:42//H
 OMO SAPIENS (HUMAN).//P08547
 F-MAMMA1001751//TWK-8 PROTEIN.//2.9e-15:77:36//CAENORHABDITIS ELEGANS.//
 P34410
 F-MAMMA1001754//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.019:20:45//DROSO
 PHILA MELANOGASTER (FRUIT FLY).//Q01645
 F-MAMMA1001757//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3' REGION.//0.94:30:4
 3//PSEUDOMONAS PUTIDA.//P25753
 F-MAMMA1001760//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//4.6e-34:103:5
 9//HOMO SAPIENS (HUMAN).//P39191
 F-MAMMA1001764
 F-MAMMA1001768//HYPOTHETICAL PROTEIN UL61.//0.042:167:33//HUMAN CYTOMEGA
 LOVIRUS (STRAIN AD169).//P16818
 F-MAMMA1001769//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-29:97:69/
 /HOMO SAPIENS (HUMAN).//P39194
 F-MAMMA1001771//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//3.3e-09:123:32//HO
 MO SAPIENS (HUMAN).//P51805
 F-MAMMA1001783//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-09:55:61//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1001785//RAS-RELATED PROTEIN RABC.//1.9e-06:120:25//DICTYOSTELIUM
 DISCOIDEUM (SLIME MOLD).//P34143

F-MAMMA1001788//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.3e-29:46:76//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1001790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-24:69:69//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001806//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION.//0.95:58:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042

F-MAMMA1001812//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.8e-12:53:69//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001815//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.11:30:70//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1001817//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:86:55//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001818

F-MAMMA1001820//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).//0.0030:63:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13238

F-MAMMA1001824//APTOTOXIN VII (PARALYTIC PEPTIDE VII) (PP VII).//0.99:26:34//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49271

F-MAMMA1001836//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-35:77:88//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001837//ZINC FINGER PROTEIN 191.//1.3e-27:106:58//HOMO SAPIENS (HUMAN).//O14754

F-MAMMA1001848//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0e-19:92:58//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001851

F-MAMMA1001854

F-MAMMA1001858//ISOTOCIN-NEUROPHYSIN IT 1 PRECURSOR.//0.93:42:38//CATOSTOMUS COMMERSONI (WHITE SUCKER).//P15210

F-MAMMA1001864//PROBABLE ABC TRANSPORTER PERMEASE PROTEIN MG189.//0.77:1

61:27//MYCOPLASMA GENITALIUM.//P47435
 F-MAMMA1001868//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).//0.00013:219:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38911
 F-MAMMA1001874//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.0075:76:31//MUS MUSCULUS (MOUSE).//P07978
 F-MAMMA1001878//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//0.020:10:80//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157
 F-MAMMA1001880
 F-MAMMA1001890//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.1e-34:56:83//HOMO SAPIENS (HUMAN).//P39192
 F-MAMMA1001907//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-12:44:68//HOMO SAPIENS (HUMAN).//P39194
 F-MAMMA1001908//HYPOTHETICAL 16.2 KD PROTEIN IN PRP24-RRN9 INTERGENIC REGION.//0.00013:77:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03525
 F-MAMMA1001931//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.//0.41:106:29//CAENORHABDITIS ELEGANS.//Q09564
 F-MAMMA1001956//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.00053:149:30//MUS MUSCULUS (MOUSE).//Q06666
 F-MAMMA1001963//HYPOTHETICAL PROTEIN IN NAC 5' REGION (ORF X) (FRAGMENT).//1.0:46:28//KLEBSIELLA AEROGENES.//Q08600
 F-MAMMA1001969//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.7e-34:97:68//HOMO SAPIENS (HUMAN).//P08547
 F-MAMMA1001970//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.2e-07:67:37//HOMO SAPIENS (HUMAN).//P08547
 F-MAMMA1001992//PROTEIN Q300.//0.53:14:71//MUS MUSCULUS (MOUSE).//Q02722
 F-MAMMA1002009//PROBABLE E5 PROTEIN.//0.17:56:32//HUMAN PAPILLOMAVIRUS TYPE 31.//P17385

F-MAMMA1002011//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L P
ROTEIN).//1.0:100:31//HOMO SAPIENS (HUMAN).//P29966

F-MAMMA1002032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.1e-21:86:65//
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002033//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.5e-20:67:58//
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002041//MALE SPECIFIC SPERM PROTEIN MST84DC.//1.0:17:52//DROSOPH
ILA MELANOGASTER (FRUIT FLY).//Q01644

F-MAMMA1002042//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.19:45:46//HO
MO SAPIENS (HUMAN).//P39192

F-MAMMA1002047//TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXO
GLUTARATE AMINOTRANSFERASE) (TAT).//0.0017:50:46//RATTUS NORVEGICUS (RAT
).//P04694

F-MAMMA1002056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.2e-37:70:77/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002058//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-08:26:76//
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002068//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:78:46//HO
MO SAPIENS (HUMAN).//P08547

F-MAMMA1002078//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:26:46/
/COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P50682

F-MAMMA1002082//SUPPRESSOR PROTEIN SRP40.//0.23:95:32//SACCHAROMYCES CER
EVISIAE (BAKER'S YEAST).//P32583

F-MAMMA1002084//HYPOTHETICAL 7.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS
(STRAIN COPENHAGEN).//P20520

F-MAMMA1002093

F-MAMMA1002108//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00
079:143:33//STREPTOMYCES FRADIAE.//P20186

F-MAMMA1002118//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:43:34//
 METRIDIIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//047493
 F-MAMMA1002125//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.9e-14:60:68/
 /HOMO SAPIENS (HUMAN).//P39192
 F-MAMMA1002132
 F-MAMMA1002140//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.4e-24:69:65//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1002143//SERUM PROTEIN MSE55.//2.1e-16:166:43//HOMO SAPIENS (HUMAN).//Q00587
 F-MAMMA1002145//36.4 KD PROLINE-RICH PROTEIN.//0.00014:84:29//LYCOPERSICON ESCULENTUM (TOMATO).//Q00451
 F-MAMMA1002153
 F-MAMMA1002155
 F-MAMMA1002156//METALLOPROTEINASE INHIBITOR PRECURSOR.//0.90:58:34//STREPTOMYCES NIGRESCENS.//P01077
 F-MAMMA1002158
 F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.0e-66:157:70//HOMO SAPIENS (HUMAN).//P15880
 F-MAMMA1002174//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.5e-25:56:64//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B).//9.0e-09:28:100//HOMO SAPIENS (HUMAN).//P32119
 F-MAMMA1002209//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.0023:132:33//HOMO SAPIENS (HUMAN).//000268
 F-MAMMA1002215//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.00032:68:35//
 HOMO SAPIENS (HUMAN).//P02452

F-MAMMA1002219//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.0079:22
4:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-MAMMA1002230

F-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-
2B GDP-GTP EXCHANGE FACTOR).//1.4e-118:151:94//RATTUS NORVEGICUS (RAT)./
/P70541

F-MAMMA1002243//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.028:
112:33//MUS MUSCULUS (MOUSE).//P70315

F-MAMMA1002250//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.0012:8
0:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333

F-MAMMA1002267//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.17:13
9:28//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-MAMMA1002268//60S RIBOSOMAL PROTEIN L22.//0.00026:163:30//DROSOPHILA M
ELANOGASTER (FRUIT FLY).//P50887

F-MAMMA1002269//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.35:14:57//
HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

F-MAMMA1002282//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-05:32:65/
/HOMO SAPIENS (HUMAN).//P39192

F-MAMMA1002292//TROPOMYOSIN 2.//1.4e-05:100:30//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P40414

F-MAMMA1002293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-25:127:44/
/HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002294//ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).//0.00011:138:3
8//BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).//P30020

F-MAMMA1002297//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.15:144:30/
/SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-MAMMA1002298//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.0e-05:40:50//MU
S MUSCULUS (MOUSE).//P05143

F-MAMMA1002299//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0

.84:65:32//STRUTHIO CAMELUS (OSTRICH).//021405
 F-MAMMA1002308//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-29:61:73//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1002310//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.0001
 6:70:38//MUS MUSCULUS (MOUSE).//P15265
 F-MAMMA1002311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.4e-09:84:54/
 /HOMO SAPIENS (HUMAN).//P39189
 F-MAMMA1002312//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REG
 ION (URF Y).//0.48:48:33//BACTERIOPHAGE T4.//P33084
 F-MAMMA1002317
 F-MAMMA1002319//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR
 ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//0.011:128:27//MUS MUSCULUS (M
 OUSE).//P11369
 F-MAMMA1002322//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.2e-20:92:57/
 /HOMO SAPIENS (HUMAN).//P39195
 F-MAMMA1002329//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.051:33:36
 //XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931
 F-MAMMA1002332//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.5e-20:116:51//H
 OMO SAPIENS (HUMAN).//P08547
 F-MAMMA1002333//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:214:31//B
 OS TAURUS (BOVINE).//P02453
 F-MAMMA1002339//COPPER-METALLOTHIONEIN (CU-MT).//0.59:42:38//HELIX POMAT
 IA (ROMAN SNAIL) (EDIBLE SNAIL).//P55947
 F-MAMMA1002347//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.43:26:61//HOM
 O SAPIENS (HUMAN).//P39188
 F-MAMMA1002351//HYPOTHETICAL PROTEIN MJ0304.//2.3e-07:139:25//METHANOCOC
 CUS JANNASCHII.//Q57752
 F-MAMMA1002352
 F-MAMMA1002353//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00028:31:80//

HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1002355//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.2e-28:87:73/
 /HOMO SAPIENS (HUMAN).//P39193
 F-MAMMA1002356//RELAXIN.//0.95:31:35//SQUALUS ACANTHIAS (SPINY DOGFISH).
 //P11953
 F-MAMMA1002359//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.93:44:36//GUIL
 LARDIA THETA (CRYPTOMONAS PHI).//078487
 F-MAMMA1002360//LATE L2 MU CORE PROTEIN PRECURSOR (PROTEIN X).//0.94:30:
 43//BOVINE ADENOVIRUS TYPE 2 (MASTADENOVIRUS BOS2).//Q96626
 F-MAMMA1002361//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.0e-08:45:68//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1002362//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.58:23:26/
 /LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942
 F-MAMMA1002380//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.23:100:27//DRO
 SOPHILA SIMULANS (FRUIT FLY).//P13729
 F-MAMMA1002384
 F-MAMMA1002385//HYPOTHETICAL 40.9 KD PROTEIN IN ORC2-TIP1 INTERGENIC REG
 ION.//3.8e-14:125:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38241
 F-MAMMA1002392//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:17:58//
 BRANCHIOSTOMA LANCEOLATUM (COMMON LANCELET) (AMPHIOXUS).//021003
 F-MAMMA1002411//30S RIBOSOMAL PROTEIN S17.//0.85:49:32//SYNECHOCYSTIS SP
 . (STRAIN PCC 6803).//P73311
 F-MAMMA1002413//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRA
 GMENT).//0.97:41:39//DROSOPHILA AFFINIS (FRUIT FLY).//P51926
 F-MAMMA1002417//RFBJ PROTEIN.//0.99:31:35//SHIGELLA FLEXNERI.//P37786
 F-MAMMA1002427//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.6e-33:135:59
 //HOMO SAPIENS (HUMAN).//P39194
 F-MAMMA1002428//HYPOTHETICAL PROTEIN C18.//0.97:34:44//SWINEPOX VIRUS (S
 TRAIN KASZA) (SPV).//P32217

F-MAMMA1002434//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.1e-36:56:78/
/HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1002446

F-MAMMA1002454//EARLY NODULIN 20 PRECURSOR (N-20).//0.77:57:45//MEDICAGO
TRUNCATULA (BARREL MEDIC).//P93329

F-MAMMA1002461//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.3e-05:1
93:32//CANIS FAMILIARIS (DOG).//P50551

F-MAMMA1002470//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REG
ION.//1.0e-75:231:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

F-MAMMA1002475//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BET
A) (BRG-1 PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA
PROTEIN HOMOLOG 1).//0.013:99:30//HOMO SAPIENS (HUMAN).//P51532

F-MAMMA1002480//NONSTRUCTURAL PROTEIN 5B.//1.0:23:43//HUMAN CORONAVIRUS
(STRAIN 229E).//P19741

F-MAMMA1002485//STANNIOCALCIN PRECURSOR.//2.1e-23:88:46//HOMO SAPIENS (H
UMAN).//P52823

F-MAMMA1002494//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS C
LARKII (RED SWAMP CRAYFISH).//P55848

F-MAMMA1002498//6.7 KD PROTEIN (ORF 5).//1.0:26:42//BARLEY YELLOW DWARF
VIRUS (ISOLATE PAV) (BYDV).//P09517

F-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC RE
GION.//5.0e-26:222:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43571

F-MAMMA1002530//CYTOSOLIC PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHA
TIDYLCHOLINE 2-ACYLHYDROLASE) / LYSOPHOSPHOLIPASE (EC 3.1.1.5).//4.5e-12
:88:44//HOMO SAPIENS (HUMAN).//P47712

F-MAMMA1002545//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-29:97:71/
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002554//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7
.6) (RPB1) (FRAGMENT).//0.46:54:40//CRICETULUS GRISEUS (CHINESE HAMSTER)

./P11414

F-MAMMA1002556//METALLOTHIONEIN 20-I ISOFORMS A AND B (MT-20-IA AND MT-20-IB).//0.99:21:47//MYTILUS EDULIS (BLUE MUSSEL).//P80251

F-MAMMA1002566//TRANSCRIPTION FACTOR P65 (NUCLEAR FACTOR NF-KAPPA-B P65 SUBUNIT).//0.70:130:30//MUS MUSCULUS (MOUSE).//Q04207

F-MAMMA1002571//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (FRAGMENT).//0.54:45:51//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P35084

F-MAMMA1002573//PARATHYMOSIN.//1.5e-07:69:46//HOMO SAPIENS (HUMAN).//P20962

F-MAMMA1002585//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.38:36:36//MUS MUSCULUS (MOUSE).//P09542

F-MAMMA1002590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.99:22:77//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002597//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.1e-18:44:70//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002598//60S RIBOSOMAL PROTEIN L7.//1.8e-16:40:100//HOMO SAPIENS (HUMAN).//P18124

F-MAMMA1002603

F-MAMMA1002612//30S RIBOSOMAL PROTEIN S16 (FRAGMENT).//1.0:29:37//THERMUS AQUATICUS.//007348

F-MAMMA1002617//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.00041:81:34//RATTUS NORVEGICUS (RAT).//P10164

F-MAMMA1002618//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT).//0.11:18:50//PSYCHODA CINEREA.//Q02027

F-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.8e-13:110:40//CAENORHABDITIS ELEGANS.//Q09931

F-MAMMA1002622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.4e-05:53:58//
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002623//PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR
(EC 1.14.17.3) (PAM).//2.6e-07:37:78//HOMO SAPIENS (HUMAN).//P19021

F-MAMMA1002625

F-MAMMA1002629//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-19:49:73//
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002636//COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).//1.7e-07:189:32//
HOMO SAPIENS (HUMAN).//P12110

F-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//7.7e-54:227:52//RATTUS NORVE
GICUS (RAT).//P37285

F-MAMMA1002646//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PR
OTEIN) (NF-H).//0.034:199:25//MUS MUSCULUS (MOUSE).//P19246

F-MAMMA1002650//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOL
OG 2).//1.7e-07:104:32//MUS MUSCULUS (MOUSE).//P97303

F-MAMMA1002655//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.
0:25:44//HOMO SAPIENS (HUMAN).//P22532

F-MAMMA1002662

F-MAMMA1002665//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.3e-07:54:57/
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA
LIGASE) (ACYL- ACTIVATING ENZYME).//1.4e-10:144:31//ESCHERICHIA COLI.//P
27550

F-MAMMA1002673//BREVICAN CORE PROTEIN PRECURSOR.//0.76:64:39//BOS TAURUS
(BOVINE).//Q28062

F-MAMMA1002684//HYPOTHETICAL 11.8 KD PROTEIN IN GP55-NRDG INTERGENIC REG
ION.//0.094:77:27//BACTERIOPHAGE T4.//P07079

F-MAMMA1002685//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:177:34//R
ATTUS NORVEGICUS (RAT).//P02454

F-MAMMA1002698

F-MAMMA1002699//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//1.2e-28:127:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-MAMMA1002701//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0:14:92//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002708//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.9e-27:52:65//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1002711//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.7e-24:54:75//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002721

F-MAMMA1002727//SOX-13 PROTEIN (FRAGMENT).//0.70:36:38//MUS MUSCULUS (MOUSE).//Q04891

F-MAMMA1002728//HYPOTHETICAL 6.0 KD PROTEIN.//1.0:25:44//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19305

F-MAMMA1002744//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//1.0:52:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834

F-MAMMA1002746//HYPOTHETICAL 5.6 KD PROTEIN (ORF A-45).//1.0:22:40//SULFOLOBUS VIRUS-LIKE PARTICLE SSV1.//P20198

F-MAMMA1002748

F-MAMMA1002754//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.1e-21:56:64//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002758//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.37:14:64//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-MAMMA1002764//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.7e-32:79:60//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002765//PARATHYMOSIN.//0.79:63:28//BOS TAURUS (BOVINE).//P08814

F-MAMMA1002769//GAR2 PROTEIN.//0.00037:192:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-MAMMA1002775//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.//

5.4e-54:240:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704
 F-MAMMA1002780
 F-MAMMA1002782//MARGATOXIN (MGTX).//1.0:31:38//CENTRUROIDES MARGARITATUS
 (SCORPION).//P40755
 F-MAMMA1002796//ICE NUCLEATION PROTEIN.//0.0018:100:41//PSEUDOMONAS FLUO
 RESCENS.//P09815
 F-MAMMA1002807//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.3e-23:100:59/
 /HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1002820//NEUROTOXIN IV (LQQ IV).//1.0:18:50//LEIURUS QUINQUESTRIA
 TUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01489
 F-MAMMA1002830//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.7e-24:55:74/
 /HOMO SAPIENS (HUMAN).//P39195
 F-MAMMA1002833//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.6e-31:95:73/
 /HOMO SAPIENS (HUMAN).//P39189
 F-MAMMA1002835//HYPOTHETICAL 42.1 KD PROTEIN F13G3.3 IN CHROMOSOME I.//1
 .0:54:37//CAENORHABDITIS ELEGANS.//Q19417
 F-MAMMA1002838//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.5e-27:99:70/
 /HOMO SAPIENS (HUMAN).//P39193
 F-MAMMA1002842//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.3e-13:65:63/
 /HOMO SAPIENS (HUMAN).//P39195
 F-MAMMA1002843//METALLOTHIONEIN-II (MT-II).//0.97:19:47//MUS MUSCULUS (M
 OUSE).//P02798
 F-MAMMA1002844//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGI
 ON.//4.9e-08:119:36//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (A
 CMNPV).//P41479
 F-MAMMA1002858//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.98:37:37/
 /PAN TROGLODYTES (CHIMPANZEE).//Q35647
 F-MAMMA1002868//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.8e-10:51:62//
 HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//1.8e-95:194:78//HOMO SAPIENS (HUMAN).//P48059

F-MAMMA1002871//G-PROTEIN COUPLED RECEPTOR HOMOLOG R33.//1.0:51:35//RAT CYTOMEGALOVIRUS (STRAIN MAASTRICHT).//012000

F-MAMMA1002880

F-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//3.3e-22:180:35//HOMO SAPIENS (HUMAN).//P48060

F-MAMMA1002886//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//0.00011:148:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706

F-MAMMA1002887

F-MAMMA1002890//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.030:142:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-MAMMA1002892

F-MAMMA1002895//HYPOTHETICAL PROTEIN UL61.//0.00099:143:35//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

F-MAMMA1002908//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.12:44:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333

F-MAMMA1002909//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00011:28:75//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002930//BOMBYXIN A-7 PRECURSOR (BBX-A7) (4K-PROTHORACICOTROPIC HORMONE) (4K-PTTH).//0.99:45:46//BOMBYX MORI (SILK MOTH).//P26730

F-MAMMA1002937//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//6.5e-24:147:34//HOMO SAPIENS (HUMAN).//P28698

F-MAMMA1002938//CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE).//4.7e-11:44:68//MUS MUSCULUS (MOUSE).//Q61147

F-MAMMA1002941//PROTEIN Q300.//0.0076:21:61//MUS MUSCULUS (MOUSE).//Q02722

F-MAMMA1002947//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//1.9e-08:152:38//STREPTOMYCES FRADIAE.//P20186

F-MAMMA1002964

F-MAMMA1002970//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.0057:55:43//
HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1002972//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (
OCT-T1) (HOMEBOX/POU DOMAIN PROTEIN RDC-1).//0.84:53:41//HOMO SAPIENS (
HUMAN).//Q01851

F-MAMMA1002973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//4.6e-11:54:68/
/HOMO SAPIENS (HUMAN).//P39192

F-MAMMA1002982

F-MAMMA1002987//HYPOTHETICAL 11.9 KD PROTEIN IN RPC8-MFA2 INTERGENIC REG
ION.//0.17:47:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53906

F-MAMMA1003003//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.6e-09:30:73/
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1003004//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0071:41:58//
HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1003007//SPERM PROTAMINE P1.//0.0076:51:37//TACHYGLOSSUS ACULEATU
S ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

F-MAMMA1003011//HISTONE MACRO-H2A.1.//1.8e-60:175:70//RATTUS NORVEGICUS
(RAT).//Q02874

F-MAMMA1003013//ACTIN BINDING PROTEIN.//0.097:83:31//SACCHAROMYCES EXIGU
US (YEAST).//P38479

F-MAMMA1003015

F-MAMMA1003019//MYOTUBULARIN.//0.022:56:37//HOMO SAPIENS (HUMAN).//Q1349
6

F-MAMMA1003026//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0014:208:27//OR
GYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341

F-MAMMA1003031//PROBABLE E4 PROTEIN (E1^E4).//0.14:49:32//HUMAN PAPILLOM
AVIRUS TYPE 6B.//P06459

F-MAMMA1003035//HYPOTHETICAL 24.4 KD PROTEIN IN LPD 3' REGION (ORF4).//5.

1e-12:112:34//ZYMOMONAS MOBILIS.//066114
 F-MAMMA1003039//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-07:68:54//
 HOMO SAPIENS (HUMAN).//P39188
 F-MAMMA1003040//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/2.8e-39:90:57
 //HOMO SAPIENS (HUMAN).//P39190
 F-MAMMA1003044
 F-MAMMA1003047//SPERM HISTONE P2 PRECURSOR (PROTAMINE 2).//0.18:25:44//B
 OS TAURUS (BOVINE).//P19782
 F-MAMMA1003049//PROBABLE E4 PROTEIN.//0.50:67:29//HUMAN PAPILLOMAVIRUS T
 YPE 6C.//P20969
 F-MAMMA1003055//WEAK TOXIN CM-2.//0.99:23:30//NAJA HAJE HAJE (EGYPTIAN C
 OBRA).//P01415
 F-MAMMA1003056//EXPORTED PROTEIN 7 (FRAGMENT).//1.0:52:32//STREPTOCOCCUS
 PNEUMONIAE.//P35597
 F-MAMMA1003057//MD6 PROTEIN.//1.5e-85:168:95//MUS MUSCULUS (MOUSE).//Q60
 584
 F-MAMMA1003066//REGB PROTEIN.//1.0:62:27//PSEUDOMONAS AERUGINOSA.//Q0338
 1
 F-MAMMA1003089//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/5.1e-15:44:77
 //HOMO SAPIENS (HUMAN).//P39190
 F-MAMMA1003099//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE F
 ILAMIN) (FILAMIN 1).//4.8e-20:80:62//HOMO SAPIENS (HUMAN).//P21333
 F-MAMMA1003104//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII.//0.98:22:40/
 /SYNECHOCOCCUS ELONGATUS NAEGELI.//P25900
 F-MAMMA1003113//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.6
 7:35:45//GALLUS GALLUS (CHICKEN).//P02467
 F-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//5.2e-34:141:56//MUS MUSCULU
 S (MOUSE).//P46735
 F-MAMMA1003135//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC RE

GION.//3.6e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
 F-MAMMA1003140
 F-MAMMA1003146//MALE SPECIFIC SPERM PROTEIN MST87F.//1.0:33:36//DROSOPHI
 LA MELANOGASTER (FRUIT FLY).//P08175
 F-MAMMA1003150//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II./
 /4.4e-10:254:30//CAENORHABDITIS ELEGANS.//Q09625
 F-MAMMA1003166//BRAIN PROTEIN H5.//4.0e-42:182:48//HOMO SAPIENS (HUMAN).
 //043236
 F-NT2RM1000001//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC RE
 GION (ORF70).//0.15:38:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
 F-NT2RM1000018
 F-NT2RM1000032//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.51:17:41/
 /CYPRINUS CARPIO (COMMON CARP).//P24948
 F-NT2RM1000035//3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC 1.1.
 1.34) (HMG-COA REDUCTASE).//0.00011:114:27//BLATTELLA GERMANICA (GERMAN
 COCKROACH).//P54960
 F-NT2RM1000037//METALLOTHIONEIN-II (MT-II).//0.025:19:47//SCYLLA SERRATA
 (MUD CRAB).//P02806
 F-NT2RM1000039//VITELLINE MEMBRANE VM34CA PROTEIN PRECURSOR.//0.00083:84
 :33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q06521
 F-NT2RM1000055//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.1e-07:34:55//P
 LASMODIUM LOPHURAE.//P04929
 F-NT2RM1000059//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACT
 OR-LIKE PROTEIN 2) (XMEF2) (RSRFR2).//0.18:83:36//HOMO SAPIENS (HUMAN)./
 /Q02080
 F-NT2RM1000062//PROLINE-RICH PEPTIDE P-B.//0.54:34:44//HOMO SAPIENS (HUM
 AN).//P02814
 F-NT2RM1000080//HYPOTHETICAL 35.7 KD PROTEIN SLR1128.//2.1e-20:119:40//S
 YNECHOCYSTIS SP. (STRAIN PCC 6803).//P72655

F-NT2RM1000086//SALIVARY PROLINE-RICH PROTEIN P0 (ALLELE K) [CONTAINS: P
EPTIDE P-D] (FRAGMENT).//0.20:56:35//HOMO SAPIENS (HUMAN).//P10162

F-NT2RM1000092//COLLAGEN-LIKE PROTEIN.//0.0017:44:45//HERPESVIRUS SAIMIR
I (SUBGROUP C / STRAIN 488).//P22576

F-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY
SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//5.7e-07:109:28//NEUROSPORA
CRASSA.//P87072

F-NT2RM1000119//TRANSCRIPTIONAL REGULATOR IE63 (VMW63) (ICP27).//0.0050:
135:32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P28276

F-NT2RM1000127//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.032:6
8:32//SORGHUM VULGARE (SORGHUM).//P24152

F-NT2RM1000131//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR)
(GIF).//0.82:33:39//BOS TAURUS (BOVINE).//P37359

F-NT2RM1000132//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR
(EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A).//2.7e-59:124
:91//HOMO SAPIENS (HUMAN).//075380

F-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//2.5e-08:
148:29//HOMO SAPIENS (HUMAN).//P49902

F-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY
SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.9e-07:109:27//NEUROSPORA
CRASSA.//P87072

F-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELI
CASE SPAC10F6.02C.//1.0e-12:94:46//SCHIZOSACCHAROMYCES POMBE (FISSION YE
AST).//042643

F-NT2RM1000199//CUTICLE COLLAGEN 12 PRECURSOR.//0.46:130:33//CAENORHABDI
TIS ELEGANS.//P20630

F-NT2RM1000242//PUTATIVE ATP SYNTHASE J CHAIN, MITOCHONDRIAL (EC 3.6.1.3
4).//0.85:38:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013931

F-NT2RM1000244//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X./

/0.0055:98:36//CAENORHABDITIS ELEGANS.//Q11102

F-NT2RM1000252//TRICHOHYALIN.//2.9e-06:88:36//OVIS ARIES (SHEEP).//P2279

3

F-NT2RM1000256//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT).//2.9e-54:153:67//MUS MUSCULUS (MOUSE).//P47856

F-NT2RM1000257//MAGO NASHI PROTEIN.//5.9e-64:136:89//DROSOPHILA MELANOGASTER (FRUIT FLY).//P49028

F-NT2RM1000260

F-NT2RM1000271//GALACTOKINASE (EC 2.7.1.6).//0.99:41:39//BACILLUS SUBTILIS.//P39574

F-NT2RM1000272//HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III.//8.8e-25:131:45//CAENORHABDITIS ELEGANS.//Q09357

F-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//2.5e-63:121:94//BOS TAURUS (BOVINE).//P39942

F-NT2RM1000300//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN).//0.51:145:26//HOMO SAPIENS (HUMAN).//Q13428

F-NT2RM1000314

F-NT2RM1000318//50S RIBOSOMAL PROTEIN L23.//0.83:28:35//AQUIFEX AEOLICUS.//066433

F-NT2RM1000341

F-NT2RM1000354//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5' REGION (ORF55).//0.95:43:37//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159

F-NT2RM1000355//SPERM-SPECIFIC PROTEIN PHI-1.//0.0016:73:43//MYTILUS EDULIS (BLUE MUSSEL).//Q04621

F-NT2RM1000365//HYPOTHETICAL PROTEIN KIAA0140.//3.5e-10:83:49//HOMO SAPIENS (HUMAN).//Q14153

F-NT2RM1000377//DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC 3.1.3.16) (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE PHOSPHATASE 4) (MKP-4).//4.9e-18:113:38//HOMO SAPIENS (HUMAN).//Q99956

F-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00023:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915

F-NT2RM1000394//HISTONE H3.3 (H3.B) (H3.3Q).//4.7e-52:71:91//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), ORYCTOLAGUS CUNICULUS (RABBIT), GALLUS GALLUS (CHICKEN), SPISULA SOLIDISSIMA (ATLANTIC SURF-CLAM), DROSOPHILA MELANOGASTER (FRUIT FLY), AND DROSOPHILA HYDEI (FRUIT FLY).//P06351

F-NT2RM1000399//ENDOTHELIN-2 PRECURSOR (ET-2) (FRAGMENT).//0.92:24:45//CANIS FAMILIARIS (DOG).//P12064

F-NT2RM1000421//CUTICLE COLLAGEN 2C (FRAGMENT).//0.12:93:33//HAEMONCHUS CONTORTUS.//P16252

F-NT2RM1000430//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).//0.13:86:31//NICOTIANA TABACUM (COMMON TOBACCO).//Q03211

F-NT2RM1000499//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//2.9e-17:75:49//HOMO SAPIENS (HUMAN).//Q15057

F-NT2RM1000539//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//2.9e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089

F-NT2RM1000553//GLYCOLIPID TRANSFER PROTEIN (GLTP).//6.4e-06:103:33//SUS SCROFA (PIG).//P17403

F-NT2RM1000555//UNR PROTEIN.//8.7e-77:105:95//RATTUS NORVEGICUS (RAT).//P18395

F-NT2RM1000563//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.15:20:50//HOMO SAPIENS (HUMAN).//P30808

F-NT2RM1000623//CLARA CELL PHOSPHOLIPID-BINDING PROTEIN PRECURSOR (CCBP) (CLARA CELLS 10 KD SECRETORY PROTEIN) (CC10).//0.17:70:34//HOMO SAPIENS (HUMAN).//P11684

F-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.0e-22:133:42//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43636

F-NT2RM1000661//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR)
(GIF) (GIFB).//0.0060:24:33//HOMO SAPIENS (HUMAN).//P25713

F-NT2RM1000666//COLD SHOCK PROTEIN SCOF.//9.1e-07:67:41//STREPTOMYCES CO
ELICOLOR.//P48859

F-NT2RM1000669//CHLOROPLAST 50S RIBOSOMAL PROTEIN L31.//0.071:69:31//POR
PHYRA PURPUREA.//P51290

F-NT2RM1000672//SIGNAL RECOGNITION PARTICLE SEC65 SUBUNIT (FRAGMENT).//0
.27:42:42//KLUYVEROMYCES LACTIS (YEAST).//013475

F-NT2RM1000691//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//4.3e-42:241:
42//HOMO SAPIENS (HUMAN).//P29375

F-NT2RM1000699//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR
(EC 2.1.1.32).//0.94:48:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
P15565

F-NT2RM1000702//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1.//0.00
13:139:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P26308

F-NT2RM1000725//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:15:60//HOMO
SAPIENS (HUMAN).//P02811

F-NT2RM1000741//STATHMIN (CLONE X020) (FRAGMENT).//1.0:53:32//XENOPUS LA
EVIS (AFRICAN CLAWED FROG).//Q09005

F-NT2RM1000742//HYPOTHETICAL 24.1 KD. PROTEIN IN DHFR 3' REGION (ORF2).//1
.0:54:42//HERPESVIRUS SAIMIRI (STRAIN 484-77).//P25049

F-NT2RM1000746//HYPOTHETICAL 16.8 KD. PROTEIN C29E6.04 IN CHROMOSOME I.//
0.11:87:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09858

F-NT2RM1000770//DXS6673E PROTEIN.//2.0e-38:190:48//HOMO SAPIENS (HUMAN).
//Q14202

F-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.3e-12:14
1:30//PODOSPORA ANSERINA.//Q00808

F-NT2RM1000780//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:34:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-NT2RM1000781

F-NT2RM1000800//24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.//7.9e-11:135:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28707

F-NT2RM1000802//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I).//0.43:62:35//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII).//P09921

F-NT2RM1000811

F-NT2RM1000826//UNR PROTEIN.//1.1e-110:144:83//RATTUS NORVEGICUS (RAT).//P18395

F-NT2RM1000829//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:38:34//DROSOPHILA SIMULANS (FRUIT FLY).//P50270

F-NT2RM1000833//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.4e-62:145:84//CANIS FAMILIARIS (DOG).//P38377

F-NT2RM1000850//TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-).//6.1e-08:136:33//RATTUS NORVEGICUS (RAT).//Q63572

F-NT2RM1000852//ATP-DEPENDENT RNA HELICASE ROK1.//1.6e-34:212:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818

F-NT2RM1000857//HISTONE H1.M6.1.//0.76:31:48//TRYPANOSOMA CRUZI.//P40273

F-NT2RM1000867//MICROSOMAL SIGNAL PEPTIDASE 10.8 KD SUBUNIT (EC 3.4.-.-).//0.0082:76:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46965

F-NT2RM1000874//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.38:12:58//HOMO SAPIENS (HUMAN).//P30808

F-NT2RM1000882//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312

F-NT2RM1000883//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.79:22:59//HOMO SAPIENS (HUMAN).//P30808

F-NT2RM1000885//HYPOTHETICAL 5.8 KD PROTEIN.//0.76:18:38//CLOVER YELLOW

MOSAIC VIRUS (CYMV).//P16485

F-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//6.2e-70:153:88//RATTUS NORVEGICUS (RAT).//054888

F-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//4.3e-12:159:28//OXYTRICHA FALLAX.//P02583

F-NT2RM1000905//GLUTATHIONE S-TRANSFERASE 1-1 (EC 2.5.1.18) (CLASS-THETA).//0.98:39:35//LUCILIA CUPRINA (GREENBOTTLE FLY) (AUSTRALIAN SHEEP BLOW FLY).//P42860

F-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.3e-11:169:28//CAENORHABDITIS ELEGANS.//P46577

F-NT2RM1000927//CUTICLE COLLAGEN 1.//0.00048:141:31//CAENORHABDITIS ELEGANS.//P08124

F-NT2RM1000962//HYPOTHETICAL 35.8 KD PROTEIN C4F8.04 IN CHROMOSOME I.//7.1e-13:169:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014180

F-NT2RM1000978//HYPOTHETICAL 20.2 KD PROTEIN IN MNN4-PTK1 INTERGENIC REGION.//0.61:82:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36045

F-NT2RM1001003//ALPHA-2 CATENIN (ALPHA N-CATENIN) (NEURAL ALPHA-CATENIN).//1.6e-21:211:31//GALLUS GALLUS (CHICKEN).//P30997

F-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3.2e-15:119:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RM1001043//ENDOTHELIN-1 (ET-1) (FRAGMENT).//0.78:32:34//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28469

F-NT2RM1001044

F-NT2RM1001059//LORICRIN.//8.6e-08:108:39//HOMO SAPIENS (HUMAN).//P23490

F-NT2RM1001066//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.99:24:50//LYCOPERSICON ESCULENTUM (TOMATO).//Q43513

F-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II)

(PLC-148).//4.7e-15:148:33//HOMO SAPIENS (HUMAN).//P19174
 F-NT2RM1001074//HYPOTHETICAL PROTEIN F-215.//8.6e-05:126:30//HUMAN ADENO
 VIRUS TYPE 2.//P03291
 F-NT2RM1001082//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//6.5e-19:75:54/
 /HOMO SAPIENS (HUMAN).//P39195
 F-NT2RM1001085//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.49:29:41//DROSOP
 HILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RM1001092//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.8e
 -42:200:38//HOMO SAPIENS (HUMAN).//P51522
 F-NT2RM1001102//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC R
 EGION.//1.7e-18:161:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5333
 1
 F-NT2RM1001105//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e
 -05:157:35//STREPTOMYCES FRADIAE.//P20186
 F-NT2RM1001112//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.18:20:55//BOS
 TAURUS (BOVINE).//P02313
 F-NT2RM1001115
 F-NT2RM1001139//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR
 (GRP 1.8).//2.0e-25:156:46//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEA
 N).//P10496
 F-NT2RM2000006//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.76:45:35//LEISHM
 ANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940
 F-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2
 .7.7.6) (RNA POLYMERASE III SUBUNIT 2).//3.9e-87:238:65//DROSOPHILA MELA
 NOGASTER (FRUIT FLY).//P25167
 F-NT2RM2000030//TOXINS 1 AND 2.//0.98:21:42//TRIMERESURUS WAGLERI (WAGLE
 R'S PIT VIPER) (TROPIDOLAEMUS WAGLERI).//P24335
 F-NT2RM2000032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00059:53:49//
 HOMO SAPIENS (HUMAN).//P39188

F-NT2RM2000042//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.
0:68:26//HOMO SAPIENS (HUMAN).//P22532

F-NT2RM2000092//HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC R
EGION.//7.0e-11:80:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38748

F-NT2RM2000093//OVARY MATURATING PARSIN (OMP).//1.0:26:38//LOCUSTA MIGRA
TORIA (MIGRATORY LOCUST).//P80045

F-NT2RM2000101//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//3
.3e-09:56:35//CAENORHABDITIS ELEGANS.//Q11096

F-NT2RM2000124//CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT (
EC 2.7.1.37) (PKA C-ALPHA).//3.1e-35:77:96//MUS MUSCULUS (MOUSE).//P0513
2

F-NT2RM2000191//3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4
.17) (PDEASE REGA).//3.3e-05:181:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOL
D).//Q23917

F-NT2RM2000192//REPLICATION PROTEIN E1 (FRAGMENTS).//0.019:148:25//COTTO
NTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN WASHINGTON B) (CRPV).//P5189
4

F-NT2RM2000239//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.00032:111:32//M
US MUSCULUS (MOUSE).//P05143

F-nnnnnnnnnnnnn//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.046:59:33//LYCOP
ERSICON ESCULENTUM (TOMATO).//Q43512

F-NT2RM2000250//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN)
(IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35)
(CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.054:46:34//RATTUS N
ORVEGICUS (RAT).//P08699

F-NT2RM2000259//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN)
(IER 2.9/ER2.6).//0.27:112:33//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
//P29128

F-NT2RM2000260//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-22:191:35//M

US MUSCULUS (MOUSE).//P05143
 F-NT2RM2000287//HYPOTHETICAL 11.8 KD PROTEIN C1B3.02C IN CHROMOSOME I.//
 5.0e-19:83:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013868
 F-NT2RM2000322//DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) (DAP DECARBO
 XYLASE).//0.47:117:29//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P561
 29
 F-NT2RM2000359//SPORE GERMINATION PROTEIN 270-11.//0.12:83:36//DICTYOSTE
 LIUM DISCOIDEUM (SLIME MOLD).//P22698
 F-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.3e-16:203:30//HOMO
 SAPIENS (HUMAN).//P11274
 F-NT2RM2000368//DEK PROTEIN.//0.00027:100:32//HOMO SAPIENS (HUMAN).//P35
 659
 F-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (
 POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE).//6.8e-36:170:47//ESCHERICHIA COL
 I.//P05055
 F-NT2RM2000374//NODAL PRECURSOR.//1.1e-32:64:95//MUS MUSCULUS (MOUSE).//
 P43021
 F-NT2RM2000395//IMMEDIATE-EARLY PROTEIN IE180.//0.31:41:43//PSEUDORABIES
 VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
 F-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PRO
 TEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC
 INTERMEDIATE COMPONENT).//1.2e-30:228:32//SACCHAROMYCES CEREVISIAE (BAKE
 R' S YEAST).//P32802
 F-NT2RM2000407//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.032:105:30//HOMO
 SAPIENS (HUMAN).//P51805
 F-NT2RM2000420//METALLOTHIONEIN (MT).//0.88:42:38//PLEURONECTES PLATESSA
 (PLAICE).//P07216
 F-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//2.0e-
 117:237:87//RATTUS NORVEGICUS (RAT).//Q08469

F-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//1.1e-08:157:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36113

F-NT2RM2000469//70 KD ANTIGEN.//0.050:207:23//SHIGELLA FLEXNERI.//P18010

F-NT2RM2000490//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.022:25:44//HOMO SAPIENS (HUMAN).//P02811

F-NT2RM2000502//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0037:17:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RM2000504//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//1.7e-22:195:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42908

F-NT2RM2000522//RAS-RELATED PROTEIN RABA (FRAGMENT).//3.6e-05:67:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141

F-NT2RM2000540//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//8.4e-33:214:38//CAENORHABDITIS ELEGANS.//Q18262

F-NT2RM2000556//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-09:133:36//HOMO SAPIENS (HUMAN).//P56524

F-NT2RM2000566//INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F).//2.2e-60:244:51//HOMO SAPIENS (HUMAN).//P23229

F-NT2RM2000567//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.3e-09:192:34//MUS MUSCULUS (MOUSE).//P05143

F-NT2RM2000569//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.0e-08:43:72//HOMO SAPIENS (HUMAN).//P39188

F-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//9.1e-54:225:45//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505

F-NT2RM2000581//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.079:111:34//HOMO SAPIENS (HUMAN).//Q15427

F-NT2RM2000588//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//2.3e-09:193:32//HOMO SAPIENS (HUMAN).//P56524

F-NT2RM2000594//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.18:33:42//HOMO

SAPIENS (HUMAN).//P02811
 F-NT2RM2000599//DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.MMUI).//1.5e-09:68:45//MUS MUSCULUS (MOUSE).//P13864
 F-NT2RM2000609//GRANULIN 2.//0.83:42:35//CYPRINUS CARPIO (COMMON CARP).//P81014
 F-NT2RM2000612//ZINC FINGER PROTEIN GCS1.//7.2e-05:155:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197
 F-NT2RM2000623//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//1.8e-09:196:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 F-NT2RM2000624//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.070:113:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730
 F-NT2RM2000635//SPERM PROTAMINE P1.//0.54:47:38//ANTECHINUS STUARTII.//P42129
 F-NT2RM2000636//OUTER MEMBRANE PROTEIN H.8 PRECURSOR.//0.096:62:35//NEISSERIA GONORRHOEAE.//P11910
 F-NT2RM2000639//HYPOTHETICAL PROTEIN MJ0243.//0.99:32:34//METHANOCOCCUS JANNASCHII.//Q57694
 F-NT2RM2000649//NEURONAL CALCIUM SENSOR 1 (NCS-1).//0.00049:70:35//RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P36610
 F-NT2RM2000669//50S RIBOSOMAL PROTEIN L34.//1.0:34:44//BACILLUS SUBTILIS.//P05647
 F-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//7.0e-116:243:87//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE).//P32391
 F-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.8e-21:174:35//HOMO SAPIENS (HUMAN).//Q15404
 F-NT2RM2000718//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.0022:174:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P13695

F-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.6e-102:24
6:74//HOMO SAPIENS (HUMAN).//P28160

F-NT2RM2000740//HYPOTHETICAL 131.1 KD HELICASE IN ALG7-ENP1 INTERGENIC R
EGION.//8.5e-51:212:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P3814
4

F-NT2RM2000795//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.0e-41:125:53
//HOMO SAPIENS (HUMAN).//P39189

F-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//1
.1e-128:291:89//RATTUS NORVEGICUS (RAT).//P23514

F-NT2RM2000837//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT K
INASE INHIBITOR P57) (P57KIP2).//3.9e-05:113:36//HOMO SAPIENS (HUMAN).//
P49918

F-NT2RM2000951//HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME III./
/2.5e-49:273:39//CAENORHABDITIS ELEGANS.//P30646

F-NT2RM2000952//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PR
OTEIN) (NF-H) (FRAGMENT).//0.037:234:23//RATTUS NORVEGICUS (RAT).//P1688
4

F-NT2RM2000984//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III./
/6.3e-44:216:43//CAENORHABDITIS ELEGANS.//P41879

F-NT2RM2001004//SYNAPSINS IA AND IB.//0.15:178:32//RATTUS NORVEGICUS (RA
T).//P09951

F-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.4e-87:188:90//MUS MU
SCULUS (MOUSE).//Q60809

F-NT2RM2001065//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.53:12
2:31//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.
//3.4e-13:171:30//CAENORHABDITIS ELEGANS.//P46577

F-NT2RM2001105//SPORE COAT PROTEIN SP96.//7.8e-06:141:34//DICTYOSTELIUM
DISCOIDEUM (SLIME MOLD).//P14328

F-NT2RM2001131//PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03.//2.3e-18
:249:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10475
F-NT2RM2001141//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.
//0.050:134:26//CAENORHABDITIS ELEGANS.//P34681
F-NT2RM2001152
F-NT2RM2001177//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//0.86:4
2:40//GALLUS GALLUS (CHICKEN).//P32018
F-NT2RM2001194//SMOOTHHELIN.//4.7e-05:77:32//HOMO SAPIENS (HUMAN).//P5381
4
F-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.7e-18:218:35//M
US MUSCULUS (MOUSE).//P05143
F-NT2RM2001201//CYSTEINE STRING PROTEIN (CCCS1).//0.041:22:59//TORPEDO C
ALIFORNICA (PACIFIC ELECTRIC RAY).//P56101
F-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP
10).//1.3e-13:183:32//RATTUS NORVEGICUS (RAT).//P97924
F-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)
(L-GLUTAMINE AMIDOHYDROLASE).//6.5e-121:218:98//RATTUS NORVEGICUS (RAT)
.//P13264
F-NT2RM2001243//HYPOTHETICAL 200.0 KD PROTEIN IN GZF3-IME2 INTERGENIC RE
GION.//0.00019:177:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42945
F-NT2RM2001247//LEGUMIN B (FRAGMENT).//0.22:54:35//PISUM SATIVUM (GARDEN
PEA).//P14594
F-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.8e-109
:207:98//MUS MUSCULUS (MOUSE).//P53995
F-NT2RM2001291//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0
16:22:40//HOMO SAPIENS (HUMAN).//P22531
F-NT2RM2001306//REF(2)P PROTEIN.//0.61:51:33//DROSOPHILA MELANOGASTER (F
RUIT FLY).//P14199
F-NT2RM2001312//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.2e-11:33:72/

/HOMO SAPIENS (HUMAN).//P39195

F-NT2RM2001319

F-NT2RM2001324//ZYXIN.//5.1e-22:91:38//GALLUS GALLUS (CHICKEN).//Q04584

F-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//7.4e-10:15

9:27//PODOSPORA ANSERINA.//Q00808

F-NT2RM2001360//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)

.//1.0:27:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P05623

F-NT2RM2001370//NAPE PROTEIN.//0.98:44:31//PARACOCCLUS DENITRIFICANS (SUB

SP. THIOSPHAERA PANTOTROPHA).//Q56348

F-NT2RM2001393//VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-

IN; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2].//0.0024:163:31//ICHTHYOMYZON

UNICUSPUS (SILVER LAMPREY).//Q91062

F-NT2RM2001420

F-NT2RM2001424//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.4

e-41:140:59//HOMO SAPIENS (HUMAN).//Q00839

F-NT2RM2001499//HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1)

(CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LE

UKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG)./

/3.7e-71:201:68//HOMO SAPIENS (HUMAN).//P30825

F-NT2RM2001504//CUTICLE COLLAGEN 2.//0.028:41:39//CAENORHABDITIS ELEGANS

.//P17656

F-NT2RM2001524//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III./

/6.7e-47:190:42//CAENORHABDITIS ELEGANS.//Q09316

F-NT2RM2001544//TELOMERE-BINDING PROTEIN 51 KD SUBUNIT.//0.0027:136:33//

EUPLOTES CRASSUS.//Q06184

F-NT2RM2001547//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REG

ION.//8.5e-18:91:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564

F-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)

) (RO(SS-A)).//3.9e-35:212:41//HOMO SAPIENS (HUMAN).//P19474

F-NT2RM2001582//RESA PROTEIN.//0.0033:72:27//BACILLUS SUBTILIS.//P35160
 F-NT2RM2001588//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//1.0e-06
 :115:32//ZEA MAYS (MAIZE).//P14918
 F-NT2RM2001592//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).
 //0.033:156:23//HOMO SAPIENS (HUMAN).//P26371
 F-NT2RM2001605//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//1.1e-116:249
 :82//HOMO SAPIENS (HUMAN).//P29375
 F-NT2RM2001613//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.2e-97:
 192:100//RATTUS NORVEGICUS (RAT).//P38378
 F-NT2RM2001632//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00068:145:
 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 F-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEM
 BRANE PROTEIN OF 121 KD) (P145).//1.1e-39:235:47//RATTUS NORVEGICUS (RAT
).//P52591
 F-NT2RM2001637//HYPOTHETICAL BHLF1 PROTEIN.//0.075:197:29//EPSTEIN-BARR
 VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-NT2RM2001641//NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R).//0.013:
 29:68//HOMO SAPIENS (HUMAN).//P00387
 F-NT2RM2001648//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//3.2e-65:
 132:100//CANIS FAMILIARIS (DOG).//P38377
 F-NT2RM2001652//PROTEIN TRANSPORT PROTEIN SEC7.//1.6e-32:261:32//SACCHAR
 OMYCES CEREVISIAE (BAKER'S YEAST).//P11075
 F-NT2RM2001659//CARBOXYPEPTIDASE A INHIBITOR.//0.83:30:46//ASCARIS SUUM
 (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P19399
 F-NT2RM2001664//IKI3 PROTEIN.//1.3e-31:265:34//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//Q06706
 F-NT2RM2001668//TONB PROTEIN.//0.32:39:41//XANTHOMONAS CAMPESTRIS (PV. C
 AMPESTRIS).//034261
 F-NT2RM2001670//ZINC FINGER PROTEIN 174.//3.6e-21:172:39//HOMO SAPIENS (

HUMAN).//Q15697
 F-NT2RM2001671//HYPOTHETICAL 118.6 KD PROTEIN C29E6.03C IN CHROMOSOME I.
 //1.6e-10:229:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09857
 F-NT2RM2001675//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS).//1.0
 :184:21//METHANOCOCCUS JANNASCHII.//Q57695
 F-NT2RM2001681//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1)
 .//0.0039:199:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54399
 F-NT2RM2001688//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REG
 ION.//2.6e-21:162:33//BACILLUS SUBTILIS.//P42966
 F-NT2RM2001695//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.9e-41:60:81/
 /HOMO SAPIENS (HUMAN).//P39194
 F-NT2RM2001696//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGI
 ON.//9.8e-16:126:38//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
 F-NT2RM2001698//PENAEIDIN-3B PRECURSOR (P3-B).//0.36:52:34//PENAEUS VANN
 AMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81059
 F-NT2RM2001699//TRANSCRIPTION INITIATION FACTOR TFIID 30 KD SUBUNIT (TAF
 II-30) (TAFII30).//0.0012:79:40//HOMO SAPIENS (HUMAN).//Q12962
 F-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3
 .99.-) (VLCAD) (FRAGMENT).//1.0e-30:140:53//MUS MUSCULUS (MOUSE).//P5054
 4
 F-NT2RM2001706//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.5e-33:95:75/
 /HOMO SAPIENS (HUMAN).//P39195
 F-NT2RM2001716//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC RE
 GION PRECURSOR.//0.010:116:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 //P47179
 F-NT2RM2001718//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00029:77:37
 //BACILLUS SUBTILIS.//P39217
 F-NT2RM2001723//POSTERIOR PITUITARY PEPTIDE.//0.94:26:53//BOS TAURUS (BO

VINE).//P01154

F-NT2RM2001727//E7 PROTEIN.//0.91:46:34//HUMAN PAPILLOMAVIRUS TYPE 23.//
P50781

F-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//4.9e-07:139:29//CAENORHABDITIS ELEGANS.//Q09931

F-NT2RM2001743//PROENKEPHALIN A PRECURSOR.//0.75:65:35//CAVIA PORCELLUS (GUINEA PIG).//P47969

F-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//1.5e-14:119:36//HOMO SAPIENS (HUMAN).//Q92609

F-NT2RM2001760//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.3e-58:119:99//CANIS FAMILIARIS (DOG).//P38377

F-NT2RM2001768//HYPOTHETICAL PROTEIN UL25.//0.45:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16761

F-NT2RM2001771//ZINC FINGER PROTEIN 135.//4.6e-80:224:60//HOMO SAPIENS (HUMAN).//P52742

F-NT2RM2001782//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//7.0e-06:61:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

F-NT2RM2001784//HYPOTHETICAL PROTEIN UL61.//0.00070:145:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

F-NT2RM2001785//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//1.5e-08:127:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RM2001797//ZINC FINGER PROTEIN 135.//1.6e-73:267:49//HOMO SAPIENS (HUMAN).//P52742

F-NT2RM2001800//HYPOTHETICAL HELICASE MG018/MG017/MG016 HOMOLOG.//3.9e-12:171:33//MYCOPLASMA PNEUMONIAE.//P75093

F-NT2RM2001803//IKI3 PROTEIN.//1.6e-38:283:36//SACCHAROMYCES CEREVISIAE

(BAKER'S YEAST).//Q06706
 F-NT2RM2001805//COLD SHOCK-LIKE PROTEIN CSPH.//0.51:46:32//SALMONELLA TY
 PHIMURIUM.//033793
 F-NT2RM2001813//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN
 C14B1.4 IN CHROMOSOME III.//5.0e-05:82:32//CAENORHABDITIS ELEGANS.//Q179
 63
 F-NT2RM2001823//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//3.
 6e-49:233:45//HOMO SAPIENS (HUMAN).//014647
 F-NT2RM2001839//RETICULOCALBIN 1 PRECURSOR.//5.2e-65:222:56//HOMO SAPIEN
 S (HUMAN).//Q15293
 F-NT2RM2001840//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.6e-33:102:68
 //HOMO SAPIENS (HUMAN).//P39194
 F-NT2RM2001855//BASP1 PROTEIN.//0.054:120:30//HOMO SAPIENS (HUMAN).//P80
 723
 F-NT2RM2001867//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC RE
 GION.//4.1e-19:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
 F-NT2RM2001879//HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I./
 /5.9e-15:76:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09800
 F-NT2RM2001886//HYPOTHETICAL 126.9 KD PROTEIN C22G7.04 IN CHROMOSOME I./
 /1.4e-41:249:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09798
 F-NT2RM2001896//HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC REG
 ION.//2.1e-59:197:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25582
 F-NT2RM2001903//HYPOTHETICAL PROTEIN MJ0263.//0.070:132:31//METHANOCOCCU
 S JANNASCHII.//006917
 F-NT2RM2001930//THROMBOSPONDIN 2 PRECURSOR.//7.1e-05:53:47//MUS MUSCULUS
 (MOUSE).//Q03350
 F-NT2RM2001935//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.00046:116:35//CAE
 NORHABDITIS ELEGANS.//Q21184
 F-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27

:216:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320
 F-NT2RM2001950//HIRUDIN HV1 (BUFRUDIN).//0.59:43:34//HIRUDINARIA MANILLE
 NSIS (BUFFALO LEECH).//P81492
 F-NT2RM2001982//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-
 8 SUBUNIT (G GAMMA-C).//0.72:35:42//BOS TAURUS (BOVINE).//P50154
 F-NT2RM2001983//PROLINE-RICH PEPTIDE P-B.//0.00035:23:52//HOMO SAPIENS (
 HUMAN).//P02814
 F-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//8.6e-
 24:197:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37838
 F-NT2RM2001997
 F-NT2RM2001998//IMMEDIATE-EARLY PROTEIN IE180.//0.076:92:27//PSEUDORABIE
 S VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
 F-NT2RM2002004//SLF1 PROTEIN.//3.5e-06:235:27//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//Q12034
 F-NT2RM2002014//HYPOTHETICAL PROTEIN HI0568.//2.1e-17:235:29//HAEMOPHILU
 S INFLUENZAE.//P71353
 F-NT2RM2002030//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOM
 ERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-
 PHOSPHATE AMIDOTRANSFERASE) (GFAT).//9.5e-105:271:76//MUS MUSCULUS (MOU
 SE).//P47856
 F-NT2RM2002049//SMALL PROLINE-RICH PROTEIN 2-1.//0.099:41:41//HOMO SAPIE
 NS (HUMAN).//P35326
 F-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.01-
 2:217:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q07878
 F-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRN
 P X) (CBP).//1.1e-09:65:53//MUS MUSCULUS (MOUSE).//Q61990
 F-NT2RM2002091//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC R
 EGION.//0.072:74:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
 F-NT2RM2002100//ATP-DEPENDENT RNA HELICASE ROK1.//4.5e-50:289:41//SACCHA

ROMYCES CEREVISIAE (BAKER'S YEAST).//P45818

F-NT2RM2002109//NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TR
KC TYROSINE KINASE) (GP145-TRKC) (TRK-C).//1.4e-14:203:32//RATTUS NORVEG
ICUS (RAT).//Q03351

F-NT2RM2002128//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.
0025:139:31//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//9.2e-20:42:73//BRACH
YDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P47805

F-NT2RM2002145//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR.//0
.0085:200:26//TRITICUM AESTIVUM (WHEAT).//P08488

F-NT2RM2002178//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//5.8e-05:56:39/
/BOS TAURUS (BOVINE).//P25508

F-NT2RM2002580//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF
-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2
.9e-14:96:37//PETROMYZON MARINUS (SEA LAMPREY).//P25210

F-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2
.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//8.6e-95:271:67//DROSOPHILA MELA
NOGASTER (FRUIT FLY).//P25167

F-NT2RM4000027//INTERFERON-ACTIVATABLE PROTEIN 202 (IFI-202).//0.99:72:3
1//MUS MUSCULUS (MOUSE).//P15091

F-NT2RM4000030//LAS1 PROTEIN.//1.4e-14:184:32//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P36146

F-NT2RM4000046//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.99:120:28//RA
TTUS NORVEGICUS (RAT).//P13941

F-NT2RM4000061

F-NT2RM4000085//ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (C
NDH II) (DEAD BOX PROTEIN 9) (MHDL-5).//8.5e-40:263:38//MUS MUSCULUS (MO
USE).//070133

F-NT2RM4000086//HYPOTHETICAL PROTEIN HI1497.//1.0:27:37//HAEMOPHILUS INF

LUENZAE.//P44221

F-NT2RM4000104//ZINC FINGER PROTEIN 134.//1.0e-26:64:56//HOMO SAPIENS (HUMAN).//P52741

F-NT2RM4000139//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:38:42//THERMOTOGA MARITIMA.//P35874

F-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//6.3e-34:181:40//HOMO SAPIENS (HUMAN).//P26639

F-NT2RM4000156//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//4.6e-12:142:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-NT2RM4000167//KINESIN-LIKE PROTEIN KIF4.//3.4e-123:269:91//MUS MUSCULUS (MOUSE).//P33174

F-NT2RM4000169//M PROTEIN, SEROTYPE 2.2 PRECURSOR.//9.7e-10:229:26//STREPTOCOCCUS PYOGENES.//P50469

F-NT2RM4000191//P68-LIKE PROTEIN.//2.1e-11:104:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P24783

F-NT2RM4000197//CUTICLE PROTEIN CP463 (CPCP463).//0.84:29:37//CANCER PAGURUS (ROCK CRAB).//P81587

F-NT2RM4000199//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//1.8e-06:187:34//HOMO SAPIENS (HUMAN).//P10162

F-NT2RM4000200//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3' REGION (ORF3).//0.52:42:40//BACILLUS LICHENIFORMIS.//P22754

F-NT2RM4000202//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.00044:168:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P14282

F-NT2RM4000210//EXTENSIN PRECURSOR.//0.27:129:27//DAUCUS CAROTA (CARROT).//P06599

F-NT2RM4000215//MAK16 PROTEIN.//2.0e-65:234:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10962

F-NT2RM4000229//GAR2 PROTEIN.//0.13:217:26//SCHIZOSACCHAROMYCES POMBE (F

ISSION YEAST).//P41891
 F-NT2RM4000233//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.047:108:30//HOMO
 SAPIENS (HUMAN).//P51805
 F-NT2RM4000244//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.67:59:27/
 /BALAENOPTERA PHYSALUS (FINBACK WHALE) (COMMON RORQUAL).//P24947
 F-NT2RM4000251//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0059:108:35//MU
 S MUSCULUS (MOUSE).//P05143
 F-NT2RM4000265//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.1e-38:70:70//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RM4000290//TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3).//1.6e-115:209
 :94//HOMO SAPIENS (HUMAN).//Q04726
 F-NT2RM4000324//PRESPORE PROTEIN DP87 PRECURSOR.//0.14:136:30//DICTYOSTE
 LIUM DISCOIDEUM (SLIME MOLD).//Q04503
 F-NT2RM4000327//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION
 .//0.91:73:28//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV
).//P41703
 F-NT2RM4000344//YME1 PROTEIN HOMOLOG (EC 3.4.24.-).//9.4e-78:241:55//CAE
 NORHABDITIS ELEGANS.//P54813
 F-NT2RM4000349//CYSTEINE STRING PROTEIN (CCCS1).//0.055:22:59//TORPEDO C
 ALIFORNICA (PACIFIC ELECTRIC RAY).//P56101
 F-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//4.6e-26:
 208:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371
 F-NT2RM4000356//COAT PROTEIN.//0.11:105:36//SATELLITE TOBACCO MOSAIC VIR
 US (STMV).//P17574
 F-NT2RM4000366//IMMEDIATE-EARLY PROTEIN.//1.2e-05:215:24//HERPESVIRUS SA
 IMIRI (STRAIN 11).//Q01042
 F-NT2RM4000368//HYPOTHETICAL 7.3 KD PROTEIN IN RPBA-GP46 INTERGENIC REGI
 ON.//0.54:46:36//BACTERIOPHAGE RB69.//064300
 F-NT2RM4000386//RHSC PROTEIN PRECURSOR.//0.0096:162:29//ESCHERICHIA COLI

./P16918

F-NT2RM4000395//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC
REGION.//4.5e-66:256:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P436
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F-NT2RM4000414//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5' REGION.//0.13:33:
48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

F-NT2RM4000421//MRNA TRANSPORT REGULATOR MTR10.//5.0e-13:171:29//SACCHAR
OMYCES CEREVISIAE (BAKER'S YEAST).//Q99189

F-NT2RM4000425//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.1e-25:46:80/
/HOMO SAPIENS (HUMAN).//P39193

F-NT2RM4000433//CUTICLE COLLAGEN 3A3.//2.5e-06:77:38//HAEMONCHUS CONTORT
US.//P16253

F-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I
.//4.3e-09:215:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10297

F-NT2RM4000471//TRNA SPLICING PROTEIN SPL1.//6.7e-73:163:65//CANDIDA ALB
ICANS (YEAST).//P87185

F-NT2RM4000486//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.0012:121:34//GA
LLUS GALLUS (CHICKEN).//P15988

F-NT2RM4000496//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7
.6) (RNA POLYMERASE II SUBUNIT 1).//5.9e-09:175:35//SCHIZOSACCHAROMYCES
POMBE (FISSION YEAST).//P36594

F-NT2RM4000511//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.020:122:31//DR
OSOPHILA SIMULANS (FRUIT FLY).//P13729

F-NT2RM4000514//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.46:68
:32//ARTEMIA SANFRANCISCANA (BRINE SHRIMP) (ARTEMIA FRANCISCANA).//Q3770

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F-NT2RM4000515//GAR2 PROTEIN.//3.2e-05:198:27//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST).//P41891

F-NT2RM4000520//HYPOTHETICAL 7.5 KD PROTEIN (ORF 63).//0.011:55:38//SPIN

ACIA OLERACEA (SPINACH).//P08974
 F-NT2RM4000531//ZINC FINGER PROTEIN 169 (FRAGMENT).//3.6e-44:244:42//HOMO SAPIENS (HUMAN).//Q14929
 F-NT2RM4000532//PUTATIVE MEMBRANE PROTEIN 53.//1.0:47:34//HERPESVIRUS SATIVUM (STRAIN 11).//Q01049
 F-NT2RM4000534//HYPOTHETICAL 5.9 KD PROTEIN IN WRBA-PUTA INTERGENIC REGION.//0.75:26:46//ESCHERICHIA COLI.//P56614
 F-NT2RM4000585//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; CORE PROTEIN P26].//0.019:86:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLISY) (HIV-2).//P12450
 F-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//5.0e-23:224:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RM4000595//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//3.8e-62:226:50//CAENORHABDITIS ELEGANS.//P34284
 F-NT2RM4000603//SRC SUBSTRATE CORTACTIN (AMPLAXIN) (EMS1 ONCOGENE).//0.077:132:22//HOMO SAPIENS (HUMAN).//Q14247
 F-NT2RM4000611//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//1.9e-06:82:32//CAENORHABDITIS ELEGANS.//Q17963
 F-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME).//5.3e-79:213:62//ESCHERICHIA COLI.//P27550
 F-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.3e-11:147:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P74168
 F-NT2RM4000689
 F-NT2RM4000698//CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 12 PRECURSOR (HC-A.12).//0.26:45:33//BOMBYX MORI (SILK MOTH).//P05687
 F-NT2RM4000700//THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//0.95:165:25//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//P53364

F-NT2RM4000712//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3
(EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING P
ROTEASE) (DEUBIQUITINATING ENZYME).//2.2e-82:152:63//CAENORHABDITIS ELEG
ANS.//P34547

F-NT2RM4000717//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.80:54:40//DROS
OPHILA SIMULANS (FRUIT FLY).//P13729

F-NT2RM4000733//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.5e-08:139:28//MUS MUSC
ULUS (MOUSE).//Q06666

F-NT2RM4000734//GASTRULA ZINC FINGER PROTEIN XLCGF26.1 (FRAGMENT).//7.2e
-20:205:28//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18715

F-NT2RM4000741//SPERM PROTAMINE P1.//0.89:52:38//ISOODON MACROURUS (SHOR
T-NOSED BANDICOOT).//P42136

F-NT2RM4000751//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT
) .//5.2e-77:246:52//MUS MUSCULUS (MOUSE).//P10076

F-NT2RM4000764//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.062:33:42//OV
IS ARIES (SHEEP).//Q02958

F-NT2RM4000778

F-NT2RM4000779//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.014:53:4
5//VOLVOX CARTERI.//P21997

F-NT2RM4000787//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BM
P-1).//0.00011:73:39//MUS MUSCULUS (MOUSE).//P98063

F-NT2RM4000790//SPORE COAT PROTEIN SP96.//0.00083:157:29//DICTYOSTELIUM
DISCOIDEUM (SLIME MOLD).//P14328

F-NT2RM4000795//CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLH
YDROLASE) (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (PSEUDOCOLINE
STERASE).//7.4e-41:271:36//HOMO SAPIENS (HUMAN).//P06276

F-NT2RM4000796//5-METHYLCYTOSINE-SPECIFIC RESTRICTION ENZYME B (EC 3.1.2
1.-).//0.28:82:30//ESCHERICHIA COLI.//P15005

F-NT2RM4000798//PROTEIN TRANSPORT PROTEIN SEC7.//4.7e-38:165:48//SACCHAR

OMYCES CEREVISIAE (BAKER'S YEAST).//P11075
 F-NT2RM4000813//METALLOTHIONEIN-IB.//0.0025:25:44//OVIS ARIES (SHEEP).//
 P09577
 F-NT2RM4000820
 F-NT2RM4000833//HYPOTHETICAL PROTEIN MJ1136.//6.5e-42:206:41//METHANOCOC
 CUS JANNASCHII.//Q58536
 F-NT2RM4000848//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (
 BRN-3.0).//0.00060:159:33//MUS MUSCULUS (MOUSE).//P17208
 F-NT2RM4000852//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.0076:13:69//H
 OMO SAPIENS (HUMAN).//P35325
 F-NT2RM4000855//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0060:68:44//
 HOMO SAPIENS (HUMAN).//P39194
 F-NT2RM4000887//RTS1 PROTEIN (SCS1 PROTEIN).//0.23:153:24//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P38903
 F-NT2RM4000895//HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC REG
 ION.//3.3e-09:80:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43123
 F-NT2RM4000950//HYPOTHETICAL PROTEIN MJ0572.//0.090:68:29//METHANOCOCCUS
 JANNASCHII.//Q57992
 F-NT2RM4000971//KINESIN LIGHT CHAIN (KLC).//0.79:201:24//LOLIGO PEALEII
 (LONGFIN SQUID).//P46825
 F-NT2RM4000979//MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN R
 LC).//1.2e-07:25:96//HOMO SAPIENS (HUMAN).//P19105
 F-NT2RM4000996//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC
 ZINC FINGER PROTEIN).//1.4e-56:253:46//MUS MUSCULUS (MOUSE).//P17141
 F-NT2RM4001002
 F-NT2RM4001016//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT
 PROTEIN P12; CORE SHELL PROTEIN P30].//0.25:101:31//FBR MURINE OSTEOSARC
 OMA VIRUS.//P29175
 F-NT2RM4001032//CUTICLE COLLAGEN 2.//2.6e-07:130:39//CAENORHABDITIS ELEG

ANS.//P17656

F-NT2RM4001047//MO25 PROTEIN.//5.6e-107:252:80//MUS MUSCULUS (MOUSE).//Q
06138

F-NT2RM4001054//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.0e-109
:209:94//CANIS FAMILIARIS (DOG).//P38377

F-NT2RM4001084//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXUR-IADA INTE
RGENIC REGION.//0.57:95:30//ESCHERICHIA COLI.//P39376

F-NT2RM4001092//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.
//2.5e-47:231:47//CAENORHABDITIS ELEGANS.//Q09531

F-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II./
/1.3e-08:243:23//CAENORHABDITIS ELEGANS.//Q09417

F-NT2RM4001140//HOMEBOX PROTEIN MSH-D.//7.1e-13:103:38//BRACHYDANIO RER
IO (ZEBRAFISH) (ZEBRA DANIO).//Q01704

F-NT2RM4001151//SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).//0.26:96:34//HO
MO SAPIENS (HUMAN).//P17600

F-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//3.6e-103:201:91//BOS TAU
RUS (BOVINE).//Q27969

F-NT2RM4001160//GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) (CLASS-PHI) (FRA
GMENTS).//1.0:33:36//BRASSICA OLERACEA (CAULIFLOWER).//P48438

F-NT2RM4001187//PREPROTEIN TRANSLOCASE SECA SUBUNIT.//0.44:158:27//MYCOP
LASMA GENITALIUM.//P47318

F-NT2RM4001191//LONG NEUROTOXIN 2 (TOXIN C).//0.99:44:43//ASTROTIA STOKES
SI (STOKES'S SEA SNAKE) (DSTEIRA STOKESI).//P01381

F-NT2RM4001200//ZINC FINGER PROTEIN 135.//2.2e-82:245:59//HOMO SAPIENS (
HUMAN).//P52742

F-NT2RM4001203//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC R
EGION.//0.028:94:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RM4001204//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.
0096:182:34//HOMO SAPIENS (HUMAN).//Q15428

F-NT2RM4001217//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-21:221:29//DRO
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RM4001256//CBP3 PROTEIN PRECURSOR.//0.30:55:32//SACCHAROMYCES CEREV
ISIAE (BAKER'S YEAST).//P21560

F-NT2RM4001258//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00
031:132:39//STREPTOMYCES FRADIAE.//P20186

F-NT2RM4001309//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CON
TAINS: BASIC PEPTIDE P-F] (FRAGMENT).//0.048:132:28//HOMO SAPIENS (HUMAN
).//P02812

F-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137)
(PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//2.6e-37:124:65//DICTYOSTELIUM DI
SCOIDEUM (SLIME MOLD).//P54676

F-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR
(EC 1.3.99.3) (MCAD).//1.7e-10:185:30//RATTUS NORVEGICUS (RAT).//P08503

F-NT2RM4001320//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO
/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//1.5e-08:197:26//MUS
MUSCULUS (MOUSE).//P52734

F-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//7.7e-14:82
:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32626

F-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC
REGION.//3.3e-16:128:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53
742

F-NT2RM4001347//HYPOTHETICAL 76.9 KD PROTEIN IN RPM2-TUB1 INTERGENIC REG
ION.//0.067:111:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04511

F-NT2RM4001371

F-NT2RM4001382//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.0e-08:82:39//P
LASMODIUM LOPHURAE.//P04929

F-NT2RM4001384

F-NT2RM4001410//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//2.1e-08:185:

31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 F-NT2RM4001411//EARLY NODULIN 20 PRECURSOR (N-20).//5.3e-05:105:38//MEDI
 CAGO TRUNCATULA (BARREL MEDIC).//P93329
 F-NT2RM4001412//GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVAT
 OR) (P120GAP) (RASGAP).//6.2e-17:109:41//RATTUS NORVEGICUS (RAT).//P5090
 4
 F-NT2RM4001414//ZINC FINGER PROTEIN 177.//8.3e-06:54:50//HOMO SAPIENS (H
 UMAN).//Q13360
 F-NT2RM4001437//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-24:87:65/
 /HOMO SAPIENS (HUMAN).//P39192
 F-NT2RM4001444//PROBABLE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUC
 INE--TRNA LIGASE) (ILERS) (FRAGMENT).//2.6e-45:197:47//CIONA INTESTINALI
 S.//Q94425
 F-NT2RM4001454//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//0.0060:95:29/
 /HOMO SAPIENS (HUMAN).//Q15057
 F-NT2RM4001455//PROBABLE E5B PROTEIN.//0.41:44:36//HUMAN PAPILLOMAVIRUS
 TYPE 6B.//P06461
 F-NT2RM4001483//ZINC FINGER PROTEIN 136.//1.7e-28:85:64//HOMO SAPIENS (H
 UMAN).//P52737
 F-NT2RM4001489//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.086:111:34//HOM
 O SAPIENS (HUMAN).//P23246
 F-NT2RM4001519//ACID UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROL
 ASE).//0.82:51:47//LACTOBACILLUS FERMENTUM.//P26929
 F-NT2RM4001522//TROPOMYOSIN.//0.030:117:23//SCHIZOSACCHAROMYCES POMBE (F
 ISSION YEAST).//Q02088
 F-NT2RM4001557
 F-NT2RM4001565//HYPOTHETICAL 44.3 KD PROTEIN C1F7.07C IN CHROMOSOME I.//
 0.99:42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09919
 F-NT2RM4001566//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-AL

PHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.054:190:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-NT2RM4001569//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (ACTIVATED PROTEIN KINASE C RECEPTOR HOMOLOG).//0.72:64:31//TRYPANOSOMA BRUCEI BRUCEI.//Q94775

F-NT2RM4001582

F-NT2RM4001592//DNA REPAIR PROTEIN RAD9.//0.00037:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14737

F-NT2RM4001594//IMMEDIATE-EARLY PROTEIN IE180.//1.9e-05:147:34//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-NT2RM4001597//THIOL:DISULFIDE INTERCHANGE PROTEIN TLPA (CYTOCHROME C BIOGENESIS PROTEIN TLPA).//5.7e-06:122:29//BRADYRHIZOBIUM JAPONICUM.//P43221

F-NT2RM4001605//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//1.7e-128:249:96//RATTUS NORVEGICUS (RAT).//P37199

F-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//1.5e-35:128:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36024

F-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//5.8e-42:254:37//HOMO SAPIENS (HUMAN).//Q13368

F-NT2RM4001650//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.62:19:57//GALLUS GALLUS (CHICKEN).//P17277

F-NT2RM4001662//PROTEIN KINASE C, ALPHA TYPE (EC 2.7.1.-) (PKC-ALPHA).//0.29:90:32//HOMO SAPIENS (HUMAN).//P17252

F-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//1.1e-31:137:44//ESCHERICHIA COLI.//P37339

F-NT2RM4001682//PROBABLE 60S RIBOSOMAL PROTEIN L22.//0.98:55:29//CAENORHABDITIS ELEGANS.//P52819

F-NT2RM4001710//HYPOTHETICAL PROTEIN KIAA0039 (FRAGMENT).//0.56:113:28//

HOMO SAPIENS (HUMAN).//Q15054
 F-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//1.4e-108:255:77//HOMO SAPIENS (HUMAN).//Q14141
 F-NT2RM4001715//HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I (FRAGMENT).//2.1e-36:148:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10342
 F-NT2RM4001731//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III./1.1e-05:90:33//CAENORHABDITIS ELEGANS.//P34284
 F-NT2RM4001741//TALIN.//1.1e-106:208:99//MUS MUSCULUS (MOUSE).//P26039
 F-NT2RM4001746//EBNA-1 NUCLEAR PROTEIN.//1.6e-09:155:38//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03211
 F-NT2RM4001754//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.93:158:33//HOMO SAPIENS (HUMAN).//P29400
 F-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//5.1e-113:277:79//HOMO SAPIENS (HUMAN).//P27448
 F-NT2RM4001776//MYOSIN I ALPHA (MMI-ALPHA).//2.2e-73:262:54//MUS MUSCULUS (MOUSE).//P46735
 F-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT).//5.3e-26:169:39//MUS MUSCULUS (MOUSE).//P55200
 F-NT2RM4001810//MALE SPECIFIC SPERM PROTEIN MST84DB.//2.3e-05:68:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RM4001813//RHODOCETIN ALPHA SUBUNIT.//2.3e-05:115:34//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA).//P81397
 F-NT2RM4001819//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.7e-06:159:25//MUS MUSCULUS (MOUSE).//Q61549
 F-NT2RM4001823//ZINC FINGER PROTEIN ZIC1 (ZINC FINGER PROTEIN OF THE CEREBELLUM 1).//2.6e-18:114:40//MUS MUSCULUS (MOUSE).//P46684
 F-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.0e-81:253:59//HOMO SAPIENS (HUMAN).//P51523

F-NT2RM4001836//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.21:1
76:30//NEPHILA CLAVIPES (ORB SPIDER).//P46804

F-NT2RM4001841//PROLINE-RICH PEPTIDE P-B.//0.046:27:40//HOMO SAPIENS (HUMAN).//P02814

F-NT2RM4001842//HYPOTHETICAL 7.0 KD PROTEIN B03B8.1 IN CHROMOSOME III.//
0.98:35:42//CAENORHABDITIS ELEGANS.//Q11104

F-NT2RM4001856//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//2.3e-37:242:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722

F-NT2RM4001858//T-BOX PROTEIN VEGT (T-BOX PROTEIN BRAT) (T-BOX PROTEIN ANTIPODEAN).//1.8e-23:78:64//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P8737
7

F-NT2RM4001865//NEURONAL CALCIUM SENSOR 2 (NCS-2).//0.012:83:28//CAENORHABDITIS ELEGANS.//P36609

F-NT2RM4001876//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//3.8e-10:242:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179

F-NT2RM4001880//EC PROTEIN HOMOLOG.//0.22:59:32//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P93746

F-NT2RM4001905//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.57:20:60//HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P14
793

F-NT2RM4001922

F-NT2RM4001930//PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 (EC 2.4.1.-).//5.5e-45:167:53//CAENORHABDITIS ELEGANS.//Q09226

F-NT2RM4001938//RTOA PROTEIN (RATIO-A).//0.0036:120:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681

F-NT2RM4001940//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 (FRAGMENT).//0.32:31:48//HOMO SAPIENS (HUMAN).//P78415

F-NT2RM4001953//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.2e-43:56:85/

/HOMO SAPIENS (HUMAN).//P39192
 F-NT2RM4001965//IG ALPHA-1 CHAIN C REGION.//0.56:73:34//GORILLA GORILLA
 GORILLA (LOWLAND GORILLA).//P20758
 F-NT2RM4001969//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4
 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.0016:140:27//H.
 OMO SAPIENS (HUMAN).//P04280
 F-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9e
 -21:103:51//HOMO SAPIENS (HUMAN).//P51523
 F-NT2RM4001984//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.0034:50:40//MUS MUSC
 ULUS (MOUSE).//P15974
 F-NT2RM4001987//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PRO
 TEIN).//6.9e-17:115:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180
 F-NT2RM4002013//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN
 ZC302.2 IN CHROMOSOME V.//0.0062:117:28//CAENORHABDITIS ELEGANS.//Q23256
 F-NT2RM4002018//SPORE COAT PROTEIN SP96.//4.3e-06:203:28//DICTYOSTELIUM
 DISCOIDEUM (SLIME MOLD).//P14328
 F-NT2RM4002034//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//0.7
 8:132:25//HOMO SAPIENS (HUMAN).//P98171
 F-NT2RM4002044//VITELLOGENIN I PRECURSOR (MINOR VITELLOGENIN) [CONTAINS:
 LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP42].//
 0.062:201:24//GALLUS GALLUS (CHICKEN).//P87498
 F-NT2RM4002054//DUPLICATE PROCYCLIN.//0.0079:44:52//TRYPANOSOMA BRUCEI B
 RUCEI.//P14044
 F-NT2RM4002055//PUTATIVE Z PROTEIN.//0.82:39:30//OVIS ARIES (SHEEP).//P0
 8105
 F-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA
 LIGASE) (ASPRS).//7.0e-37:80:52//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)
 .//P36419
 F-NT2RM4002063//SARCOSINE OXIDASE (EC 1.5.3.1).//2.2e-25:216:31//BACILLU

S SP. (STRAIN NS-129).//P23342
 F-NT2RM4002066//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//1.1e-94:260:7
 1//HOMO SAPIENS (HUMAN).//Q93074
 F-NT2RM4002067//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-15:51:70//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RM4002073//ELASTIN PRECURSOR (TROPOLASTIN).//4.9e-05:88:36//HOMO S
 APIENS (HUMAN).//P15502
 F-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//7.2e-43:220:41//DRO
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RM4002093//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOU
 S NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB
 -1).//1.8e-93:255:72//HOMO SAPIENS (HUMAN).//P26599
 F-NT2RM4002109//KINESIN-LIKE PROTEIN KIF4.//3.7e-101:260:78//MUS MUSCULU
 S (MOUSE).//P33174
 F-NT2RM4002128//HYPOTHETICAL PROTEIN IN CYCB 3' REGION PRECURSOR (ORF2) (
 FRAGMENT).//0.91:49:32//PARACOCUS DENITRIFICANS.//P29969
 F-NT2RM4002140//GROUCHO PROTEIN (ENHANCER OF SPLIT M9/10).//0.36:104:22/
 /DROSOPHILA MELANOGASTER (FRUIT FLY).//P16371
 F-NT2RM4002145//SLIT PROTEIN PRECURSOR.//8.6e-13:127:33//DROSOPHILA MELA
 NOGASTER (FRUIT FLY).//P24014
 F-NT2RM4002146//MAGO NASHI PROTEIN.//7.9e-69:143:91//DROSOPHILA MELANOGA
 STER (FRUIT FLY).//P49028
 F-NT2RM4002161//DUAL SPECIFICITY PROTEIN PHOSPHATASE (EC 3.1.3.48) (EC 3
 .1.3.16).//0.0062:99:26//CHLAMYDOMONAS EUGAMETOS.//Q39491
 F-NT2RM4002174//MRP PROTEIN.//4.5e-50:183:55//ESCHERICHIA COLI.//P21590
 F-NT2RM4002189//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.6e-14:233:29/
 /HOMO SAPIENS (HUMAN).//Q02817
 F-NT2RM4002194//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.92:108:28//HOMO
 SAPIENS (HUMAN).//P51805

F-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5
 .8e-39:122:72//RATTUS NORVEGICUS (RAT).//Q07803

F-NT2RM4002213//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III./
 /9.9e-27:110:43//CAENORHABDITIS ELEGANS.//Q03565

F-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//1.3e-21:147:41//DROSO
 PHILA MELANOGASTER (FRUIT FLY).//P40809

F-NT2RM4002251//PROTEIN EF-7 (FRAGMENT).//0.00082:45:42//MUS MUSCULUS (M
 OUSE).//P97805

F-NT2RM4002256//COLD-REGULATED PROTEIN 1 (FRAGMENT).//0.00015:114:42//HO
 RDEUM VULGARE (BARLEY).//P23251

F-NT2RM4002266//CUTICLE COLLAGEN 2.//0.00013:142:33//CAENORHABDITIS ELEG
 ANS.//P17656

F-NT2RM4002278//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC
 REGION.//1.0:40:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288

F-NT2RM4002281

F-NT2RM4002287//GAR2 PROTEIN.//0.00055:225:23//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST).//P41891

F-NT2RM4002294//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//1.1e-60:152:75/
 /HOMO SAPIENS (HUMAN).//Q92556

F-NT2RM4002301//GENERAL STRESS PROTEIN CTC (FRAGMENT).//0.56:43:39//BACI
 LLUS CALDOLYTICUS.//P42832

F-NT2RM4002323//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.0080:73:35//BO
 S TAURUS (BOVINE).//P02313

F-NT2RM4002339//METALLOTHIONEIN 10-III (MT-10-III).//0.67:34:38//MYTILUS
 EDULIS (BLUE MUSSEL).//P80248

F-NT2RM4002344//METALLOTHIONEIN-I (MT-I).//0.84:41:31//MUS MUSCULUS (MOU
 SE).//P02802

F-NT2RM4002373//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DY10 PRECURSOR./
 /0.0019:190:28//TRITICUM AESTIVUM (WHEAT).//P10387

F-NT2RM4002374//5E5 ANTIGEN.//0.0059:170:32//RATTUS NORVEGICUS (RAT).//Q
63003

F-NT2RM4002383//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.13:17:88//HO
MO SAPIENS (HUMAN).//P39193

F-NT2RM4002390

F-NT2RM4002398//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PR
OTEIN).//0.034:110:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38074

F-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA
LIGASE) (ACYL- ACTIVATING ENZYME).//4.0e-20:179:31//METHANOTHRIX SOEHNGE
NII.//P27095

F-NT2RM4002438//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.7e-15:41:95/
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RM4002446//CRYPTIDIN-RELATED PROTEIN 4C-1 PRECURSOR (CRS4C).//0.0058
:24:50//MUS MUSCULUS (MOUSE).//P17534

F-NT2RM4002452//METALLOTHIONEIN 10-II (MT-10-II).//0.83:48:37//MYTILUS E
DULIS (BLUE MUSSEL).//P80247

F-NT2RM4002457//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//4.9e-07:52:63/
/HOMO SAPIENS (HUMAN).//P39192

F-NT2RM4002460//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.92:43:30//HORDEU
M VULGARE (BARLEY).//P17992

F-NT2RM4002479//RNA HELICASE-LIKE PROTEIN DB10.//1.7e-28:200:41//NICOTIA
NA SYLVESTRIS (WOOD TOBACCO).//P46942

F-NT2RM4002482//HYPOTHETICAL 65.9 KD PROTEIN YPR065W.//8.8e-26:123:49//S
ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12514

F-NT2RM4002493//LARVAL CUTICLE PROTEIN I PRECURSOR.//0.17:126:27//DROSOP
HILA MIRANDA (FRUIT FLY).//P91627

F-NT2RM4002499//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.4e-34:92:80/
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RM4002504//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.4e-19:55:83/

/HOMO SAPIENS (HUMAN).//P39189
 F-NT2RM4002527//WD-40 REPEAT PROTEIN MSI2.//3.0e-07:193:27//ARABIDOPSIS
 THALIANA (MOUSE-EAR CRESS).//022468
 F-NT2RM4002532//AEROLYSIN REGULATORY PROTEIN.//0.97:19:47//AEROMONAS SOB
 RIA.//P09165
 F-NT2RM4002534//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32
).//0.76:86:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25348
 F-NT2RM4002558//LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).//4.2e-55
 :204:50//MUS MUSCULUS (MOUSE).//Q60714
 F-NT2RM4002565//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//1.0:16:62//
 ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852
 F-NT2RM4002567//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REG
 ION.//2.7e-10:184:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
 F-NT2RM4002571//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.
 41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTI
 DE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.4e-25:124:47//HO
 MO SAPIENS (HUMAN).//Q10472
 F-NT2RM4002593//HYPOTHETICAL 9.1 KD PROTEIN IN TETB-EXOA INTERGENIC REGI
 ON.//0.95:36:38//BACILLUS SUBTILIS.//P37509
 F-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//9.0e-68:227:60//CAENORHABDITIS EL
 EGANS.//P54815
 F-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA
 LIGASE) (ASPRS).//3.3e-54:243:47//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//
 P73851
 F-NT2RP1000018//SUPPRESSOR PROTEIN SRP40.//0.0023:131:25//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P32583
 F-NT2RP1000035//RING CANAL PROTEIN (KELCH PROTEIN).//1.0e-06:63:34//DROS
 OPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP1000040//LETHAL NEUROTOXIN TX1.//0.69:21:47//PHONEUTRIA NIGRIVENT

ER (BRAZILIAN ARMED SPIDER).//P17727
 F-NT2RP1000063//HYPOTHETICAL 25.1 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION.//3.8e-14:130:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40359
 F-NT2RP1000086//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION.//0.16:44:40//ESCHERICHIA COLI.//P22847
 F-NT2RP1000101//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//1.9e-06:74:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344
 F-NT2RP1000111//COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1).//2.7e-19:135:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43254
 F-NT2RP1000112//DUAL SPECIFICITY PROTEIN KINASE TTK (EC 2.7.1.-) (PYT).//1.2e-39:91:62//HOMO SAPIENS (HUMAN).//P33981
 F-NT2RP1000124//ATP-DEPENDENT PROTEASE LA 2 (EC 3.4.21.53).//0.074:131:24//MYXOCOCCUS XANTHUS.//P36774
 F-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//1.5e-49:186:56//MUS MUSCULUS (MOUSE).//P51859
 F-NT2RP1000163//METALLOTHIONEIN (MT).//0.98:41:34//PLEURONECTES PLATESSA (PLAICE).//P07216
 F-NT2RP1000170//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.85:64:35//HOMO SAPIENS (HUMAN).//P10162
 F-NT2RP1000174//IMMEDIATE-EARLY PROTEIN IE180.//0.00056:89:37//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
 F-NT2RP1000191//NIFU PROTEIN.//0.53:78:35//FRANKIA ALNI.//P46045
 F-NT2RP1000202//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//9.1e-21:148:39//HOMO SAPIENS (HUMAN).//Q01485
 F-NT2RP1000243//HYPOTHETICAL PROTEIN MJ1136.//1.4e-37:219:36//METHANOCOCCUS JANNASCHII.//Q58536
 F-NT2RP1000259//HYPOTHETICAL PROTEIN TP0318.//0.18:25:44//TREPONEMA PALLIDUM.//083338
 F-NT2RP1000272//SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MRNA SPLICI

NG FACTOR SRP20) (X16 PROTEIN).//1.6e-18:133:36//HOMO SAPIENS (HUMAN), A
ND MUS MUSCULUS (MOUSE).//P23152
F-NT2RP1000324
F-NT2RP1000326//HYPOTHETICAL 29.8 KD PROTEIN ZC97.1 IN CHROMOSOME III.//
1.0e-23:129:36//CAENORHABDITIS ELEGANS.//P34599
F-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//2.5e-45:147:57//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32447
F-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.8e-14:
119:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343
F-NT2RP1000357//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGME
NT).//1.0:43:32//TRYPANOSOMA CRUZI.//Q26327
F-NT2RP1000358//HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3' REGION.//7.9
e-28:244:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39744
F-NT2RP1000363//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.
2e-07:178:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
F-NT2RP1000376//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./
/1.5e-20:254:31//HOMO SAPIENS (HUMAN).//P16157
F-NT2RP1000409//CYTOCHROME C3 (CYTOCHROME C7) (C551.5).//1.0:34:26//DESU
LFUROMONAS ACETOXIDANS (CHLOROPSEUDOMONAS ETHYLICA).//P00137
F-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//3.7e-
131:230:97//RATTUS NORVEGICUS (RAT).//P55161
F-NT2RP1000416//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.83:54:40//DROS
OPHILA SIMULANS (FRUIT FLY).//P13729
F-NT2RP1000418//HYPOTHETICAL 9.9 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC
REGION.//0.24:91:35//BACILLUS SUBTILIS.//P49779
F-NT2RP1000439//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//
0.13:172:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429
F-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUC
TASE) (ZETA- CRYSTALLIN).//1.9e-08:167:24//HOMO SAPIENS (HUMAN).//Q08257

F-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//1.0e-18:149:34//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).//P17624

F-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//1.3e-43:180:47//CAENORHABDITIS ELEGANS.//P34580

F-NT2RP1000478//TUBULIN BETA-6 CHAIN (CLASS-VI).//1.5e-45:85:63//GALLUS GALLUS (CHICKEN).//P09207

F-NT2RP1000481//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5' REGION (ORF55).//0.083:21:47//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159

F-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//6.6e-11:139:31//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P33194

F-NT2RP1000513//60S RIBOSOMAL PROTEIN L22.//0.017:92:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887

F-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//0.0055:86:36//MUS MUSCULUS (MOUSE).//Q61068

F-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.2e-09:69:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P49020

F-NT2RP1000574//HOMEODOMAIN PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//6.0e-39:141:65//MUS MUSCULUS (MOUSE).//P97367

F-NT2RP1000577//PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W.//0.00016:48:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12389

F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR.//0.00017:61:50//HOMO SAPIENS (HUMAN).//P04275

F-NT2RP1000609//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//4.4e-07:128:31//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RP1000629//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT)

T) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)./
/4.2e-70:167:86//MUS MUSCULUS (MOUSE).//P35585

F-NT2RP1000630//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC RE
GION PRECURSOR.//0.0011:238:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
.//P47179

F-NT2RP1000677//COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.//0.99:71:33//HOMO
SAPIENS (HUMAN).//Q07092

F-NT2RP1000688//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.0024:19:94//
HOMO SAPIENS (HUMAN).//P39193

F-NT2RP1000695//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III./
/2.2e-30:185:37//CAENORHABDITIS ELEGANS.//Q18262

F-NT2RP1000701//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.2e-65:12
8:93//RATTUS NORVEGICUS (RAT).//P54319

F-NT2RP1000721//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA
FII-135) (TAFII135) (TAFII-130) (TAFII130).//2.3e-06:139:34//HOMO SAPIEN
S (HUMAN).//O00268

F-NT2RP1000730//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR I
SOFORM (FRAGMENT).//0.89:40:40//MUS MUSCULUS (MOUSE).//P09542

F-NT2RP1000733//METALLOTHIONEIN-LIKE PROTEIN CRS5.//0.024:24:45//SACCHAR
OMYCES CEREVISIAE (BAKER'S YEAST).//P41902

F-NT2RP1000738//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSO
R (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C
) [CONTAINS: PEPTIDE P-C].//0.040:82:36//HOMO SAPIENS (HUMAN).//P02810

F-NT2RP1000746//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION
.//2.0e-30:170:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201

F-NT2RP1000767//PSEUDOMONAPEPSIN PRECURSOR (EC 3.4.23.37) (PEPSTATIN-INS
ENSITIVE CARBOXYL PROTEINASE).//0.99:75:34//PSEUDOMONAS SP. (STRAIN 101)
.//P42790

F-NT2RP1000782//CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTI

C LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMO
SOME, SURFACE MARKER 1).//2.3e-23:159:35//HOMO SAPIENS (HUMAN).//P41732
F-NT2RP1000796//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL P
ROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.00018:79:32//SUS SCROFA (PI
G).//P35323
F-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPA
SE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//3
.1e-37:89:64//HOMO SAPIENS (HUMAN).//Q07960
F-NT2RP1000833//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.3
2:29:48//HOMO SAPIENS (HUMAN).//P22531
F-NT2RP1000834//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//6.4e-67:202
:68//RATTUS NORVEGICUS (RAT).//P70473
F-NT2RP1000836//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//1
.0:35:54//HUMAN ADENOVIRUS TYPE 41.//P23691
F-NT2RP1000846//SMALL PROLINE-RICH PROTEIN 2-1.//0.013:35:48//HOMO SAPIE
NS (HUMAN).//P35326
F-NT2RP1000851//PERIOD CLOCK PROTEIN (FRAGMENT).//0.082:28:57//DROSOPHIL
A SALTANS (FRUIT FLY).//Q04536
F-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27)
(MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//2.5e-26:190:30//MUS MUS
CULUS (MOUSE).//035566
F-NT2RP1000860//POTENTIAL TRANSCRIPTIONAL ADAPTOR.//0.13:86:36//SACCHARO
MYCES CEREVISIAE (BAKER'S YEAST).//Q02336
F-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.
//7.6e-11:200:35//CAENORHABDITIS ELEGANS.//Q09531
F-NT2RP1000915//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENI
C REGION.//1.4e-06:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40
010
F-NT2RP1000916//SUPPRESSOR PROTEIN SRP40.//0.40:90:35//SACCHAROMYCES CER

EVISIAE (BAKER'S YEAST).//P32583
 F-NT2RP1000943//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.099:75:34//HO
 MO SAPIENS (HUMAN).//Q02817
 F-NT2RP1000944//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//7.6e-06:65:41//OR
 GYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341
 F-NT2RP1000947//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (U
 BIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//3.6
 e-12:27:77//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICU
 S (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669
 F-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//2.8e-15:169:28//DRO
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP1000958//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENI
 C REGION.//4.2e-16:162:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P4
 0010
 F-NT2RP1000959//CORNIFIN A (SMALL PROLINE-RICH PROTEIN 1A) (SPR-1A) (SPR
 K).//0.0031:34:44//HOMO SAPIENS (HUMAN).//P35321
 F-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//1.5e-52:110:95//HOMO SAPIENS (
 HUMAN).//P19338
 F-NT2RP1000980//LIGHT-HARVESTING PROTEIN B-1015, ALPHA CHAIN PRECURSOR (
 ANTENNA PIGMENT PROTEIN, ALPHA CHAIN).//0.87:37:45//RHODOPSEUDOMONAS VIR
 IDIS.//P04123
 F-NT2RP1000988
 F-NT2RP1001011//PROTEIN P19.//0.96:30:50//BACTERIOPHAGE PRD1.//P17638
 F-NT2RP1001013//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0:20:45//BACTE
 RIOPHAGE T4.//P16012
 F-NT2RP1001014
 F-NT2RP1001033//TUBULIN GAMMA CHAIN.//2.5e-16:112:42//SCHIZOSACCHAROMYCE
 S POMBE (FISSION YEAST).//P25295
 F-NT2RP1001073//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC RE

GION.//7.6e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089
 F-NT2RP1001079//SARCOSINE OXIDASE (EC 1.5.3.1).//4.8e-15:95:40//ARTHROBA
 CTER SP. (STRAIN TE1826).//P40873
 F-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.4e-29:126:4
 6//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06218
 F-NT2RP1001113//SMALL PROLINE-RICH PROTEIN 2-1.//0.49:38:39//HOMO SAPIEN
 S (HUMAN).//P35326
 F-NT2RP1001173//RHOMBOTIN-1 (CYSTEINE RICH PROTEIN TTG-1) (T-CELL TRANSL
 OCATION PROTEIN 1) (LIM-ONLY PROTEIN 1).//0.99:54:37//HOMO SAPIENS (HUMA
 N).//P25800
 F-NT2RP1001177//HISTONE MACRO-H2A.1.//1.6e-29:85:76//RATTUS NORVEGICUS (
 RAT).//Q02874
 F-NT2RP1001185
 F-NT2RP1001199//NEUROTOXIN I.//1.0:23:47//CENTRUROIDES SCULPTURATUS (BAR
 K SCORPION).//P01491
 F-NT2RP1001247//TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4)
 (ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR).//3.3e-08:28:89//HOMO SAPIENS
 (HUMAN).//000292
 F-NT2RP1001248//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.33:
 49:28//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P1880
 4
 F-NT2RP1001253//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSA
 MINE-6- PHOSPHATE DEAMINASE) (GNPDA) (OSCILLIN) (KIAA0060).//3.8e-46:115
 :81//HOMO SAPIENS (HUMAN).//P46926
 F-NT2RP1001286//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN)
 (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35)
 (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDI
 NG LECTIN).//0.16:48:37//MUS MUSCULUS (MOUSE).//P16110
 F-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//6.1e-05:92:34//SAC

CHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.2e-05:92:33//SAC

CHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP1001310//PROBABLE E4 PROTEIN.//0.99:109:26//HUMAN PAPILLOMAVIRUS
TYPE 5.//P06924

F-NT2RP1001311//SODIUM/HYDROGEN EXCHANGER 5 (NA(+)/H(+)) EXCHANGER 5) (NH
E-5) (FRAGMENT).//0.99:94:31//HOMO SAPIENS (HUMAN).//Q14940

F-NT2RP1001313//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P40312

F-NT2RP1001361//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.
3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//1.2e-47:117:74//BOS TA
URUS (BOVINE).//Q02827

F-NT2RP1001385//CELL DIVISION PROTEIN FTSN.//0.64:107:28//ESCHERICHIA CO
LI.//P29131

F-NT2RP1001395//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.2
5:35:45//GALLUS GALLUS (CHICKEN).//P02467

F-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//2.2e-41:129:67//C
AENORHABDITIS ELEGANS.//P91917

F-NT2RP1001424//UREASE ACCESSORY PROTEIN UREF (FRAGMENT).//0.87:24:45//E
SCHERICHIA COLI.//Q03286

F-NT2RP1001432//CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB).//1.0
:35:42//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//Q10993

F-NT2RP1001449//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).
//0.053:37:37//OVIS ARIES (SHEEP).//P26372

F-NT2RP1001457//HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN
IN CPR4-SSK22 INTERGENIC REGION.//2.9e-16:159:30//SACCHAROMYCES CEREVISI
AE (BAKER'S YEAST).//P25382

F-NT2RP1001466//HYPOTHETICAL PROTEIN MJ0284.//5.3e-15:162:35//METHANOCOC
CUS JANNASCHII.//Q57732

F-NT2RP1001475//HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UBI1 INTERGENIC REGION.//0.69:119:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40457

F-NT2RP1001482//PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9).//1.0:58:32//HOMO SAPIENS (HUMAN).//P25789

F-NT2RP1001494//MALE STERILITY PROTEIN 2.//2.4e-12:84:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

F-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//6.3e-37:94:52//SPIRODELA POLYRRHIZA.//P42803

F-NT2RP1001546//LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53).//9.3e-11:98:29//HOMO SAPIENS (HUMAN).//P19397

F-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//2.2e-64:159:84//MUS MUSCULUS (MOUSE).//P47758

F-NT2RP1001616//HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME III.//9.2e-05:49:42//CAENORHABDITIS ELEGANS.//Q09506

F-NT2RP1001665//REGB PROTEIN.//0.99:29:37//PSEUDOMONAS AERUGINOSA.//Q0381

F-NT2RP2000001//SMALL PROLINE-RICH PROTEIN 2-1.//0.64:36:41//HOMO SAPIENS (HUMAN).//P35326

F-NT2RP2000006//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.7e-19:74:52//HOMO SAPIENS (HUMAN).//P25685

F-NT2RP2000007//TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM36) (TME1) (TM1).//0.93:126:23//HOMO SAPIENS (HUMAN).//P06468

F-NT2RP2000008//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIA A0065) (HA0946) (FRAGMENT).//4.2e-35:156:54//HOMO SAPIENS (HUMAN).//Q067

30

F-NT2RP2000027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.95:41:39//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P50665

F-NT2RP2000032//BAX PROTEIN, CYTOPLASMIC ISOFORM GAMMA.//1.0:35:34//HOMO
SAPIENS (HUMAN).//Q07815

F-NT2RP2000040//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0024:58:36//HOMO SAP
IENS (HUMAN).//P04281

F-NT2RP2000045//DNAJ PROTEIN.//1.1e-12:42:66//THERMUS AQUATICUS (SUBSP.
THERMOPHILUS).//Q56237

F-NT2RP2000054//GONADOLIBERIN III PRECURSOR (GONADOTROPIN-RELEASING HORM
ONE III) (GNRH-III) (LH-RH III) (LULIBERIN III).//0.20:46:36//ONCORHYNCH
US MASOU (CHERRY SALMON) (MASU SALMON).//P30973

F-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3
.48) (R-PTP- EPSILON).//1.3e-18:45:100//MUS MUSCULUS (MOUSE).//P49446

F-NT2RP2000067//HOMEBOX PROTEIN HOX-A5 (S12-B) (FRAGMENT).//0.71:44:40/
/SALMO SALAR (ATLANTIC SALMON).//P09637

F-NT2RP2000070//INSULIN.//0.94:30:43//HYSTRIX CRISTATA (CRESTED PORCUPIN
E).//P01328

F-NT2RP2000076//ETS-LIKE PROTEIN POINTED P1 (D-ETS-2).//0.0013:76:40//DR
OSOPHILA MELANOGASTER (FRUIT FLY).//P51022

F-NT2RP2000077//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C).//0.24:49:40
//HOMO SAPIENS (HUMAN).//P09234

F-NT2RP2000079//PLATELET FACTOR 4 (PF-4).//0.15:52:30//SUS SCROFA (PIG).
//P30034

F-NT2RP2000088//HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REG
ION.//1.0:36:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53245

F-NT2RP2000091//HYPOTHETICAL PROTEIN HI0149 PRECURSOR.//0.22:38:47//HAEM
OPHILUS INFLUENZAE.//P43953

F-NT2RP2000097//VIRUS ATTACHMENT PROTEIN (O61R).//0.75:33:36//AFRICAN SW
INE FEVER VIRUS (STRAIN BA71V) (ASFV).//P32510

F-NT2RP2000098

F-NT2RP2000108//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.4e-09:50:70/

/HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP2000114//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.024:52:44//H
 OMO SAPIENS (HUMAN).//P42768
 F-NT2RP2000120//5.8 KD PROTEIN IN HMC OPERON (ORF 4).//0.67:37:32//DESUL
 FOVIBRIO VULGARIS (STRAIN HILDENBOROUGH).//P33391
 F-NT2RP2000126//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.
 5e-23:94:47//HOMO SAPIENS (HUMAN).//O14646
 F-NT2RP2000133//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//5.
 6e-10:82:39//HOMO SAPIENS (HUMAN).//Q15427
 F-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOC
 IATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNI
 T) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)./
 /6.7e-89:96:98//MUS MUSCULUS (MOUSE).//P35585
 F-NT2RP2000153//PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPRO
 LYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE).//1.7e-05:136:33//BRUGIA
 MALAYI.//Q27450
 F-NT2RP2000157//ML02 PROTEIN.//2.7e-06:62:40//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST).//Q09329
 F-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//2.7e-33:173:45//CAENORHABDITIS EL
 EGANS.//Q17632
 F-NT2RP2000173//HYPOTHETICAL 10.5 KD PROTEIN IN SODA-COMGA INTERGENIC RE
 GION.//0.99:62:25//BACILLUS SUBTILIS.//P54499
 F-NT2RP2000175//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.19:41:43//DROSOP
 HILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SP
 ECIFIC PROTEIN NSP60).//4.1e-19:114:44//BOS TAURUS (BOVINE).//002675
 F-NT2RP2000195//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:30:33/
 /MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P24949
 F-NT2RP2000205//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURS

OR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN)
 .//0.098:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54
 463
 F-NT2RP2000208//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.020:19:57//DROSO
 PHILA MELANOGASTER (FRUIT FLY).//Q01645
 F-NT2RP2000224//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.0058:159:32//CAENO
 RHABDITIS ELEGANS.//Q09455
 F-NT2RP2000232//P55-C-FOS PROTO-ONCOGENE PROTEIN (FRAGMENT).//1.0:44:38/
 /OVIS ARIES (SHEEP).//002761
 F-NT2RP2000233//GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR)
 (CCK-BR).//0.34:53:43//CANIS FAMILIARIS (DOG).//P30552
 F-NT2RP2000239//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRA
 GMENT).//0.019:69:33//RATTUS NORVEGICUS (RAT).//P10164
 F-NT2RP2000248//OVOMUCOID (FRAGMENT).//0.88:18:55//POLYPLECTRON EMPHANUM
 (PALAWAN PEACOCK-PHEASANT).//P52250
 F-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//6.4e-09:83:37//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556
 F-NT2RP2000258//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.081:217:28//DICTYO
 STELIUM DISCOIDEUM (SLIME MOLD).//P08799
 F-NT2RP2000270//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-17:80:57//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP2000274//HYPOTHETICAL 5.8 KD PROTEIN.//0.082:22:45//CLOVER YELLOW
 MOSAIC VIRUS (CYMV).//P16485
 F-NT2RP2000283//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III./
 /0.39:38:34//CAENORHABDITIS ELEGANS.//P34535
 F-NT2RP2000288
 F-NT2RP2000289//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGI
 ON.//0.40:38:42//ESCHERICHIA COLI.//P22847
 F-NT2RP2000297//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1)

.//2.3e-62:206:47//HOMO SAPIENS (HUMAN).//Q03923
 F-NT2RP2000298//CUTICLE COLLAGEN 12 PRECURSOR.//0.55:81:40//CAENORHABDIT
 IS ELEGANS.//P20630
 F-NT2RP2000310//RUBREDOXIN (RD).//0.13:43:41//TREPONEMA PALLIDUM.//08395
 6
 F-NT2RP2000327//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:46:30//
 GADUS MORHUA (ATLANTIC COD).//P15996
 F-NT2RP2000328//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REG
 ION.//2.0e-21:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313
 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (
 AK3).//1.8e-91:155:92//BOS TAURUS (BOVINE).//P08760
 F-NT2RP2000337//PROTEIN A54.//0.75:48:35//VACCINIA VIRUS (STRAIN WR), AN
 D VACCINIA VIRUS (STRAIN COPENHAGEN).//P21072
 F-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.
 //9.7e-13:114:42//MUS MUSCULUS (MOUSE).//P17564
 F-NT2RP2000369//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//0.98:47:34//MUS
 MUSCULUS (MOUSE).//Q09098
 F-NT2RP2000412//SHORT NEUROTOXIN D PRECURSOR.//0.66:57:36//AIPYSURUS LAE
 VIS (OLIVE SEA SNAKE).//P19960
 F-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//1.
 0e-27:96:67//HOMO SAPIENS (HUMAN).//P52597
 F-NT2RP2000420//ZINC FINGER PROTEIN 191.//0.16:47:38//HOMO SAPIENS (HUMA
 N).//014754
 F-NT2RP2000422//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (A
 CETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE)./
 /3.6e-19:148:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687
 F-NT2RP2000438//TUBULIN GAMMA CHAIN.//0.86:190:27//RETICULOMYXA FILOSA./
 /P54405
 F-NT2RP2000448//OXYSTEROL-BINDING PROTEIN.//3.7e-13:140:42//HOMO SAPIENS

(HUMAN).//P22059
 F-NT2RP2000459//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//1.0:45:35//HOMO SAPIENS (HUMAN).//Q16612
 F-NT2RP2000498//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//0.062:25:68//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP2000503
 F-NT2RP2000510//TOXIN IV-5.//1.0:51:33//TITYUS BAHIENSIS (BRAZILIAN SCORPION).//P56608
 F-NT2RP2000516//SLYX PROTEIN.//1.0:52:32//ESCHERICHIA COLI.//P30857
 F-NT2RP2000523//PHORBOLIN I (FRAGMENTS).//1.4e-06:36:47//HOMO SAPIENS (HUMAN).//P31941
 F-NT2RP2000603//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-III).//0.93:119:26//TRITICUM AESTIVUM (WHEAT).//P04723
 F-NT2RP2000617//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.056:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT).//P04102
 F-NT2RP2000634//NEDD-4 PROTEIN (EC 6.3.2.-) (KIAA0093) (FRAGMENT).//1.8e-05:128:28//HOMO SAPIENS (HUMAN).//P46934
 F-NT2RP2000644//HYPOTHETICAL PROTEIN HI1566 PRECURSOR.//0.85:48:39//HAEMOPHILUS INFLUENZAE.//P44257
 F-NT2RP2000656//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (NERVE GROWTH FACTOR-INDUCED PROTEIN A) (NGFI-A).//1.0:111:24//RATTUS NORVEGICUS (RAT).//P08154
 F-NT2RP2000658//URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE ISOMERASE) (URONIC ISOMERASE).//0.49:79:31//ESCHERICHIA COLI.//P42607
 F-NT2RP2000668//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KD MEROZOITE SURFACE ANTIGEN).//0.020:115:30//PLASMODIUM FALCIPARUM (ISOLATE 3 D7).//P50498
 F-NT2RP2000678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00085:38:68//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000704//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-17:55:74//
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA
LIGASE) (ASPRS).//8.9e-47:106:59//TREPONEMA PALLIDUM.//083950

F-NT2RP2000715

F-NT2RP2000731//CONIDIATION-SPECIFIC PROTEIN 10.//0.094:31:41//NEUROSPOR
A CRASSA.//P10713

F-NT2RP2000758//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00027:31:74//
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000764//NIFS PROTEIN.//2.7e-27:175:47//ANABAENA SP. (STRAIN PCC
7120).//P12623

F-NT2RP2000809//HYPOTHETICAL PROTEIN MG381 HOMOLOG.//0.91:85:25//MYCOPLA
SMA PNEUMONIAE.//P75219

F-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//2.8e
-07:133:31//MUS MUSCULUS (MOUSE).//Q99104

F-NT2RP2000814//40S RIBOSOMAL PROTEIN S27A.//0.93:44:38//LYCOPERSICON ES
CULENTUM (TOMATO), AND SOLANUM TUBEROSUM (POTATO).//P27083

F-NT2RP2000816//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III./
/3.3e-21:123:39//CAENORHABDITIS ELEGANS.//Q03565

F-NT2RP2000819//TROPOMYOSIN 5, CYTOSKELETAL TYPE.//1.0:71:30//MUS MUSCUL
US (MOUSE).//P21107

F-NT2RP2000841//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//0.0011:133
:26//MUS MUSCULUS (MOUSE).//P27671

F-NT2RP2000842//LYSOPHOSPHATIDIC ACID RECEPTOR (EDG-2).//6.4e-13:22:95//
HOMO SAPIENS (HUMAN).//Q92633

F-NT2RP2000845//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//0.92:24:4
1//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321

F-NT2RP2000863//N-MYC PROTO-ONCOGENE PROTEIN.//0.010:148:27//XENOPUS LAE
VIS (AFRICAN CLAWED FROG).//P24793

F-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//4.0e-100:1
99:94//HOMO SAPIENS (HUMAN).//O60841

F-NT2RP2000892//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHOND
ROCALCIN].//0.43:45:44//MUS MUSCULUS (MOUSE).//P28481

F-NT2RP2000931//MATRIN 3.//2.8e-46:104:92//RATTUS NORVEGICUS (RAT).//P43
244

F-NT2RP2000932//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDEN
T RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.9e-07:113:31//MUS MU
SCULUS (MOUSE).//Q05921

F-NT2RP2000938//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).
//0.026:59:45//RATTUS NORVEGICUS (RAT).//Q01956

F-NT2RP2000943//HYPOTHETICAL PROTEIN KIAA0079 (HA3543).//5.9e-18:161:42/
/HOMO SAPIENS (HUMAN).//P53992

F-NT2RP2000965//INNER CENTROMERE PROTEIN (INCENP).//0.062:156:25//GALLUS
GALLUS (CHICKEN).//P53352

F-NT2RP2000970//EC PROTEIN HOMOLOG.//1.0:50:30//ARABIDOPSIS THALIANA (MO
USE-EAR CRESS).//P93746

F-NT2RP2000985//HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REG
ION.//2.5e-06:53:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36159

F-NT2RP2000987//INSECT TOXIN 4 (INSECT TOXIN AAH IT4).//1.0:32:34//ANDRO
CTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P21150

F-NT2RP2001036//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.2e-33:65:81/
/HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2001044//HIRUSTASIN.//0.97:15:66//HIRUDO MEDICINALIS (MEDICINAL L
EECH).//P80302

F-NT2RP2001056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-24:85:65/
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2001065//BOWMAN-BIRK TYPE SEED TRYPSIN AND CHYMOTRYPSIN INHIBITOR
(BTCI).//0.41:50:32//VIGNA UNGUICULATA (COWPEA).//P17734

F-NT2RP2001070//PROBABLE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5)
(PNP/PMP OXIDASE) (FPRA PROTEIN).//6.2e-18:64:48//MYXOCOCCUS XANTHUS.//P
21159

F-NT2RP2001081//SYNAPTOTAGMIN IV.//7.8e-16:94:46//RATTUS NORVEGICUS (RAT
)..//P50232

F-NT2RP2001094//METALLOTHIONEIN-I (MT-I).//1.0:24:33//RATTUS NORVEGICUS
(RAT)..//P02803

F-NT2RP2001119//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.5e-11:61:63/
/HOMO SAPIENS (HUMAN).//P39195

F-NT2RP2001127//XE169 PROTEIN (SMCX PROTEIN) (FRAGMENTS).//1.0e-47:155:5
8//MUS MUSCULUS (MOUSE).//P41230

F-NT2RP2001137//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.10:68:39//BO
S TAURUS (BOVINE).//P25508

F-NT2RP2001149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-13:81:59//
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2001168//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0
.0071:77:33//RATTUS NORVEGICUS (RAT).//P20468

F-NT2RP2001173//CYTOSKELETON-ASSOCIATED PROTEIN CKAPI (TUBULIN FOLDING C
OFACITOR B).//1.0:36:41//HOMO SAPIENS (HUMAN).//Q99426

F-NT2RP2001174//ZINC FINGER PROTEIN 137.//7.2e-11:65:43//HOMO SAPIENS (H
UMAN).//P52743

F-NT2RP2001196//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//1.
0:95:26//CAPRA HIRCUS (GOAT).//Q36346

F-NT2RP2001218//HYPOTHETICAL 59.2 KD PROTEIN IN MOB1-SGA1 INTERGENIC REG
ION.//0.00024:80:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40486

F-NT2RP2001226//RABPHILIN-3A (FRAGMENT).//4.6e-05:121:39//MUS MUSCULUS (
MOUSE).//P47708

F-NT2RP2001233//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.2e-61:153:56//
HOMO SAPIENS (HUMAN).//P16415

F-NT2RP2001245//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//4.9e-05
 :230:21//HOMO SAPIENS (HUMAN).//Q15431
 F-NT2RP2001268//HOMEBOX PROTEIN CEH-32.//0.23:159:25//CAENORHABDITIS EL
 EGANS.//Q23175
 F-NT2RP2001277
 F-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-AL
 PHA HOMOLOG) (BRAIN PROTEIN I47) (FRAGMENT).//1.0e-86:131:97//MUS MUSCUL
 US (MOUSE).//P28663
 F-NT2RP2001295
 F-NT2RP2001312//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14)
 (G6S) (GLUCOSAMINE-6-SULFATASE).//0.64:80:33//CAPRA HIRCUS (GOAT).//P504
 26
 F-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHEL
 IAL (B12 PROTEIN).//1.0e-36:118:65//HOMO SAPIENS (HUMAN).//Q13829
 F-NT2RP2001328//PROBABLE E5 PROTEIN.//1.0:46:41//HUMAN PAPILLOMAVIRUS TY
 PE 33.//P06426
 F-NT2RP2001347//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.5e-19:66:62/
 /HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2001366//SPERM-SPECIFIC PROTEIN PHI-1.//0.66:55:32//MYTILUS EDULI
 S (BLUE MUSSEL).//Q04621
 F-NT2RP2001378//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
 (FRAGMENT).//0.060:78:33//HOMO SAPIENS (HUMAN).//Q14003
 F-NT2RP2001381//26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG) (XSUG1)
 .//1.0:167:26//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P46470
 F-NT2RP2001392//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3.//0.0080:82:3
 2//OVIS ARIES (SHEEP).//P02441
 F-NT2RP2001394//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN.//0.024:39:53//D
 ROSOPHILA MELANOGASTER (FRUIT FLY).//P39769
 F-NT2RP2001397//G2/MITOTIC-SPECIFIC CYCLIN B2.//1.4e-46:125:78//MESOCRIC

ETUS AURATUS (GOLDEN HAMSTER).//P37883
 F-NT2RP2001420//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4
 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H] .//0.00018:113:38//
 HOMO SAPIENS (HUMAN).//P04280
 F-NT2RP2001423//HYPOTHETICAL 9.4 KD PROTEIN IN GP31-CD INTERGENIC REGION
 (ORF A).//0.90:23:43//BACTERIOPHAGE T4.//P17307
 F-NT2RP2001427//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-11:38:68//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP2001436//DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC (LIC53/55)
 (LIC-2).//0.25:124:28//RATTUS NORVEGICUS (RAT).//Q62698
 F-NT2RP2001440//14-3-3 PROTEIN GAMMA (PROTEIN KINASE C INHIBITOR PROTEIN
 -1) (KCIP-1).//4.8e-62:145:90//RATTUS NORVEGICUS (RAT).//P35214
 F-NT2RP2001445
 F-NT2RP2001449//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
 SUBUNIT (CPSF 100 KD SUBUNIT).//9.5e-118:226:95//BOS TAURUS (BOVINE).//Q
 10568
 F-NT2RP2001450
 F-NT2RP2001467//SHORT NEUROTOXIN 1 (TOXIN V-II-1).//1.0:25:40//BUNGARUS
 FASCIATUS (BANDED KRAIT).//P10808
 F-NT2RP2001506
 F-NT2RP2001511//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.
 //0.49:124:29//CAENORHABDITIS ELEGANS.//P34681
 F-NT2RP2001520//VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN, INTESTINAL
 (CABP) (CALBINDIN D9K).//0.035:71:33//HOMO SAPIENS (HUMAN).//P29377
 F-NT2RP2001526
 F-NT2RP2001536//METALLOTHIONEIN-I (MT-1).//1.0:19:42//COLUMBA LIVIA (DOM
 ESTIC PIGEON).//P15786
 F-NT2RP2001560//CUTICLE COLLAGEN 12 PRECURSOR.//0.0018:144:35//CAENORHAB
 DITIS ELEGANS.//P20630

F-NT2RP2001569//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-31:102:67
 //HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP2001576//SMP3 PROTEIN.//0.00016:75:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04174
 F-NT2RP2001581//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.040:46:36//HOMO SAPIENS (HUMAN).//P51805
 F-NT2RP2001597//PROBABLE E4 PROTEIN.//0.00042:113:34//HUMAN PAPILLOMAVIRUS TYPE 5.//P06924
 F-NT2RP2001601
 F-NT2RP2001613//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.14:59:32//GALLUS GALLUS (CHICKEN).//P19601
 F-NT2RP2001628//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.056:140:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 F-NT2RP2001634//ALPHA-CATENIN.//7.1e-12:152:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P35220
 F-NT2RP2001660//HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION.//0.43:119:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40358
 F-NT2RP2001663//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON- NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).//1.2e-26:126:56//HOMO SAPIENS (HUMAN).//P06733
 F-NT2RP2001675//HYPOTHETICAL 107.7 KD PROTEIN IN RPSO 5' REGION (ORF1).//0.25:148:25//CAMPYLOBACTER JEJUNI.//Q46089
 F-NT2RP2001677//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.010:101:31//RATTUS NORVEGICUS (RAT).//P10164
 F-NT2RP2001678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-18:83:61//HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP2001699//PROTEIN C14.//0.98:51:31//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21045
 F-NT2RP2001720//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC F

ORM 1).//0.16:145:30//PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA).//
Q99317
F-NT2RP2001721//MALE-SPECIFIC LETHAL-2 PROTEIN.//0.00090:48:39//DROSOPHI
LA MELANOGASTER (FRUIT FLY).//P50534
F-NT2RP2001740//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.50:43:25//BOS TAURU
S (BOVINE).//P20072
F-NT2RP2001748//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P
EPTIDE P-D] (FRAGMENT).//0.77:111:28//HOMO SAPIENS (HUMAN).//P10162
F-NT2RP2001762
F-NT2RP2001813//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I).//1.0
:22:40//PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA).//047040
F-NT2RP2001839//SCY1 PROTEIN.//6.8e-17:204:27//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P53009
F-NT2RP2001861//D15KZ1 PROTEIN (FRAGMENT).//0.31:56:39//MUS MUSCULUS (MO
USE).//Q61466
F-NT2RP2001869//CORNEODESMOSIN (S PROTEIN) (FRAGMENT).//0.97:78:30//SUS
SCROFA (PIG).//019084
F-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM
BINDING ADAPTER MOLECULE 1).//3.5e-36:106:66//HOMO SAPIENS (HUMAN).//P5
5008
F-NT2RP2001883//CATHEPSIN L (EC 3.4.22.15).//0.95:29:41//OVIS ARIES (SHE
EP).//Q10991
F-NT2RP2001898//TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECU
RSOR (EC 3.1.3.56) (5PTASE) (FRAGMENT).//1.6e-84:185:88//HOMO SAPIENS (H
UMAN).//P32019
F-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//1.1e-17:180:34//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P53946
F-NT2RP2001907//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.13
:108:27//CANDIDA ALBICANS (YEAST).//P46593

F-NT2RP2001926//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.55:57:26//CYANOPHORA PARADOXA.//P48273

F-NT2RP2001936

F-NT2RP2001943//HYPOTHETICAL 57.7 KD PROTEIN IN AIP1-CTF13 INTERGENIC REGION.//1.8e-13:208:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04305

F-NT2RP2001946//HYPOTHETICAL 13.0 KD PROTEIN IN ALGR3 3' REGION.//0.59:76:28//PSEUDOMONAS AERUGINOSA.//P21485

F-NT2RP2001947//ZINC FINGER PROTEIN DAN (N03).//0.53:68:29//RATTUS NORVEGICUS (RAT).//Q06880

F-NT2RP2001969//CHLOROPLAST 30S RIBOSOMAL PROTEIN S18.//0.0015:52:34//CHLORELLA VULGARIS.//P56353

F-NT2RP2001976//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//9.5e-07:201:22//MUS MUSCULUS (MOUSE).//Q99104

F-NT2RP2001985//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.016:90:32//MUS MUSCULUS (MOUSE).//P05142

F-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//8.0e-14:47:76//RATTUS NORVEGICUS (RAT).//Q08469

F-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//2.9e-30:211:42//GALLUS GALLUS (CHICKEN).//P35331

F-NT2RP2002032//FLOCCULANT-ACTIVE PROTEINS MO2.1 AND MO2.2.//0.23:20:40//MORINGA OLEIFERA (HORSE RADISH TREE) (MORINGA PTERYGOSPERMA).//P24303

F-NT2RP2002033//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.88:27:62//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2002041

F-NT2RP2002046//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//1.0:85:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027

F-NT2RP2002047

F-NT2RP2002058//DOM34 INTERACTING PROTEIN 2.//9.4e-25:165:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027

CES CEREVISIAE (BAKER'S YEAST).//Q12220
 F-NT2RP2002066//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)./
 /5.7e-12:108:41//HOMO SAPIENS (HUMAN).//Q07157
 F-NT2RP2002070//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGME
 NT).//0.88:28:50//ASTERINA PECTINIFERA (STARFISH).//P11958
 F-NT2RP2002076//TRP-ASP REPEATS CONTAINING PROTEIN RBA-2.//0.0031:124:27
 //CAENORHABDITIS ELEGANS.//P90916
 F-NT2RP2002078//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.82:30:40//OVI
 S ARIES (SHEEP).//Q02958
 F-NT2RP2002079//OUTER DENSE FIBER PROTEIN.//0.34:41:39//HOMO SAPIENS (HU
 MAN).//Q14990
 F-NT2RP2002099//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//5.2
 e-08:81:48//HOMO SAPIENS (HUMAN).//Q00839
 F-NT2RP2002105//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0012:100:34//BOS TAURU
 S (BOVINE).//P23206
 F-NT2RP2002124//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSC
 RIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225).//0.74:72:31//H
 OMO SAPIENS (HUMAN).//P18146
 F-NT2RP2002137//NEUROTOXIN B-II.//1.0:27:44//CEREBRATULUS LACTEUS (MILKY
 RIBBON WORM).//P01526
 F-NT2RP2002154//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN)
 (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35)
 (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDI
 NG LECTIN).//0.0029:112:34//MUS MUSCULUS (MOUSE).//P16110
 F-NT2RP2002172
 F-NT2RP2002185//UBIQUITIN-LIKE PROTEIN DSK2.//1.8e-07:87:40//SACCHAROMYC
 ES CEREVISIAE (BAKER'S YEAST).//P48510
 F-NT2RP2002192
 F-NT2RP2002193//CUTICLE COLLAGEN 40.//0.0062:70:37//CAENORHABDITIS ELEGA

NS.//P34804

F-NT2RP2002208//PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10).//0.00011
:45:40//HOMO SAPIENS (HUMAN).//060683

F-NT2RP2002219

F-NT2RP2002231//V-TYPE SODIUM ATP SYNTHASE SUBUNIT E (EC 3.6.1.34) (NA(+)-
)- TRANSLOCATING ATPASE SUBUNIT E).//1.0:68:32//ENTEROCOCCUS HIRAE.//P43
436

F-NT2RP2002235//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP
34.5).//0.0022:66:45//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CVG-2).//P37
318

F-NT2RP2002252//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7
.6) (RPB1) (FRAGMENT).//0.071:110:31//CRICETULUS GRISEUS (CHINESE HAMSTE
R).//P11414

F-NT2RP2002256//CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLI
ZING CYTOCHROME) (P450RA1) (RETINOIC ACID 4-HYDROXYLASE).//3.1e-31:75:84
//MUS MUSCULUS (MOUSE).//055127

F-NT2RP2002259//L-MYC-1 PROTO-ONCOGENE PROTEIN.//1.9e-17:41:90//HOMO SAP
IENS (HUMAN).//P12524

F-NT2RP2002270//HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC REG
ION.//2.1e-27:164:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53930

F-NT2RP2002292//IMMEDIATE-EARLY PROTEIN RSP40.//0.018:107:23//PSEUDORABI
ES VIRUS (STRAIN KAPLAN) (PRV).//P24827

F-NT2RP2002312//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DI
GLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLY
CEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG
SYNTHASE).//1.4e-52:174:55//HOMO SAPIENS (HUMAN).//Q92903

F-NT2RP2002316//HISTONE H1.C6/H1.C9.//1.0:40:40//TRYPANOSOMA CRUZI.//P40
269

F-NT2RP2002325//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A

).//2.2e-06:145:26//CANDIDA BOIDINII (YEAST).//Q00316
 F-NT2RP2002333//HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REG
 ION (ORF 3).//0.30:86:32//ESCHERICHIA COLI.//P23524
 F-NT2RP2002373//SYNAPSINS IA AND IB.//0.080:145:31//BOS TAURUS (BOVINE).
 //P17599
 F-NT2RP2002385//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS:
 KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN].//0.021:66:28//MINK CE
 LL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CI-3).//P03388
 F-NT2RP2002394
 F-NT2RP2002408//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00030:107:37//
 BOS TAURUS (BOVINE).//P02453
 F-NT2RP2002426
 F-NT2RP2002439//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.00032:79:32/
 /PLASMODIUM BERGHEI (STRAIN ANKA).//P23093
 F-NT2RP2002442//HESA PROTEIN.//6.0e-16:163:30//PLECTONEMA BORYANUM.//P46
 037
 F-NT2RP2002457
 F-NT2RP2002464//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I./
 /9.3e-18:165:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264
 F-NT2RP2002475//CYSTEINE-RICH HEART PROTEIN (HCRHP).//0.91:45:35//HOMO S
 APIENS (HUMAN).//P50238
 F-NT2RP2002479//ATP-BINDING CASSETTE TRANSPORTER 7 PRECURSOR (ABC TRANSP
 ORTER 7 PROTEIN).//6.8e-96:186:94//HOMO SAPIENS (HUMAN).//075027
 F-NT2RP2002498//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.65:37:
 45//PSEUDOMONAS AERUGINOSA.//P04139
 F-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//1.3e-31:124:59//HOMO
 SAPIENS (HUMAN).//Q02386
 F-NT2RP2002504//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155)
 (155 KD NUCLEOPORIN) (P140).//1.2e-123:240:92//RATTUS NORVEGICUS (RAT).

//P37199

F-NT2RP2002520//ACIDIC PROLINE-RICH PROTEIN HP43A PRECURSOR.//0.94:83:28

//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P06680

F-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4

.0e-10:194:23//CAENORHABDITIS ELEGANS.//Q11073

F-NT2RP2002546

F-NT2RP2002549//G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN) (FRAGMENT).//0.98:65:30//DAUCUS CAROTA (CARROT).//P25010

F-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.6e-19:60:61//HOMO SAPIENS (HUMAN).//P51523

F-NT2RP2002595//ANNEXIN VII (SYNEXIN).//1.2e-15:121:49//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q92125

F-NT2RP2002606//PROTEIN TRANSPORT PROTEIN SEC2.//0.00034:98:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065

F-NT2RP2002609//HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SPT6 INTERGENIC REGION.//0.00022:79:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53264

F-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-).//6.2e-37:180:44//RATTUS NORVEGICUS (RAT).//Q63009

F-NT2RP2002621//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.98:37:35//LEMUR CATTAL (RING-TAILED LEMUR).//Q34879

F-NT2RP2002643//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.042:77:32//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319

F-NT2RP2002672//PROTEIN Q300.//0.0018:41:43//MUS MUSCULUS (MOUSE).//Q02722

F-NT2RP2002701//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3.6e-17:100:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RP2002706//IMMEDIATE-EARLY PROTEIN IE180.//0.00027:139:33//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//6.9e-09:96:40//MUS MUSCULUS
(MOUSE).//P55194

F-NT2RP2002727//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//3.6e-20
:160:36//RATTUS NORVEGICUS (RAT).//P49816

F-NT2RP2002736

F-NT2RP2002740

F-NT2RP2002741//RH01 GDP-GTP EXCHANGE PROTEIN 2.//2.0e-07:178:28//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST).//P51862

F-NT2RP2002750//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.6e-09:43:72
//HOMO SAPIENS (HUMAN).//P39191

F-NT2RP2002752//LOW CALCIUM RESPONSE LOCUS PROTEIN T.//0.95:33:39//YERSI
NIA PSEUDOTUBERCULOSIS.//Q00932

F-NT2RP2002753//ENDOGLUCANASE EG-1 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA
-GLUCANASE) (CELLULASE).//0.71:78:33//TRICHODERMA LONGIBRACHIATUM.//Q127
14

F-NT2RP2002769//50 KD SPICULE MATRIX PROTEIN PRECURSOR.//0.44:76:32//STR
ONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P11994

F-NT2RP2002778

F-NT2RP2002800//CRAMBIN.//0.99:20:50//CRAMBE ABYSSINICA (ABYSSINIAN CRAM
BE).//P01542

F-NT2RP2002839//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CON
TAINS: BASIC PEPTIDE P-F] (FRAGMENT).//0.010:87:31//HOMO SAPIENS (HUMAN)
.//P02812

F-NT2RP2002857//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).//0.
00018:57:45//RATTUS NORVEGICUS (RAT).//P04474

F-NT2RP2002862//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION
.//7.2e-27:140:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201

F-NT2RP2002880//DNA REPAIR PROTEIN RAD32.//0.83:67:28//SCHIZOSACCHAROMYC
ES POMBE (FISSION YEAST).//Q09683

F-NT2RP2002891//HOMEBOX PROTEIN DLX-2 (DLX-5) (FRAGMENT).//0.99:70:24//
RATTUS NORVEGICUS (RAT).//Q64204

F-NT2RP2002925//ALPHA-1D ADRENERGIC RECEPTOR (ALPHA 1D-ADRENOCEPTOR) (ALPHA-1A ADRENERGIC RECEPTOR).//0.31:48:43//HOMO SAPIENS (HUMAN).//P25100

F-NT2RP2002928//CELL DIVISION CONTROL PROTEIN 40.//2.8e-26:142:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40968

F-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//2.0e-31:186:35//CAENORHABDITIS ELEGANS.//Q18964

F-NT2RP2002939//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATASE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//0.0022:98:39//CANIS FAMILIARIS (DOG).//P30803

F-NT2RP2002954//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A').//0.0019:107:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43333

F-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//2.8e-11:33:81//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669

F-NT2RP2002979

F-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.1e-09:98:36//MYCOPLASMA CAPRICOLUM.//P10129

F-NT2RP2002986//RING CANAL PROTEIN (KELCH PROTEIN).//1.1e-19:141:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP2002987//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.3e-07:78:47//HOMO SAPIENS (HUMAN).//P39192

F-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.0e-77:165:85//RATTUS NORVEGICUS (RAT).//O54888

F-NT2RP2003000//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.8e-19:62:64/

/HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP2003034//HYPOTHETICAL PROTEIN HI1458.//1.0:42:35//HAEMOPHILUS INF
 LUENZAE.//P44204
 F-NT2RP2003073//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.0051:16:87//
 HOMO SAPIENS (HUMAN).//P39189
 F-NT2RP2003099
 F-NT2RP2003108//BASIC PROLINE-RICH PEPTIDE IB-1.//0.84:47:34//HOMO SAPIE
 NS (HUMAN).//P04281
 F-NT2RP2003117
 F-NT2RP2003121//HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REG
 ION.//9.0e-08:99:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43572
 F-NT2RP2003125//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOL
 OG 2).//9.2e-08:134:28//MUS MUSCULUS (MOUSE).//P97303
 F-NT2RP2003129
 F-NT2RP2003137//UBIQUITIN.//3.4e-06:70:30//NEUROSPORA CRASSA.//P13117
 F-NT2RP2003157//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//
 7.8e-13:84:40//CAENORHABDITIS ELEGANS.//Q09217
 F-NT2RP2003158//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT
 P58).//3.1e-65:155:84//HOMO SAPIENS (HUMAN).//043242
 F-NT2RP2003161//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0011:59:42//MUS
 MUSCULUS (MOUSE).//P05142
 F-NT2RP2003164//ZYGIN.//0.0037:85:36//MUS MUSCULUS (MOUSE).//Q62523
 F-NT2RP2003165//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-24:77:64/
 /HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP2003177//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.55:38:39//DROSOP
 HILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RP2003194//HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III./
 /2.3e-14:87:37//CAENORHABDITIS ELEGANS.//P30629
 F-NT2RP2003206//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.

0:100:28//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM).//P4
1306

F-NT2RP2003228//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P
1-CDC21).//9.3e-82:211:81//HOMO SAPIENS (HUMAN).//P33991

F-NT2RP2003230//SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSITOL/PHOSPHATIDY
LCHOLINE TRANSFER PROTEIN) (PI/PC TP).//1.0:51:31//CANDIDA GLABRATA (YEA
ST) (TORULOPSIS GLABRATA).//P53989

F-NT2RP2003237//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.1e-44:66:84/
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2003243//M PROTEIN, SEROTYPE 5 PRECURSOR.//0.027:204:23//STREPTOC
OCCUS PYOGENES.//P02977

F-NT2RP2003265//BP4A PROTEIN.//0.95:35:34//BRASSICA NAPUS (RAPE).//P4150
5

F-NT2RP2003272//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (F
RAGMENT).//5.5e-06:78:35//BRASSICA NAPUS (RAPE).//P40603

F-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (U
P-FRAMESHIFT SUPPRESSOR 1).//1.9e-19:145:43//SACCHAROMYCES CEREVISIAE (B
AKER'S YEAST).//P30771

F-NT2RP2003280

F-NT2RP2003286//RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-P
HOSPHATE CYCLASE) (RNA CYCLASE).//2.1e-32:137:42//SACCHAROMYCES CEREVISI
AE (BAKER'S YEAST).//Q08096

F-NT2RP2003293//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.7e
-12:175:33//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP2003295//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.055:44:45//HOMO
SAPIENS (HUMAN).//P23246

F-NT2RP2003297

F-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.0e-18:87:49//RATTUS NORVEG
ICUS (RAT).//P37285

F-NT2RP2003308//CROOKED NECK PROTEIN.//2.1e-91:244:67//DROSOPHILA MELANO
 GASTER (FRUIT FLY).//P17886

F-NT2RP2003329//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III./
 /5.8e-57:186:55//CAENORHABDITIS ELEGANS.//P34284

F-NT2RP2003339//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA).//0.98:11:72//DEND
 ROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P01416

F-NT2RP2003347//60S RIBOSOMAL PROTEIN L38.//0.83:42:33//OSTERTAGIA OSTER
 TAGI.//O61570

F-NT2RP2003367//SYNERGISTIC-TYPE VENOM PROTEIN C9S3, CHAIN 1.//1.0:37:35
 //DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01408

F-NT2RP2003391//MRNA TRANSPORT REGULATOR MTR10.//3.3e-11:229:24//SACCHAR
 OMYCES CEREVISIAE (BAKER'S YEAST).//Q99189

F-NT2RP2003393//PROTOCHLOROPHYLLIDE REDUCTASE CHLB SUBUNIT (EC 1.3.1.33)
 (NADPH- PROTOCHLOROPHYLLIDE OXIDOREDUCTASE CHLB SUBUNIT) (FRAGMENT).//O
 .94:29:34//ARAUCARIA HETEROPHYLLA.//P37843

F-NT2RP2003394

F-NT2RP2003401//60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).//0.95:
 125:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P45746

F-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.8e-78:
 178:84//RATTUS NORVEGICUS (RAT).//P38378

F-NT2RP2003445

F-NT2RP2003446//HYPOTHETICAL PROTEIN E-115.//0.00030:106:33//HUMAN ADENO
 VIRUS TYPE 2.//P03290

F-NT2RP2003456//PHOTOSYSTEM II REACTION CENTRE M PROTEIN.//1.0:27:51//MA
 RCHANTIA POLYMORPHA (LIVERWORT).//P12168

F-NT2RP2003466//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESAT
 URASE).//6.7e-06:108:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RP2003480//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2)
 (T-14-6).//7.2e-15:38:50//GALLUS GALLUS (CHICKEN).//Q98937

F-NT2RP2003499//5E5 ANTIGEN.//0.090:114:32//RATTUS NORVEGICUS (RAT).//Q6
3003

F-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.0
e-11:91:43//SUS SCROFA (PIG).//P04175

F-NT2RP2003511//PARAMYOSIN, SHORT FORM (MIMIPARAMYOSIN).//0.0020:108:25/
/DROSOPHILA MELANOGASTER (FRUIT FLY).//P35416

F-NT2RP2003513//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2e-05:96:36//HO
MO SAPIENS (HUMAN).//P23246

F-NT2RP2003517//HYPOTHETICAL 12.9 KD PROTEIN CY49.27.//0.0059:22:31//MYC
OBACTERIUM TUBERCULOSIS.//Q10696

F-NT2RP2003522//HYPOTHETICAL 10.0 KD PROTEIN.//1.0:65:30//THERMOPROTEUS
TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19283

F-NT2RP2003533//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.7e-18:94:54//HO
MO SAPIENS (HUMAN).//P08547

F-NT2RP2003543//SYNAPSINS IA AND IB.//0.045:101:35//RATTUS NORVEGICUS (R
AT).//P09951

F-NT2RP2003559//ITBA2 PROTEIN (DXS9879E).//0.98:37:37//HOMO SAPIENS (HUM
AN).//Q14657

F-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)
) (RO(SS-A)).//6.4e-35:175:44//HOMO SAPIENS (HUMAN).//P19474

F-NT2RP2003567//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X.//0
.72:82:34//CAENORHABDITIS ELEGANS.//Q22544

F-NT2RP2003581//HOMEBOX PROTEIN OTX1.//0.90:61:37//MUS MUSCULUS (MOUSE)
.//P80205

F-NT2RP2003596//ELONGATION FACTOR P (EF-P).//0.83:61:32//MYCOPLASMA GENI
TALIUM.//P47272

F-NT2RP2003604//ALPHA-CATENIN.//1.5e-11:152:33//DROSOPHILA MELANOGASTER
(FRUIT FLY).//P35220

F-NT2RP2003629//PHOSPHOLIPASE A2 ALPHA (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE

2-ACYLHYDROLASE)../0.97:85:27//CROTALUS ADAMANTEUS (EASTERN DIAMONDBACK
RATTLESNAKE)../P00623

F-NT2RP2003643//ACYLNEURAMINATE CYTIDYLYLTRANSFERASE (EC 2.7.7.43) (CMP-
N- ACETYLNEURAMINIC ACID SYNTHETASE) (CMP-NEUNAC SYNTHETASE) (CMP-SIALIC
ACID SYNTHETASE)../3.9e-12:84:40//NEISSERIA MENINGITIDIS.//Q57385

F-NT2RP2003668//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.0e-33:74:81/
/HOMO SAPIENS (HUMAN)../P39195

F-NT2RP2003687//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.7e-05:40:67//
HOMO SAPIENS (HUMAN)../P39188

F-NT2RP2003691//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.5e-37:56:67/
/HOMO SAPIENS (HUMAN)../P39194

F-NT2RP2003702//HYPOTHETICAL OXIDOREDUCTASE IN INLA 5' REGION (EC 1.-.-.-
) (ORFA)../1.3e-07:98:37//LISTERIA MONOCYTOGENES.//P25145

F-NT2RP2003704//GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (EC 2.3.2.2) (G
AMMA- GLUTAMYLTRANSFERASE 5) (GGT-REL)../0.66:23:52//HOMO SAPIENS (HUMAN
)../P36269

F-NT2RP2003706//GLUTAMYL AMINOPEPTIDASE (EC 3.4.11.7) (EAP) (AMINOPEPTID
ASE A) (APA) (DIFFERENTIATION ANTIGEN GP160)../1.2e-22:187:35//HOMO SAPI
ENS (HUMAN)../Q07075

F-NT2RP2003713//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 6 (EC 3.1.2.15) (U
BIQUITIN THIOLESTERASE 6) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 6) (DE
UBIQUITINATING ENZYME 6) (PROTO-ONCOGENE TRE-2)../2.7e-06:119:34//HOMO S
APIENS (HUMAN)../P35125

F-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7
)../6.7e-27:68:75//HOMO SAPIENS (HUMAN)../Q05481

F-NT2RP2003727//HYPOTHETICAL PROTEIN MG007 HOMOLOG.//0.64:110:30//MYCOPL
ASMA PNEUMONIAE.//P75105

F-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (U
BIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)../1.2

e-72:147:90//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGIC
US (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669
F-NT2RP2003751//EXTRACELLULAR GLOBIN PRECURSOR.//0.67:68:30//PSEUDOTERRA
NOVA DECIPIENS (COD WORM).//P26914
F-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).
//1.0e-98:235:82//BOS TAURUS (BOVINE).//P53620
F-NT2RP2003764//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.011:69:34//ORGY
IA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341
F-NT2RP2003769//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:33:36//
EQUUS CABALLUS (HORSE).//P48663
F-NT2RP2003770//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAG
MENT).//0.029:35:42//PSEUDOMONAS AERUGINOSA.//P23621
F-NT2RP2003777//HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION./
/0.041:67:34//XANTHOMONAS CAMPESTRIS (PV. VESICATORIA).//P14728
F-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//4.
7e-54:204:47//CAENORHABDITIS ELEGANS.//Q09201
F-NT2RP2003793//PSEUDO-HEVEIN (MINOR HEVEIN).//0.61:30:36//HEVEA BRASILI
ENSIS (PARA RUBBER TREE).//P80359
F-NT2RP2003825//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//1.0:35:37//CA
NIS FAMILIARIS (DOG).//P13206
F-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//2
.5e-05:80:38//CAENORHABDITIS ELEGANS.//Q11076
F-NT2RP2003857//BACTERIOCIN MICROGIN B17 PRECURSOR (MCB17).//0.54:28:50/
/ESCHERICHIA COLI.//P05834
F-NT2RP2003859//DROSOCIN PRECURSOR.//1.0:37:35//DROSOPHILA MELANOGASTER
(FRUIT FLY).//P36193
F-NT2RP2003871
F-NT2RP2003885//CUTICLE PROTEIN 32 (LM-32) (LM-ACP 32) (FRAGMENT).//1.0:
28:50//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P11736

F-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//4.8e-110:268:80//MUS MUSCULUS (MOUSE).//P519

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F-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//0.00024:92:31//RATTUS NORVEGICUS (RAT).//009175

F-NT2RP2003968//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//9.2e-05:101:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-NT2RP2003976//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-21:62:62//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//2.7e-08:165:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39702

F-NT2RP2003984//UNC-87 PROTEIN.//0.75:71:28//CAENORHABDITIS ELEGANS.//P37806

F-NT2RP2003986//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.3e-19:47:70//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2003988//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.2e-18:80:58//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.0e-52:141:77//HOMO SAPIENS (HUMAN).//P20290

F-NT2RP2004014//MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA (MIP2-ALPHA) (CINC-2-ALPHA).//0.99:45:26//RATTUS NORVEGICUS (RAT).//Q10746

F-NT2RP2004041//SYNAPSINS IA AND IB.//0.0022:51:37//BOS TAURUS (BOVINE).//P17599

F-NT2RP2004042//CRUSTACEAN HYPERGLYCEMIC HORMONE PRECURSOR (CHH) (FRAGMENT).//1.0:49:28//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//Q26181

F-NT2RP2004066//CALDESMON (CDM).//2.9e-05:175:21//GALLUS GALLUS (CHICKEN).//P12957

F-NT2RP2004081//CADMIUM-METALLOTHIONEIN (CD-MT).//0.93:59:23//HELIX POMA
TIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187

F-NT2RP2004098//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)
.//4.6e-09:121:30//HOMO SAPIENS (HUMAN).//Q15404

F-NT2RP2004124//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.068:63:31//GAL
LUS GALLUS (CHICKEN).//P02314

F-NT2RP2004142//HYPOTHETICAL 59.1 KD PROTEIN IN VPS15-YMC2 INTERGENIC RE
GION.//7.9e-05:94:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38262

F-NT2RP2004152//LAMIN L(I).//0.25:167:19//XENOPUS LAEVIS (AFRICAN CLAWED
FROG).//P09010

F-NT2RP2004165//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC R
EGION.//0.0014:124:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RP2004170//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.012:125:30//MUS
MUSCULUS (MOUSE).//P05143

F-NT2RP2004172//HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC RE
GION.//4.1e-26:214:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36051

F-NT2RP2004187//ZINC FINGER PROTEIN 174.//3.7e-12:76:47//HOMO SAPIENS (H
UMAN).//Q15697

F-NT2RP2004194//HYPOTHETICAL 10.5 KD PROTEIN C31A2.13C IN CHROMOSOME I./
/0.0013:92:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09730

F-NT2RP2004196//METALLOTHIONEIN 10-II (MT-10-II).//0.92:36:36//MYTILUS E
DULIS (BLUE MUSSEL).//P80247

F-NT2RP2004207//MALE ACCESSORY GLAND SECRETORY PROTEIN 355A PRECURSOR.//
0.92:62:35//DROSOPHILA SIMULANS (FRUIT FLY).//P33737

F-NT2RP2004226//66 KD STRESS PROTEIN (P66).//0.030:113:26//PHYSARUM POLY
CEPHALUM (SLIME MOLD).//P90587

F-NT2RP2004232//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//2.0e-
48:211:51//HOMO SAPIENS (HUMAN).//Q15139

F-NT2RP2004239//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.

//0.00038:111:36//TRITICUM AESTIVUM (WHEAT).//P08489
 F-NT2RP2004240//METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN
) (MT-CE).//1.0:39:28//CAENORHABDITIS ELEGANS.//P17512
 F-NT2RP2004242//RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN
 RGP1).//0.0036:64:28//ORYZA SATIVA (RICE).//P25766
 F-NT2RP2004245//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:21:42//
 PONGO PYGMAEUS PYGMAEUS (BORNEAN ORANGUTAN).//P92896
 F-NT2RP2004270//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.0002
 3:118:33//NEPHILA CLAVIPES (ORB SPIDER).//P46804
 F-NT2RP2004300//PROBABLE E4 PROTEIN.//0.18:77:40//HUMAN PAPILLOMAVIRUS T
 YPE 8.//P06425
 F-NT2RP2004316
 F-NT2RP2004321//HYPOTHETICAL 10.8 KD PROTEIN SSR2439.//1.0:50:28//SYNECH
 OCYSTIS SP. (STRAIN PCC 6803).//Q01904
 F-NT2RP2004339//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.0e-33:84:77/
 /HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP2004347//HYPOTHETICAL 40.9 KD PROTEIN F33H1.3 FROM CHROMOSOME II.
 //0.78:96:30//CAENORHABDITIS ELEGANS.//Q09556
 F-NT2RP2004364//MINOR OUTER CAPSID PROTEIN (NS26) (NONSTRUCTURAL PROTEIN
 VP9).//0.059:143:30//BOVINE ROTAVIRUS (STRAIN UK).//P04515
 F-NT2RP2004365//EAMZP30-47 PROTEIN (FRAGMENT).//0.27:38:39//EIMERIA ACER
 VULINA.//P21959
 F-NT2RP2004366//GLYCOPROTEIN L PRECURSOR.//0.64:71:28//MAREK'S DISEASE H
 ERPESVIRUS (STRAIN GA) (MDHV).//P52510
 F-NT2RP2004373//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE
 RICH GLYCOPROTEIN) (HPRG) (FRAGMENT).//0.59:50:40//ORYCTOLAGUS CUNICULU
 S (RABBIT).//Q28640
 F-NT2RP2004389//HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III./
 /4.0e-16:89:43//CAENORHABDITIS ELEGANS.//P34388

F-NT2RP2004392

F-NT2RP2004396//SINGLE-STRANDED NUCLEIC ACID-BINDING PROTEIN.//0.42:89:2
9//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10080

F-NT2RP2004399//SOMATOTROPIN PRECURSOR (GROWTH HORMONE).//1.0:72:34//MES
OCRICETUS AURATUS (GOLDEN HAMSTER).//P37886

F-NT2RP2004400

F-NT2RP2004412//SPERM PROTAMINE P1.//0.24:38:31//NOTORYCTES TYPHLOPS (MA
RSUPIAL MOLE).//P42143

F-NT2RP2004425//SUPPRESSOR PROTEIN SRP40.//0.0087:197:22//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP2004463//ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (AL
PHA-2AAR).//1.3e-05:121:37//MUS MUSCULUS (MOUSE).//Q01338

F-NT2RP2004476//NICKEL-SENSITIVE T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT
(RBE-II).//0.20:68:36//RATTUS NORVEGICUS (RAT).//Q07652

F-NT2RP2004490//FOS-RELATED ANTIGEN 1.//0.94:59:33//HOMO SAPIENS (HUMAN)
.//P15407

F-NT2RP2004512//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRA
GMENTS).//1.0:37:32//PISASTER OCHRACEUS (SEA STAR).//P24998

F-NT2RP2004523//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.1e-15:57:71/
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2004538//KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPT
IC VESICLES).//1.2e-48:121:60//HOMO SAPIENS (HUMAN).//Q12756

F-NT2RP2004551//HYPOTHETICAL 7.6 KD PROTEIN (ORF 65).//1.0:20:50//EUGLEN
A GRACILIS.//P32095

F-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//5.2e-07:
150:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09903

F-NT2RP2004580//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.7e-37:100:78
//HOMO SAPIENS (HUMAN).//P39192

F-NT2RP2004587//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC R

EGION.//8.2e-06:150:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5321

4

F-NT2RP2004594//HYPOTHETICAL 45.3 KD PROTEIN C09F5.7 IN CHROMOSOME II.//

0.84:105:24//CAENORHABDITIS ELEGANS.//Q09458

F-NT2RP2004600//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS).//

/0.17:127:29//RATTUS NORVEGICUS (RAT).//P30009

F-NT2RP2004602//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-05:50:58//

HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2004614//HYPOTHETICAL 11.6 KD PROTEIN.//1.0:68:33//VACCINIA VIRUS

(STRAIN COPENHAGEN).//P20561

F-NT2RP2004655//GLYCINE-RICH RNA-BINDING PROTEIN 7.//7.0e-05:70:42//ARAB

IDOPSIS THALIANA (MOUSE-EAR CRESS).//Q03250

F-NT2RP2004664//HYPOTHETICAL 104.0 KD PROTEIN C32A11.03C IN CHROMOSOME I

.//0.30:78:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10328

F-NT2RP2004675

F-NT2RP2004681

F-NT2RP2004689//HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REG

ION.//0.021:179:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34243

F-NT2RP2004709//HYPOTHETICAL PROTEIN MJ0647.//0.90:39:43//METHANOCOCCUS

JANNASCHII.//Q58063

F-NT2RP2004710//GAR2 PROTEIN.//0.085:60:30//SCHIZOSACCHAROMYCES POMBE (F

SSION YEAST).//P41891

F-NT2RP2004736//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-15:97:49//

HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2004743//MALE SPECIFIC SPERM PROTEIN MST87F.//0.43:24:41//DROSOPH

ILA MELANOGASTER (FRUIT FLY).//P08175

F-NT2RP2004767//36.4 KD PROLINE-RICH PROTEIN.//0.0051:88:27//LYCOPERSICO

N ESCULENTUM (TOMATO).//Q00451

F-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RIC

H KINASE 1).//9.0e-29:166:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./
/P38692

F-NT2RP2004775

F-NT2RP2004791//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T
RNA LIGASE) (LEURS).//7.4e-60:226:53//CAENORHABDITIS ELEGANS.//Q09996

F-NT2RP2004799//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR
(EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.2e-42:
133:57//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587

F-NT2RP2004802//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3' REGION.//0.018:86
:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-NT2RP2004816//H58 PROTEIN.//1.0e-68:145:93//MUS MUSCULUS (MOUSE).//P40
336

F-NT2RP2004841//DSRD PROTEIN.//0.83:33:39//ARCHAEOGLOBUS FULGIDUS.//P707
42

F-NT2RP2004861//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIA3A.//0.0072:41:
39//OVIS ARIES (SHEEP).//P02443

F-NT2RP2004897//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:41:41//CASUARINA G
LAUCA (SWAMP OAK).//Q39511

F-NT2RP2004933//DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINA
SE 1).//8.4e-34:102:67//HOMO SAPIENS (HUMAN).//P53355

F-NT2RP2004936//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).
//0.87:36:33//ECTOTHIORHODOSPIRA VACUOLATA.//P38524

F-NT2RP2004959//STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTO
R) (MGF) (C-KIT LIGAND).//1.0:69:28//CANIS FAMILIARIS (DOG).//Q06220

F-NT2RP2004961//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIA
A0065) (HA0946) (FRAGMENT).//2.1e-21:73:58//HOMO SAPIENS (HUMAN).//Q0673
0

F-NT2RP2004962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.17:28:57//HO
MO SAPIENS (HUMAN).//P39189

F-NT2RP2004967//HYPOTHETICAL 7.3 KD PROTEIN.//0.76:41:31//THERMOPROTEUS
TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19301

F-NT2RP2004978//SPERMATID-SPECIFIC PROTEIN T2 [CONTAINS: SPERM PROTAMINE
SP2].//0.44:40:45//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80002

F-NT2RP2004982

F-NT2RP2004985//HYPOTHETICAL PROTEIN KIAA0144.//1.2e-51:204:57//HOMO SAP
IENS (HUMAN).//Q14157

F-NT2RP2004999//LONG NEUROTOXIN 1 (ALPHA-BUNGAROTOXIN) (BGTX).//0.23:73:
26//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P01378

F-NT2RP2005000//ATPASE STABILIZING FACTOR 15 KD PROTEIN.//0.12:37:32//SA
CCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P16965

F-NT2RP2005001//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.9
0:54:31//HOMO SAPIENS (HUMAN).//P22531

F-NT2RP2005003//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.6e
-30:78:56//MUS MUSCULUS (MOUSE).//P15533

F-NT2RP2005012//NPL1 PROTEIN (SEC63 PROTEIN).//0.00024:94:35//SACCHAROMY
CES CEREVISIAE (BAKER'S YEAST).//P14906

F-NT2RP2005018//GAG POLYPROTEIN (CORE POLYPROTEIN) [CONTAINS: CORE PROTE
INS P19, P10] (FRAGMENT).//1.0:91:28//AVIAN ENDOGENOUS ROUS-ASSOCIATED V
IRUS-0 (EV-2) (AVIAN RETROVIRUS RAV-0).//P06937

F-NT2RP2005020

F-NT2RP2005022//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.9e-11:10
6:35//PODOSPORA ANSERINA.//Q00808

F-NT2RP2005031

F-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//2.2e-32:117:55//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32447

F-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL AD
DITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFER
ASE).//9.3e-28:187:40//AMBYSTOMA MEXICANUM (AXOLOTL).//057486

F-NT2RP2005108//CUTICLE COLLAGEN 2.//0.33:62:38//CAENORHABDITIS ELEGANS.
//P17656

F-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPH
A SUBUNIT (EIF-3 ALPHA).//4.0e-54:161:63//CAENORHABDITIS ELEGANS.//P3446
6

F-NT2RP2005126//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.23:
46:39//PLEUROCHRYISIS HAPTONEMOFERA.//P41552

F-NT2RP2005139//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.016:43:37//B
OS TAURUS (BOVINE).//P25508

F-NT2RP2005140//HYPOTHETICAL 7.4 KD PROTEIN YCF33.//0.96:51:39//GUILLARD
IA THETA (CRYPTOMONAS PHI).//078517

F-NT2RP2005144//TUBBY PROTEIN.//5.6e-08:66:45//MUS MUSCULUS (MOUSE).//P5
0586

F-NT2RP2005147

F-NT2RP2005159//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//
0.94:57:29//NICOTIANA TABACUM (COMMON TOBACCO), AND SPINACIA OLERACEA (S
PINACH).//P12164

F-NT2RP2005162//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REG
ION.//1.2e-33:139:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821

F-NT2RP2005168//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.8
e-33:102:61//HOMO SAPIENS (HUMAN).//Q00839

F-NT2RP2005204//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//3.9
e-28:141:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624

F-NT2RP2005227

F-NT2RP2005239//TRNA SPLICING PROTEIN SPL1.//2.0e-38:117:64//CANDIDA ALB
ICANS (YEAST).//P87185

F-NT2RP2005254//OMEGA-AGATOXIN IB (OMEGA-AGA-IB) (FRAGMENT).//0.26:29:48
//AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).//P15970

F-NT2RP2005270//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.037:82:34//GALLUS

GALLUS (CHICKEN).//P17277
 F-NT2RP2005276//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//2.0e-59:174:61//RATTUS NORVEGICUS (RAT).//035547
 F-NT2RP2005287//ZINC FINGER PROTEIN 26 (ZINC FINGER PROTEIN KOX20) (FRAGMENT).//1.5e-05:27:70//HOMO SAPIENS (HUMAN).//P17031
 F-NT2RP2005288//PROBABLE RUBREDOXIN HUPI.//1.0:42:28//RHIZOBIUM LEGUMINOSARUM (BIOVAR VICIAE).//P28151
 F-NT2RP2005289//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.1e-21:75:70//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2005293//TRANSLATION INITIATION FACTOR IF-2.//0.58:170:24//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P55972
 F-NT2RP2005315//CUTICLE COLLAGEN 7 (FRAGMENT).//0.091:65:38//CAENORHABDITIS ELEGANS.//P18832
 F-NT2RP2005325//CHROMOGANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I) [CONTAINS: PANCREASTATIN; WE-14].//9.5e-09:98:39//HOMO SAPIENS (HUMAN).//P10645
 F-NT2RP2005336//HYPOTHETICAL 68.7 KD PROTEIN IN STB1-MCK1 INTERGENIC REGION.//0.00011:124:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42846
 F-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 4 (EC 3.6.1.38).//4.7e-21:92:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12675
 F-NT2RP2005354
 F-NT2RP2005358//MYOSIN IC HEAVY CHAIN.//0.012:91:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
 F-NT2RP2005360//ACROSIN PRECURSOR (EC 3.4.21.10).//0.0022:73:36//ORYZOLAGUS CUNICULUS (RABBIT).//P48038
 F-NT2RP2005393//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.00085:135:28//CAENORHABDITIS ELEGANS.//Q09202
 F-NT2RP2005407//SQUALENE MONOOXYGENASE (EC 1.14.99.7) (SQUALENE EPOXIDASE)

E) (SE).//0.96:109:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32476
 F-NT2RP2005436//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0011:
 54:42//ZEA MAYS (MAIZE).//P14918
 F-NT2RP2005441//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.039:182:29//MUS
 MUSCULUS (MOUSE).//P05142
 F-NT2RP2005453
 F-NT2RP2005457//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.
 3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//4.0e-10:124:37//BOS TA
 URUS (BOVINE).//Q02827
 F-NT2RP2005464//HYPOTHETICAL 9.5 KD PROTEIN.//0.96:42:33//VACCINIA VIRUS
 (STRAIN COPENHAGEN).//P20553
 F-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//4.6e-09:92:42//SACC
 HAROMYCES CEREVISIAE (BAKER'S YEAST).//P38127
 F-NT2RP2005472//HYPOTHETICAL PROTEIN BB0129.//0.76:80:32//BORRELIA BURGD
 ORFERI (LYME DISEASE SPIROCHETE).//051155
 F-NT2RP2005476//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-31:39:89/
 /HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2005490//METALLOTHIONEIN-II (MT-II).//0.14:27:33//SCYLLA SERRATA
 (MUD CRAB).//P02806
 F-NT2RP2005491//DNA-DIRECTED RNA POLYMERASE SUBUNIT I (EC 2.7.7.6).//0.9
 5:45:31//METHANOCOCCUS JANNASCHII.//Q58785
 F-NT2RP2005495//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REG
 ION.//0.99:68:30//BACTERIOPHAGE T4.//Q02407
 F-NT2RP2005496//ZINC FINGER PROTEIN 135.//1.4e-54:120:59//HOMO SAPIENS (
 HUMAN).//P52742
 F-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPH
 A ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55
).//9.5e-76:146:86//RATTUS NORVEGICUS (RAT).//P36876
 F-NT2RP2005501//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN)

(IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35)
 (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29), (L-31) (GALACTOSIDE-BIN
 DING PROTEIN) (GALBP).//0.025:70:40//HOMO SAPIENS (HUMAN).//P17931
 F-NT2RP2005509//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:166:27//GAL
 LUS GALLUS (CHICKEN).//P02457
 F-NT2RP2005520//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//7.9e-45:118:79//XEN
 OPUS LAEVIS (AFRICAN CLAWED FROG).//P50533
 F-NT2RP2005525//50S RIBOSOMAL PROTEIN L11.//1.0:47:27//BORRELIA BURGDORF
 ERI (LYME DISEASE SPIROCHETE).//051354
 F-NT2RP2005531//PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (PTPASE-
 MEG1) (MEG).//9.8e-13:84:45//HOMO SAPIENS (HUMAN).//P29074
 F-NT2RP2005539//RING CANAL PROTEIN (KELCH PROTEIN).//4.9e-10:90:33//DROS
 OPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP2005540//NUCLEOTIDE BINDING PROTEIN EXPZ.//0.36:119:21//BACILLUS
 SUBTILIS.//P39115
 F-NT2RP2005549//HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III
 .//6.0e-39:179:46//CAENORHABDITIS ELEGANS.//Q09253
 F-NT2RP2005555
 F-NT2RP2005557//HYPOTHETICAL 23.7 KD PROTEIN C13G6.14 IN CHROMOSOME I.//
 4.9e-06:90:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09790
 F-NT2RP2005581
 F-NT2RP2005600//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.014:37:40//HOM
 O SAPIENS (HUMAN).//P02811
 F-NT2RP2005605//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE
 RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBE
 RIN I) (FRAGMENT).//0.64:26:42//MACACA MULATTA (RHESUS MACAQUE).//P55247
 F-NT2RP2005620//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REG
 ION.//8.7e-31:138:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
 F-NT2RP2005622//NEUROTOXIN-LIKE PROTEIN STR1 (ANATOXIN AAH STR1).//0.39:

22:40//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P80950
 F-NT2RP2005635//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REG
 ION.//5.8e-43:144:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795
 F-NT2RP2005637//VPU PROTEIN (U ORF PROTEIN).//0.91:33:45//CHIMPANZEE IMM
 UNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286
 F-NT2RP2005640//METALLOTHIONEIN-LIKE PROTEIN LSC54.//0.63:41:31//BRASSIC
 A NAPUS (RAPE).//P43402
 F-NT2RP2005645
 F-NT2RP2005651//OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4)
 .//0.0023:50:42//HOMO SAPIENS (HUMAN).//Q01860
 F-NT2RP2005654//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REG
 ION.//6.1e-16:76:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564
 F-NT2RP2005669//METALLOTHIONEIN-II (MT-II).//0.76:16:50//SCYLLA SERRATA
 (MUD CRAB).//P02806
 F-NT2RP2005675//PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL CANCER-
 1).//6.5e-26:116:54//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P49119
 F-NT2RP2005683//HYPOTHETICAL PROTEIN HI0275.//0.17:50:40//HAEMOPHILUS IN
 FLUENZAE.//P43975
 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P
 5C REDUCTASE).//1.3e-16:75:30//PISUM SATIVUM (GARDEN PEA).//Q04708
 F-NT2RP2005694//HYPOTHETICAL PROTEIN KIAA0032.//9.6e-11:135:34//HOMO SAP
 IENS (HUMAN).//Q15034
 F-NT2RP2005701//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: P
 EPTIDE P-D] (FRAGMENT).//0.084:158:32//HOMO SAPIENS (HUMAN).//P10161
 F-NT2RP2005712//METALLOTHIONEIN-II (MT-II).//0.19:14:50//STENELLA COERUL
 EOALBA (STRIPED DOLPHIN).//P14425
 F-NT2RP2005719//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTO
 LAGUS CUNICULUS (RABBIT).//P02456
 F-NT2RP2005722//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//7.8e-37:131:62//

HOMO SAPIENS (HUMAN).//P16415
 F-NT2RP2005723//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.98:23:60//HOMO SAPIENS (HUMAN).//P39192
 F-NT2RP2005726//HYPOTHETICAL PROTEIN TP0375.//0.98:30:43//TREPONEMA PALLIDUM.//083390
 F-NT2RP2005732//PERIOD CLOCK PROTEIN (FRAGMENT).//0.41:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296
 F-NT2RP2005741//SMR1 PROTEIN PRECURSOR (VCS-ALPHA 1).//0.38:58:36//RATTUS NORVEGICUS (RAT).//P13432
 F-NT2RP2005748//ZINC FINGER PROTEIN KOX23 (FRAGMENT).//0.026:19:68//HOMO SAPIENS (HUMAN).//P17034
 F-NT2RP2005752//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//0.90:101:31//HOMO SAPIENS (HUMAN).//P02461
 F-NT2RP2005753//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.50:22:59//HOMO SAPIENS (HUMAN).//P30808
 F-NT2RP2005763//PUTATIVE ATP-DEPENDENT RNA HELICASE STE13.//4.7e-14:108:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09181
 F-NT2RP2005767//NONHISTONE CHROMOSOMAL PROTEIN 6B.//4.1e-08:65:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11633
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//1.2e-14:65:61//HOMO SAPIENS (HUMAN).//P32322
 F-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).//1.3e-103:199:90//ORYCTOLAGUS CUNICULUS (RABBIT).//P42675
 F-NT2RP2005781//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.090:73:36//HOMO SAPIENS (HUMAN).//P02810
 F-NT2RP2005784//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).//3.5e-06:79:37//HERPES SIM

PLEX VIRUS (TYPE 1 / STRAIN 17).//P08393
 F-NT2RP2005804//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.8e-07:4
 3:55//OWENIA FUSIFORMIS.//P21260
 F-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REG
 ION.//6.3e-14:143:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004
 F-NT2RP2005815//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HE
 ME SYNTHETASE).//0.0017:123:37//MYCOBACTERIUM AVIUM.//007401
 F-NT2RP2005835//SHP1 PROTEIN.//1.2e-08:135:26//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//P34223
 F-NT2RP2005841//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.
 23:28:53//HOMO SAPIENS (HUMAN).//P22532
 F-NT2RP2005853//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGI
 ON.//0.99:33:48//BACTERIOPHAGE T4.//P22917
 F-NT2RP2005857//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//8.6e-84:235:66//XEN
 OPUS LAEVIS (AFRICAN CLAWED FROG).//P50532
 F-NT2RP2005859//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.017:60:40//DROSO
 PHILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RP2005868//ATP SYNTHASE B' CHAIN PRECURSOR (EC 3.6.1.34) (SUBUNIT I
 I).//0.28:121:28//SPINACIA OLERACEA (SPINACH).//P31853
 F-NT2RP2005886//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAI
 NS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA].//0.80:130:28/
 /TETRAHYMENA THERMOPHILA.//P40631
 F-NT2RP2005890
 F-NT2RP2005901//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.35:18:44/
 /DROSOPHILA YAKUBA (FRUIT FLY).//P03933
 F-NT2RP2005908//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-28:61:65/
 /HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP2005933//PERIOD CLOCK PROTEIN (P230) (FRAGMENT).//1.7e-11:85:49//
 ACETABULARIA MEDITERRANEA (MERMAID'S WINE GLASS).//P12347

F-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A
DENYLYLTRANSFERASE).//7.2e-59:216:58//BOS TAURUS (BOVINE).//P25500

F-NT2RP2005980//HYPOTHETICAL 11.5 KD PROTEIN IN RSP8A-AST1 INTERGENIC RE
GION.//1.0:49:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38185

F-NT2RP2006023//DNA REPAIR PROTEIN REC N (RECOMBINATION PROTEIN N) (FRAGM
ENT).//1.0:40:45//VIBRIO CHOLERAEE.//P52118

F-NT2RP2006038//HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III./
/4.0e-11:90:34//CAENORHABDITIS ELEGANS.//P34281

F-NT2RP2006043//LAMININ BETA-1 CHAIN VARIANT (LAMININ BETA-1-2 CHAIN) (F
RAGMENT).//0.00067:73:38//GALLUS GALLUS (CHICKEN).//Q01636

F-NT2RP2006052//METALLOTHIONEIN-I (MT-I).//0.19:31:38//CERCOPITHECUS AET
HIOPS (GREEN MONKEY) (GRIVET).//P02797

F-NT2RP2006069//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//1.0:66:34//RATTU
S NORVEGICUS (RAT).//P02466

F-NT2RP2006071//RESTIN.//0.40:156:29//GALLUS GALLUS (CHICKEN).//042184

F-NT2RP2006098//HYPOTHETICAL 21.7 KD PROTEIN IN TUP1-ABP1 INTERGENIC REG
ION.//0.99:95:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25651

F-NT2RP2006100//LONG NEUROTOXIN 4 (ALPHA-NEUROTOXIN).//0.94:43:34//OPHIO
PHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P80156

F-NT2RP2006103//50S RIBOSOMAL PROTEIN L32.//0.40:36:38//SYNECHOCYSTIS SP
. (STRAIN PCC 6803).//P73014

F-NT2RP2006106//CUTICLE COLLAGEN 1.//0.28:85:29//CAENORHABDITIS ELEGANS.
//P08124

F-NT2RP2006141//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1
.9e-08:57:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RP2006166

F-NT2RP2006184//HYPOTHETICAL 11.2 KD PROTEIN IN CSGC-MDOG INTERGENIC REG
ION PRECURSOR.//0.95:87:26//ESCHERICHIA COLI.//P75917

F-NT2RP2006186//MICROTUBULE-ASSOCIATED PROTEIN 2.//0.088:124:33//MUS MUS

CULUS (MOUSE).//P20357
 F-NT2RP2006196//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.0e-05:49:61/
 /HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2006200//PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR.//0.0013:205:32//
 HOMO SAPIENS (HUMAN).//P05997
 F-NT2RP2006219//GONADAL PROTEIN GDL.//3.5e-18:158:37//DROSOPHILA MELANOG
 ASTER (FRUIT FLY).//P22468
 F-NT2RP2006237//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEI
 N).//0.79:103:28//STREPTOCOCCUS PYOGENES.//P30141
 F-NT2RP2006238//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-07:127:39//M
 US MUSCULUS (MOUSE).//P05143
 F-NT2RP2006258//PROBABLE E5 PROTEIN.//0.78:47:34//RHESUS PAPILLOMAVIRUS
 TYPE 1 (RHPV 1).//P24834
 F-NT2RP2006261//PENAEIDIN-3A PRECURSOR (P3-A).//0.61:35:40//PENAEUS VANN
 AMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81058
 F-NT2RP2006275//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//1.
 2e-28:59:57//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401
 F-NT2RP2006312//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROT
 EIN).//1.6e-06:53:35//TETRAHYMENA PYRIFORMIS.//P40625
 F-NT2RP2006320//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGME
 NT).//0.90:24:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV
 -1).//P04612
 F-NT2RP2006321//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.0051:25:76//
 HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2006323//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.84:33:39//HO
 MO SAPIENS (HUMAN).//P42768
 F-NT2RP2006333//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.56:37:40//CROTALU
 S DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333
 F-NT2RP2006334//SUCCINYL-COA LIGASE [GDP-FORMING], ALPHA-CHAIN 3 PRECURS

OR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN 3).//0.00097:46:41
 //TRICHOMONAS VAGINALIS.//P53401

F-NT2RP2006365//NONSPECIFIC LIPID-TRANSFER PROTEIN 4.3 PRECURSOR (LTP 4.
 3).//0.18:75:29//HORDEUM VULGARE (BARLEY).//Q42842

F-NT2RP2006393//OMEGA-CONOTOXIN MVIIC PRECURSOR (FRAGMENT).//0.82:15:66/
 /CONUS MAGUS (MAGUS CONE).//P37300

F-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOME
 BOX).//1.4e-08:50:50//MUS MUSCULUS (MOUSE).//Q61658

F-NT2RP2006441//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:22:54//MIMULUS GUT
 TATUS (SPOTTED MONKEY FLOWER) (YELLOW MONKEY FLOWER).//P20238

F-NT2RP2006454//SPERM PROTAMINE P1.//0.60:47:36//TACHYGLOSSUS ACULEATUS
 ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

F-NT2RP2006456

F-NT2RP2006464//PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT
 VII) (9 KD POLYPEPTIDE) (PSI-C).//0.91:79:30//SYNECHOCOCCUS SP. (STRAIN
 PCC 7002) (AGMENELLUM QUADRUPLICATUM).//P31087

F-NT2RP2006467//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.15:53:35//CAENORH
 ABDITIS ELEGANS.//Q21184

F-NT2RP2006472//HYPOTHETICAL 19 KD PROTEIN (ORF 167).//0.33:98:26//MARCH
 ANTIA POLYMORPHA (LIVERWORT).//P12202

F-NT2RP2006534

F-NT2RP2006554//ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PRO
 TEIN AA).//0.91:50:34//BACILLUS SPHAERICUS.//O32723

F-NT2RP2006565//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 3
 7).//6.0e-66:93:96//RATTUS NORVEGICUS (RAT).//P56603

F-NT2RP2006571//CYTOCHROME P450 2B10 (EC 1.14.14.1) (CYP11B10) (TESTOSTE
 RONE 16-ALPHA HYDROXYLASE) (P450-16-ALPHA) (CLONE PF3/46).//4.5e-40:138:
 57//MUS MUSCULUS (MOUSE).//P12791

F-NT2RP2006573//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.53:46:3

9//BOS TAURUS (BOVINE).//P02318
 F-NT2RP2006598//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-12:44:77/
 /HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP3000002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.4e-19:60:63/
 /HOMO SAPIENS (HUMAN).//P39192
 F-NT2RP3000031//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV./
 /2.1e-39:210:42//CAENORHABDITIS ELEGANS.//Q20296
 F-NT2RP3000046//POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//1.
 4e-25:149:44//PSEUDOMONAS PUTIDA.//P25755
 F-NT2RP3000047//NPL4 PROTEIN.//4.7e-48:275:38//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//P33755
 F-NT2RP3000050//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//3.2e
 -72:232:59//HOMO SAPIENS (HUMAN).//P51522
 F-NT2RP3000055//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.26:57:36//DROSOP
 HILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RP3000068//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC RE
 GION.//0.0014:66:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
 F-NT2RP3000072//HYPOTHETICAL 6.7 KD PROTEIN IN NOHA-CSPI INTERGENIC REGI
 ON.//0.95:49:30//ESCHERICHIA COLI.//P77695
 F-NT2RP3000080//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.1e-17:64:68//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP3000085//BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-CO
 A CARBOXYLASE (EC 6.4.1.2)) (ACC).//4.4e-43:169:51//BACILLUS SUBTILIS.//
 P49787
 F-NT2RP3000092//CELL DIVISION CONTROL PROTEIN 1.//0.00016:103:31//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST).//P40986
 F-NT2RP3000109//ACYL CARRIER PROTEIN HOMOLOG (ACP).//0.76:83:28//MYCOPLA
 SMA GENITALIUM.//P47529
 F-NT2RP3000134

F-NT2RP3000142//GAR2 PROTEIN.//0.00098:241:20//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST).//P41891

F-NT2RP3000149//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.0014:33:3.
6//PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694

F-NT2RP3000186//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.3e-15:36:83//
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3000197//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5' REGION.//0.91:21:
52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

F-NT2RP3000207//GLUCOAMYLASE S1/S2. PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-AL
PHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.026:209:27//SA
CCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-NT2RP3000220//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)
.//1.0:26:42//HOMO SAPIENS (HUMAN).//P30808

F-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-42:249:39//DRO
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP3000235//HOMEBOX PROTEIN H40 (FRAGMENT).//0.55:45:40//APIS MELLI
FERA (HONEYBEE).//P15858

F-NT2RP3000247//HYPOTHETICAL PROTEIN KIAA0218.//1.7e-82:123:69//HOMO SAP
IENS (HUMAN).//Q93075

F-NT2RP3000251//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLO
ID PROTEIN).//1.0:53:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319

F-NT2RP3000252//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROT
EIN GENE CLUSTER 5' REGION.//2.2e-06:96:32//HALOBACTERIUM CUTIRUBRUM.//P1
7103

F-NT2RP3000255//HISTONE H1.1 (FRAGMENT).//0.95:71:33//BOS TAURUS (BOVINE
) .//P02253

F-NT2RP3000267//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGI
ON (O182).//0.38:77:33//ESCHERICHIA COLI.//P09160

F-NT2RP3000299//MYOSIN IC HEAVY CHAIN.//1.2e-11:147:34//ACANTHAMOEBA CAS

TELLANII (AMOEBA).//P10569
 F-NT2RP3000312//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.64:216:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
 F-NT2RP3000320//TRANSLATION INITIATION FACTOR IF-2.//5.2e-05:184:22//AQUIFEX AEOLICUS.//067825
 F-NT2RP3000324//HYPOTHETICAL PROTEIN HI1036.//0.69:64:35//HAEMOPHILUS INFLUENZAE.//P44097
 F-NT2RP3000333//WIR1A PROTEIN.//0.35:51:41//TRITICUM AESTIVUM (WHEAT).//Q01482
 F-NT2RP3000341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.1e-30:57:80//HOMO SAPIENS (HUMAN).//P39189
 F-NT2RP3000348
 F-NT2RP3000350//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5' REGION.//0.0011:77:35//HALOBACTERIUM CUTIRUBRUM.//P17103
 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.2e-97:222:84//BOS TAURUS (BOVINE).//P08760
 F-NT2RP3000361//PRE-MRNA SPLICING FACTOR PRP6.//2.2e-08:128:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19735
 F-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1e-107:206:99//MUS MUSCULUS (MOUSE).//P35293
 F-NT2RP3000393//HOMEODOMAIN PROTEIN HOX-C4 (HOX-3E) (CP19).//0.0023:36:52//HOMO SAPIENS (HUMAN).//P09017
 F-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAD BOX PROTEIN 13).//5.5e-27:116:44//MUS MUSCULUS (MOUSE).//035286
 F-NT2RP3000403//PRE-MRNA PROCESSING PROTEIN PRP40.//0.00044:67:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33203
 F-NT2RP3000418//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//2.2e-16:228:34//MUS MUSCULUS

(MOUSE).//P11369
 F-NT2RP3000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-17:79:55//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGI
 ON.//9.8e-10:201:26//ESCHERICHIA COLI.//P37908
 F-NT2RP3000441//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.91:48:3
 5//MYCOBACTERIUM LEPRAE.//P38388
 F-NT2RP3000449//HOMEBOX PROTEIN HOX-B8 (CHOX-2.4) (FRAGMENT).//1.0:42:3
 3//GALLUS GALLUS (CHICKEN).//P23681
 F-NT2RP3000451
 F-NT2RP3000456//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00018:178:36//
 RATTUS NORVEGICUS (RAT).//P02454
 F-NT2RP3000484//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR)
 (GIF).//0.098:40:27//BOS TAURUS (BOVINE).//P37359
 F-NT2RP3000487//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00037:16
 :81//VOLVOX CARTERI.//P21997
 F-NT2RP3000512
 F-NT2RP3000526//HYPOTHETICAL NIN REGION PROTEIN ORF56.//0.51:37:43//BACT
 ERIOPHAGE LAMBDA.//P03769
 F-NT2RP3000527//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.0e
 -16:234:30//HOMO SAPIENS (HUMAN).//P51522
 F-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//3.4e-15:
 192:30//HOMO SAPIENS (HUMAN).//P15151
 F-NT2RP3000542//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGME
 NT).//0.60:51:39//ASTERINA PECTINIFERA (STARFISH).//P11958
 F-NT2RP3000561//HYPOTHETICAL ATP-BINDING PROTEIN MJ0423.//0.79:53:32//ME
 THANOCOCCUS JANNASCHII.//Q57866
 F-NT2RP3000562//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)
 .//0.99:26:34//DROSOPHILA MAURITIANA (FRUIT FLY), AND DROSOPHILA SIMULAN

S (FRUIT FLY).//018666

F-NT2RP3000578//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.5e-26:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P3875

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F-NT2RP3000582

F-NT2RP3000584//METALLOTHIONEIN-II (MT-II).//0.28:27:29//MUS MUSCULUS (MOUSE).//P02798

F-NT2RP3000590//UVS-2 PROTEIN.//4.8e-10:113:33//NEUROSPORA CRASSA.//P33288

F-NT2RP3000592//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00087:178:31//HOMO SAPIENS (HUMAN).//000268

F-NT2RP3000596//YEMANUCLEIN-ALPHA.//1.8e-05:98:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25992

F-NT2RP3000599//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00095:90:37//HOMO SAPIENS (HUMAN).//Q15428

F-NT2RP3000603//5E5 ANTIGEN.//1.0e-09:181:34//RATTUS NORVEGICUS (RAT).//Q63003

F-NT2RP3000605//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1).//0.00098:76:34//HOMO SAPIENS (HUMAN).//P36956

F-NT2RP3000622//HYPOTHETICAL PROTEIN MG096 HOMOLOG 5 (P02_ORF427).//0.15:52:36//MYCOPLASMA PNEUMONIAE.//P75277

F-NT2RP3000624//HYPOTHETICAL PROTEIN KIAA0256.//5.4e-16:222:31//HOMO SAPIENS (HUMAN).//Q93073

F-NT2RP3000628

F-NT2RP3000632//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//2.0e-16:52:63//MUS MUSCULUS (MOUSE).//Q61967

F-NT2RP3000644//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.7e-40:102:79

//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP3000661//HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II.
 //6.0e-08:83:36//CAENORHABDITIS ELEGANS.//Q09441
 F-NT2RP3000665//HOMEODOMAIN PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY SP
 ECIFIC HOMEODOMAIN FACTOR).//0.13:48:35//HOMO SAPIENS (HUMAN).//075360
 F-NT2RP3000685//HYPOTHETICAL 33.5 KD PROTEIN IN CAT1 5' REGION (ORFY).//0
 .26:202:23//CLOSTRIDIUM KLUYVERI.//P38943
 F-NT2RP3000690//INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PH
 OSPO- HYDROLASE) (PPASE).//0.99:131:26//SACCHAROMYCES CEREVISIAE (BAKER
 'S YEAST).//P00817
 F-NT2RP3000736//HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC RE
 GION.//3.5e-27:211:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40516
 F-NT2RP3000739//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//
 6.0e-23:114:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149
 F-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS
 E DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III
).//6.7e-12:85:36//RATTUS NORVEGICUS (RAT).//P10688
 F-NT2RP3000753//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTE
 IN B) (S-LAYER PROTEIN 1).//0.00011:208:28//CLOSTRIDIUM THERMOCELLUM.//Q
 06852
 F-NT2RP3000759//ADP-RIBOSYLATION FACTOR 6.//8.1e-28:141:38//GALLUS GALLU
 S (CHICKEN).//P26990
 F-NT2RP3000815//CYTOCHROME C-551 (C551) (CYTOCHROME C8).//0.24:45:37//PS
 EUDOMONAS DENITRIFICANS.//P00103
 F-NT2RP3000825//ALPHA-LACTALBUMIN (LACTOSE SYNTHASE B PROTEIN (EC 2.4.1.
 22)).//0.82:51:39//MACROPUS RUFOGRISEUS (RED-NECKED WALLABY).//P07458
 F-NT2RP3000826//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.025:79:37//B
 OS TAURUS (BOVINE).//P25508
 F-NT2RP3000836//HYPOTHETICAL PROTEIN IN KSGA 3' REGION (ORF L5) (FRAGMENT

).//0.85:36:47//MYCOPLASMA CAPRICOLUM.//P43040
 F-NT2RP3000841//UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (E
 C 2.4.1.17) (UDPGT) (UGT1*7) (UGT1-07) (UGT1.7) (UGT1A7) (UGTP4) (FRAGME
 NT).//1.0:70:34//MUS MUSCULUS (MOUSE).//Q62452
 F-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-
).//5.2e-72:247:61//HOMO SAPIENS (HUMAN).//P27448
 F-NT2RP3000847//HYPOTHETICAL PROTEIN KIAA0161.//0.037:55:30//HOMO SAPIEN
 S (HUMAN).//P50876
 F-NT2RP3000850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-31:90:75/
 /HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP3000852//HYDROPHOBIC SEED PROTEIN (HPS).//0.33:23:69//GLYCINE MAX
 (SOYBEAN).//P24337
 F-NT2RP3000859//IMMEDIATE-EARLY PROTEIN.//3.6e-07:189:25//HERPESVIRUS SA
 IMIRI (STRAIN 11).//Q01042
 F-NT2RP3000865
 F-NT2RP3000868//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT).//
 1.4e-09:232:28//GALLUS GALLUS (CHICKEN).//P29616
 F-NT2RP3000869//CUTICLE COLLAGEN 2.//4.5e-08:58:46//CAENORHABDITIS ELEGA
 NS.//P17656
 F-NT2RP3000875//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2).
 //0.90:62:37//MUS MUSCULUS (MOUSE).//P43241
 F-NT2RP3000901//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.99:124:33//BOS
 TAURUS (BOVINE).//P02453
 F-NT2RP3000904
 F-NT2RP3000917//DHP1 PROTEIN.//6.5e-60:229:55//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST).//P40848
 F-NT2RP3000919//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//
 2.4e-19:159:34//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//3.7e-48:73:98//HOMO SAPIENS

(HUMAN), AND RATTUS NORVEGICUS (RAT).//P39027
 F-NT2RP3000980//COPA/INCA PROTEIN (REPA3 PROTEIN).//0.24:19:47//ESCHERIC
 HIA COLI.//P13946
 F-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//1.4e-10:78:48//DROSOPH
 ILA MELANOGASTER (FRUIT FLY).//P25159
 F-NT2RP3001004//HYPOTHETICAL 7.6 KD PROTEIN B0563.8 IN CHROMOSOME X.//0.
 70:50:32//CAENORHABDITIS ELEGANS.//Q11084
 F-NT2RP3001007
 F-NT2RP3001055//N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLO
 G.//1.3e-05:138:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P36416
 F-NT2RP3001057//ZINC FINGER PROTEIN 45 (BRC1744).//4.0e-28:141:51//HOMO
 SAPIENS (HUMAN).//Q02386
 F-NT2RP3001081//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III.
 //3.8e-08:144:29//CAENORHABDITIS ELEGANS.//P34568
 F-NT2RP3001084//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//3.4e-0
 6:217:32//NEPHILA CLAVIPES (ORB SPIDER).//P46804
 F-NT2RP3001096//SYNAPTONEMAL COMPLEX PROTEIN SC65.//1.1e-30:244:33//RATT
 US NORVEGICUS (RAT).//Q64375
 F-NT2RP3001107//ARYLSULFATASE F (EC 3.1.6.-) (ASF) (FRAGMENT).//0.041:47
 :44//HOMO SAPIENS (HUMAN).//P54793
 F-NT2RP3001109
 F-NT2RP3001111//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.17:28:39//DROSOP
 HILA MELANOGASTER (FRUIT FLY).//Q01644
 F-NT2RP3001113//INVOLUCRIN.//0.00036:192:23//MUS MUSCULUS (MOUSE).//P489
 97
 F-NT2RP3001115
 F-NT2RP3001116//AMINOPEPTIDASE G (EC 3.4.11.-) (FRAGMENT).//0.99:29:51//
 STREPTOMYCES LIVIDANS.//Q54340
 F-NT2RP3001119//COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT).//0.0015:73:39//BO

S TAURUS (BOVINE).//Q29442
 F-NT2RP3001120//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.3e-57:229:52//
 HOMO SAPIENS (HUMAN).//P16415
 F-NT2RP3001126//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC RE
 GION.//2.8e-07:83:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888
 F-NT2RP3001133//CALCIUM BINDING PROTEIN.//2.0e-08:171:32//DICTYOSTELIUM
 DISCOIDEUM (SLIME MOLD).//P35085
 F-NT2RP3001140//F-SPONDIN PRECURSOR.//2.0e-147:244:97//RATTUS NORVEGICUS
 (RAT).//P35446
 F-NT2RP3001147//TROPOMYOSIN 2 (TMII).//0.11:159:23//SCHISTOSOMA MANSONI
 (BLOOD FLUKE).//P42638
 F-NT2RP3001150//OCTAPEPTIDE-REPEAT PROTEIN T2.//6.2e-09:163:25//MUS MUSC
 ULUS (MOUSE).//Q06666
 F-NT2RP3001155//DNA POLYMERASE ALPHA-BINDING PROTEIN (POB1/CTF4 PROTEIN)
 (CHROMOSOME REPLICATION PROTEIN CHL15).//4.1e-05:244:23//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//Q01454
 F-NT2RP3001176//LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIA
 LOPHORIN) (CD43) (LY 48) (B CELL DIFFERENTIATION ANTIGEN LP-3).//0.21:13
 6:26//MUS MUSCULUS (MOUSE).//P15702
 F-NT2RP3001214//SAP1 PROTEIN.//0.058:133:30//SACCHAROMYCES CEREVISIAE (B
 AKER'S YEAST).//P39955
 F-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//2.1
 e-08:137:33//HOMO SAPIENS (HUMAN).//P35663
 F-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.
 11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//4.2e-05:131:26//PSEUDOMONAS SP
 . (STRAIN AK-1).//P80193
 F-NT2RP3001232//HYPOTHETICAL PROTEIN PRECURSOR IN CS5 3' REGION (FRAGMENT
).//0.75:57:31//ESCHERICHIA COLI.//P33792
 F-NT2RP3001236//TRANSFORMING PROTEIN MAF.//0.017:136:30//AVIAN MUSCULOAP

ONEUROTIC FIBROSARCOMA VIRUS AS42.//P23091
 F-NT2RP3001239//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 (FRAGMENT).//4.
 2e-55:221:49//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14400
 F-NT2RP3001245
 F-NT2RP3001253//TROPOMYOSIN 2, MUSCLE THORACIC ISOFORM (TROPOMYOSIN 1)./
 /0.0042:142:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//P09491
 F-NT2RP3001260//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0011:89:43//HOM
 O SAPIENS (HUMAN).//P53420
 F-NT2RP3001268//ZINC FINGER PROTEIN 45 (BRC1744).//9.0e-29:194:44//HOMO
 SAPIENS (HUMAN).//Q02386
 F-NT2RP3001272//HYPOTHETICAL 75.2 KD PROTEIN C13F4.08C IN CHROMOSOME 1./
 /8.2e-17:183:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10199
 F-NT2RP3001274//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP
 5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.7e-09:78:39//MUS MUSCULU
 S (MOUSE).//Q60676
 F-NT2RP3001281//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.7e-08:38:71//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP3001297//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//2.2e-57:159:70/
 /HOMO SAPIENS (HUMAN).//Q92556
 F-NT2RP3001307//SPERM PROTAMINE P1.//0.21:46:39//ORNITHORHYNCHUS ANATINU
 S (DUCKBILL PLATYPUS).//P35307
 F-NT2RP3001318
 F-NT2RP3001325//ENHANCER OF RUDIMENTARY HOMOLOG.//1.0:73:24//BRACHYDANIO
 RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q98874
 F-NT2RP3001338//ZINC FINGER PROTEIN 29 (ZINC FINGER PROTEIN KOX26) (FRAG
 MENT).//0.0021:56:35//HOMO SAPIENS (HUMAN).//P17037
 F-NT2RP3001339//CITRON PROTEIN.//3.6e-06:90:33//MUS MUSCULUS (MOUSE).//P
 49025
 F-NT2RP3001340//HYPOTHETICAL PROTEIN UL61.//7.2e-11:202:34//HUMAN CYTOME

GALOVIRUS (STRAIN AD169).//P16818

F-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//7.7e-16:129:33//HOMO SAPIENS (HUMAN).//P53007

F-NT2RP3001356//RAS-RELATED PROTEIN RABA (FRAGMENT).//0.00041:66:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141

F-NT2RP3001374

F-NT2RP3001383//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.5e-06:190:32//HOMO SAPIENS (HUMAN).//P23246

F-NT2RP3001384//CHORION PROTEIN S15.//0.00079:94:37//DROSOPHILA VIRILIS (FRUIT FLY).//P13424

F-NT2RP3001392//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//1.0:22:45//CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV).//P31834

F-NT2RP3001396//HYPOTHETICAL 8.1 KD PROTEIN (ORF4).//1.0:37:32//STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMYEA).//Q00848

F-NT2RP3001398//KRUEPPEL-RELATED ZINC FINGER PROTEIN 2 (HKR2 PROTEIN) (FRAGMENT).//1.9e-08:45:37//HOMO SAPIENS (HUMAN).//P10073

F-NT2RP3001399//SSU72 PROTEIN.//7.3e-18:84:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53538

F-NT2RP3001407//SCY1 PROTEIN.//1.5e-08:143:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009

F-NT2RP3001420//HYPOTHETICAL 7.9 KD PROTEIN.//0.25:41:26//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20542

F-NT2RP3001426//DNAJ PROTEIN.//7.5e-15:78:43//HAEMOPHILUS INFLUENZAE.//P43735

F-NT2RP3001427//WERNER SYNDROME HELICASE.//3.6e-13:159:33//HOMO SAPIENS (HUMAN).//Q14191

F-NT2RP3001428//NUCLEOPROTEIN TPR.//1.8e-53:117:99//HOMO SAPIENS (HUMAN).//P12270

F-NT2RP3001432//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:52:21//TARSUS SYRICHIA (TARSIER).//Q36151

F-NT2RP3001447//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION (ORF1).//0.96:45:35//ESCHERICHIA COLI.//P14505

F-NT2RP3001449//HOMEODOMAIN PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.0043:53:43//GALLUS GALLUS (CHICKEN).//P19601

F-NT2RP3001453//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.0048:65:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3001457//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28.//0.55:121:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02767

F-NT2RP3001459//MYOSIN IC HEAVY CHAIN.//0.10:126:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//3.0e-14:87:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11632

F-NT2RP3001490//METALLOTHIONEIN-LIKE PROTEIN LSC54.//1.0:39:35//BRASSICA NAPUS (RAPE).//P43402

F-NT2RP3001495//UBIQUITIN--PROTEIN LIGASE RSP5 (EC 6.3.2.-).//3.3e-14:148:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39940

F-NT2RP3001497//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.13:44:38//BOS TAURUS (BOVINE).//P25508

F-NT2RP3001527//SPERM PROTAMINE P1.//0.35:29:37//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305

F-NT2RP3001529//HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA IN TERGENIC REGION.//3.3e-21:125:37//ESCHERICHIA COLI.//P42641

F-NT2RP3001538//HNF3/FH TRANSCRIPTION FACTOR GENESIS (WINGED HELIX PROTEIN CWH-3).//0.13:53:39//GALLUS GALLUS (CHICKEN).//P79772

F-NT2RP3001554//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//2.3e-48:137:52//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401

F-NT2RP3001580//GERM CELL-LESS PROTEIN.//8.2e-18:100:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820

F-NT2RP3001587//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//2.0e-47:188:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488

F-NT2RP3001589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.4e-41:87:80//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP3001607//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:49:32//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362

F-NT2RP3001608//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0013:177:25//ZEA MAYS (MAIZE).//P14918

F-NT2RP3001621//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.84:29:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RP3001629//RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (FRAGMENTS).//0.91:57:24//CAVIA PORCELLUS (GUINEA PIG).//P80236

F-NT2RP3001634//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.9e-11:73:54//HOMO SAPIENS (HUMAN).//P39189

F-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//1.1e-12:117:29//HOMO SAPIENS (HUMAN).//Q92609

F-NT2RP3001646//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0092:69:34//ORGANIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341

F-NT2RP3001671//RING CANAL PROTEIN (KELCH PROTEIN).//0.0042:55:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP3001672

F-NT2RP3001676//GTP-BINDING PROTEIN LEPA (FRAGMENT).//1.2e-15:56:62//PSEUDOMONAS FLUORESCENS.//P26843

F-NT2RP3001678//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.054:187:31//NEPHILA CLAVIPES (ORB SPIDER).//P46804

F-NT2RP3001679//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III./

/1.5e-07:63:44//CAENORHABDITIS ELEGANS.//P34679
 F-NT2RP3001688//GLUCOAMYLASE S1 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) (GAI).//1.0:83:28//SACCHAROMYCES DIASTATICUS (YEAST).//P04065
 F-NT2RP3001690//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//0.021:247:24//HOMO SAPIENS (HUMAN).//P12883
 F-NT2RP3001698
 F-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//7.7e-12:73:43//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54356
 F-NT2RP3001712//CEC-1 PROTEIN.//1.9e-07:121:29//CAENORHABDITIS ELEGANS.//P34618
 F-NT2RP3001716//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.89:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
 F-NT2RP3001724//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//7.5e-41:164:48//HOMO SAPIENS (HUMAN).//O14646
 F-NT2RP3001727//HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III.//1.5e-51:240:41//CAENORHABDITIS ELEGANS.//P34669
 F-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//2.4e-122:267:86//HOMO SAPIENS (HUMAN).//Q14141
 F-NT2RP3001739//INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER).//0.99:63:34//RATTUS NORVEGICUS (RAT).//P70545
 F-NT2RP3001752//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.0e-21:60:85//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP3001753//HYPOTHETICAL PROTEIN KIAA0127.//7.9e-12:83:44//HOMO SAPIENS (HUMAN).//Q14140
 F-NT2RP3001764//DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE PYST1).//7.7e-25:146:36//HOMO SAPIENS (HUMAN).//Q16828
 F-NT2RP3001777//SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG (EC 2.7.1.

-).//0.0096:204:25//CANDIDA ALBICANS (YEAST).//Q92212
 F-NT2RP3001782//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.91:34:44/
 /PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694
 F-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.
 8e-33:159:53//HOMO SAPIENS (HUMAN).//P52272
 F-NT2RP3001799//LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (E
 HS-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN).//0.14:46:28//ECTOT
 HIORHODOSPIRA HALOCHLORIS.//P80103
 F-NT2RP3001819//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00030:77:36//
 HOMO SAPIENS (HUMAN).//P08123
 F-NT2RP3001844//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (
 FRAGMENT).//0.99:43:34//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466
 F-NT2RP3001854//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEI
 N).//9.3e-10:213:24//STREPTOCOCCUS PYOGENES.//P30141
 F-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//2.6e
 -61:220:60//HOMO SAPIENS (HUMAN).//P55347
 F-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.0e-13:21
 3:24//PODOSPORA ANSERINA.//Q00808
 F-NT2RP3001896//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.
 074:124:34//HOMO SAPIENS (HUMAN).//Q15428
 F-NT2RP3001898//REGULATORY PROTEIN E2.//0.36:131:29//CANINE ORAL PAPILLO
 MAVIRUS (COPV).//Q89420
 F-NT2RP3001915//CHITIN BIOSYNTHESIS PROTEIN CHS5 (CAL3 PROTEIN).//0.0021
 :237:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12114
 F-NT2RP3001926//HYPOTHETICAL 14.0 KD PROTEIN IN RPL15B-GCR3 INTERGENIC R
 EGION.//1.0:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03880
 F-NT2RP3001929//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-14:35:60/
 /HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP3001931//HYPOTHETICAL 59.3 KD PROTEIN IN TAP42-ARP9 INTERGENIC RE

GION.//0.86:162:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05040
 F-NT2RP3001938//GLYCOPROTEIN GP50.//0.0036:54:40//PSEUDORABIES VIRUS (ST
 RAIN RICE) (PRV).//P07645
 F-NT2RP3001943//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//
 1.0:113:27//ESCHERICHIA COLI.//P23839
 F-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.
 //4.1e-56:208:47//CAENORHABDITIS ELEGANS.//Q09251
 F-NT2RP3001969//PUFF II/9-2 PROTEIN PRECURSOR.//0.0078:149:26//SCIARA CO
 PROPHILA (FUNGUS GNAT).//P22312
 F-NT2RP3001989//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//1.0:41:31
 //MUS MUSCULUS (MOUSE).//P02319
 F-NT2RP3002002//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.2e-44:69:79/
 /HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP3002004//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2).//0.000
 24:45:40//MUS MUSCULUS (MOUSE).//Q61345
 F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEU
 RONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACEL
 LULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C).//0.21:115:28//HOMO SAPI
 ENS (HUMAN).//P24821
 F-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./
 /1.7e-25:139:48//CAENORHABDITIS ELEGANS.//Q09232
 F-NT2RP3002033//ACTIVATOR OF APOPTOSIS HARAKIRI (NEURONAL DEATH PROTEIN
 DP5).//0.14:65:41//HOMO SAPIENS (HUMAN).//O00198
 F-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALP
 HA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADA
 PTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//8.1e-108:192:98//MUS MUSCULUS (M
 OUSE).//P17427
 F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.04
 6:176:31//STREPTOMYCES FRADIAE.//P20186

F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//1.4e-07:245:
25//RATTUS NORVEGICUS (RAT).//P41777

F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN.//1.0:12:66//SIMIAN VIRUS 5 (S
TRAIN W3) (SV5).//P07577

F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR I(A)3).//1.
0:49:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P01094

F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP).//0.99:38:31//HAEMOPHILUS INF
LUENZAE.//P43709

F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//
5.8e-35:253:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429

F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC RE
GION.//6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN.//0.68:34:47//THERMOPROTEUS
TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302

F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F6.10 IN CHROMOSOME III
.//7.9e-19:179:34//CAENORHABDITIS ELEGANS.//Q21986

F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-17:37:75//
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3002146//CUTICLE COLLAGEN 40.//0.00034:90:37//CAENORHABDITIS ELEG
ANS.//P34804

F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//
0.011:166:28//HOMO SAPIENS (HUMAN).//P10163

F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING
PROTEIN GST1-HS).//4.8e-11:60:53//HOMO SAPIENS (HUMAN).//P15170

F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA
FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.028:191:29//HOMO SAPIENS
(HUMAN).//000268

F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//2.3e-131:223:9
1//MUS MUSCULUS (MOUSE).//Q02614

F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP).//1.0:65:33//LACTOBACILLU
S CASEI.//P55153

F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.4e-26:114:62
//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.25:31:38//DROSOP
HILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.069:16:
62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT).//P04102

F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MICROFIB
RIL PROTEIN) (AMF).//0.0079:187:24//GALLUS GALLUS (CHICKEN).//P55080

F-NT2RP3002255//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.6e-10:168:34//M
US MUSCULUS (MOUSE).//P05143

F-NT2RP3002273//SCD6 PROTEIN.//1.5e-11:160:33//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P45978

F-NT2RP3002276//PROBABLE E4 PROTEIN.//0.91:54:29//HUMAN PAPILLOMAVIRUS T
YPE 16.//P06922

F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C4D7.04C IN CHROMOSOME I.//
1.7e-42:191:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014171

F-NT2RP3002304

F-NT2RP3002330//NNP-1 PROTEIN.//0.52:140:18//MUS MUSCULUS (MOUSE).//P561
83

F-NT2RP3002343//5E5 ANTIGEN.//0.0056:189:30//RATTUS NORVEGICUS (RAT).//Q
63003

F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (E
C 1.5.1.15) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) MITOC
HONDRIAL PRECURSOR.//1.0e-66:196:68//HOMO SAPIENS (HUMAN).//P13995

F-NT2RP3002352//PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN 1
02) (NEUROENDOCRINE-DLG) (NE-DLG).//0.79:173:27//HOMO SAPIENS (HUMAN).//
Q92796

F-NT2RP3002377//PUTATIVE HELICASE YGR271W.//1.0e-56:216:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53327

F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6.//1.4e-19:136:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53091

F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.74:107:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204

F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT).//5.6e-06:57:42//AGROBACTERIUM TUMEFACIENS.//P50018

F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B10.04 IN CHROMOSOME I.//0.00032:52:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10438

F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FRE2-JEN1 INTERGENIC REGION.//9.4e-42:209:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36007

F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GPM1-MCR1 INTERGENIC REGION.//7.7e-32:162:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36059

F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C.//2.1e-45:241:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09805

F-NT2RP3002545

F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//2.8e-41:161:52//CAENORHABDITIS ELEGANS.//Q10010

F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180.//0.56:130:24//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-NT2RP3002587

F-NT2RP3002590

F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (THIOREDOXIN-RELATED GLYCOPROTEIN 1).//0.00091:111:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17967

F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3' REGION.//1.0:65:40//STREPTOMYCES CACA01.//P33654

F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093.//2.4e-17:101:44//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P50027

F-NT2RP3002631//METALLOTHIONEIN-IB (MT-1B).//0.092:36:33//HOMO SAPIENS (HUMAN).//P07438

F-NT2RP3002650//DUALIN.//3.0e-21:184:37//GALLUS GALLUS (CHICKEN).//Q90830

F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00016:223:33//HOMO SAPIENS (HUMAN).//P08123

F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A.//0.16:72:31//CAENORHABDITIS ELEGANS.//P37165

F-NT2RP3002663//OXYSTEROL-BINDING PROTEIN.//5.4e-23:168:41//HOMO SAPIENS (HUMAN).//P22059

F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION.//6.0e-38:203:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53893

F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.25:63:31//ARTEMIA SALINA (BRINE SHRIMP).//P19049

F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LEF3-IAP2 INTERGENIC REGION.//0.029:60:36//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (AC MNPV).//P41469

F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF1B.//5.3e-61:130:88//MUS MUSCULUS (MOUSE).//Q60575

F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//7.4e-05:109:33//MUS MUSCULUS (MOUSE).//P15265

F-NT2RP3002713//PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN 10).//0.77:70:32//HOMO SAPIENS (HUMAN).//Q13206

F-NT2RP3002763//HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I.//6.7e-11:66:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14056

F-NT2RP3002770//COLLAGEN ALPHA 1(IX) CHAIN (FRAGMENT).//0.33:87:34//MUS

MUSCULUS (MOUSE).//Q05722
 F-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//9.7e-36:
 187:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371
 F-NT2RP3002799//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-08:41:73//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP3002810//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.0034:35:65//
 HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (C
 ENP-B).//3.2e-17:148:37//MUS MUSCULUS (MOUSE).//P27790
 F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REG
 ION.//1.7e-05:95:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951
 F-NT2RP3002869//TRYPSIN INHIBITOR II (BDTI-II).//0.97:23:39//BRYONIA DIO
 ICA (RED BRYONY).//P11968
 F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).//0:
 00017:140:31//RATTUS NORVEGICUS (RAT).//P04474
 F-NT2RP3002877//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.5e-06:55:60/
 /HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BINDING PROTEIN) (BBP)./
 /4.6e-08:129:38//HOMO SAPIENS (HUMAN).//Q13625
 F-NT2RP3002911//HYPOTHETICAL PROTEIN C18.//0.99:26:50//SWINEPOX VIRUS (S
 TRAIN KASZA) (SPV).//P32217
 F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-23:113:47//DRO
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN
).//0.55:116:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450
 F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BLTR-SPOIIC INTERGENIC
 REGION.//0.87:67:37//BACILLUS SUBTILIS.//P54445
 F-NT2RP3002969//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-C
 HAIN ACYL-COA SYNTHETASE 4) (LACS 4).//6.7e-56:189:59//HOMO SAPIENS (HUM

AN).//060488

F-NT2RP3002972//HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.0028:147:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48566

F-NT2RP3002978//PROBABLE E5 PROTEIN.//0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553

F-NT2RP3002985//METALLOTHIONEIN (MT).//0.0031:49:42//PLEURONECTES PLATES SA (PLAICE).//P07216

F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).//1.0:111:29//MUS MUSCULUS (MOUSE).//Q01705

F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//0.96:112:25//CAENORHABDITIS ELEGANS.//P41879

F-NT2RP3003032

F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR.//9.7e-27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10254

F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.7e-25:167:34//HOMO SAPIENS (HUMAN).//P16157

F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SERRS) (FRAGMENT).//0.074:82:39//SULFOLOBUS SOLFATARICUS.//033780

F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0085:128:30//HOMO SAPIENS (HUMAN).//P50552

F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT).//0.028:165:31//VULPES VULPES (RED FOX).//P53353

F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TETA(C)).//1.0e-14:243:25//ESCHERICHIA COLI.//P02981

F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40.//7.4e-05:143:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65).//0.024:61:42//GALLUS GALLUS (CHICKEN).//P46936

F-NT2RP3003138//KINESIN-LIKE PROTEIN KIF4.//1.1e-118:151:93//MUS MUSCULU
S (MOUSE).//P33174

F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1.//1.0:70:30//SCHIZ
OSACCHAROMYCES POMBE (FISSION YEAST).//Q92337

F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (HMFG)
(BREAST EPITHELIAL ANTIGEN BA46) (MFGM).//2.0e-12:121:37//HOMO SAPIENS (
HUMAN).//Q08431

F-NT2RP3003150

F-NT2RP3003157//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.0e
-79:260:54//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP3003185//TROPOMYOSIN.//0.077:122:27//SCHIZOSACCHAROMYCES POMBE (F
ISSION YEAST).//Q02088

F-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.2e-91:239:65//HOMO SAPIENS (
HUMAN).//P52742

F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REG
ION.//1.3e-07:117:34//BACILLUS SUBTILIS.//P42966

F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//
9.9e-23:132:39//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-NT2RP3003204//RAS-LIKE PROTEIN RASB.//0.92:103:27//DICTYOSTELIUM DISCO
IDEUM (SLIME MOLD).//P32252

F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENI
C REGION.//0.23:106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P3819
0

F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40.//0.019:171:23//SACCHAROMYCES C
EREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP3003230//CORONIN-LIKE PROTEIN P57.//8.3e-74:183:73//BOS TAURUS (B
OVINE).//Q92176

F-NT2RP3003242//STANNIOCALCIN PRECURSOR.//1.4e-21:127:37//HOMO SAPIENS (
HUMAN).//P52823

F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//3.1e-51:198:52//MUS MUSCULUS (MOUSE).//P15533

F-NT2RP3003264//E6 PROTEIN.//1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48.//Q80920

F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//8.6e-07:80:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344

F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDNM).//8.0e-108:226:88//MUS MUSCULUS (MOUSE).//P39054

F-NT2RP3003290//BIOH PROTEIN.//0.0055:107:30//ESCHERICHIA COLI.//P13001

F-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.2.1.-).//1.3e-69:200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//064948

F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.4e-69:102:66//HOMO SAPIENS (HUMAN).//P08547

F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.18:225:26//ACANTHA MOEBA CASTELLANII (AMOEBA).//P05659

F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P EPTIDE P-D] (FRAGMENT).//0.0014:142:33//HOMO SAPIENS (HUMAN).//P10162

F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052).//8.8e-18:94:43//MUS MUSCULUS (MOUSE).//Q62191

F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-20:123:44//HOMO SAPIENS (HUMAN).//Q14681

F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC REGION.//1.0:28:42//ESCHERICHIA COLI.//P75991

F-NT2RP3003346//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//6.9e-26:74:78//HOMO SAPIENS (HUMAN).//P39191

F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D7.2 IN CHROMOSOME III.//3.7e-10:118:33//CAENORHABDITIS ELEGANS.//P30641

F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6.//1.5e-05:102:37//CAENORHABDITIS ELEGANS.//P34391

F-NT2RP3003384

F-NT2RP3003385//SKD3 PROTEIN.//5.1e-83:210:69//MUS MUSCULUS (MOUSE).//Q6
0649

F-NT2RP3003403

F-NT2RP3003409//SOX-22 PROTEIN.//0.042:173:28//HOMO SAPIENS (HUMAN).//O1
5370

F-NT2RP3003411//PROBABLE E3 PROTEIN.//0.17:91:31//BOVINE PAPILLOMAVIRUS
TYPE 2.//P11300

F-NT2RP3003427//HOLOTRICIN 3 PRECURSOR.//0.012:36:41//HOLOTRICHIA DIOMPH
ALIA.//Q25055

F-NT2RP3003433

F-NT2RP3003464//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC R
EGION.//0.0042:110:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RP3003490

F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT S
HOCK 10 KD PROTEIN).//0.99:49:34//LEPTOSPIRA INTERROGANS.//P35472

F-NT2RP3003500//SCY1 PROTEIN.//6.8e-14:192:26//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P53009

F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.0026:175:30//HO
MO SAPIENS (HUMAN).//P29400

F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.19:21:47//BOS TAURU
S (BOVINE).//P20072

F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC RE
GION.//7.3e-27:159:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40529

F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//1.0:99:30//TUR
NIP YELLOW MOSAIC VIRUS.//P10358

F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6.//0.33:128:32//CAENORH
ABDITIS ELEGANS.//P34391

F-NT2RP3003576//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//7.1e-28:58:77/

/HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10.//5.4e-54:114:94//CANIS FAMILIARIS (DOG).//P24409
 F-NT2RP3003621//COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).//2.0e-15:89:40//HOMO SAPIENS (HUMAN).//P00748
 F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.99:22:50//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
 F-NT2RP3003656//HOMEODOMAIN PROTEIN OTX3 (ZOTX3).//0.30:111:25//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q90267
 F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.1e-20:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755
 F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C).//0.34:52:34//PENAEUS VANNAMEI (PENAEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81060
 F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//8.7e-15:146:42//HOMO SAPIENS (HUMAN).//P14209
 F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION.//4.3e-25:159:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601
 F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.067:63:31//GALLUS GALLUS (CHICKEN).//P02314
 F-NT2RP3003701//F-SPONDIN PRECURSOR.//1.8e-13:193:27//RATTUS NORVEGICUS (RAT).//P35446
 F-NT2RP3003716//SLIT PROTEIN PRECURSOR.//1.3e-12:150:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
 F-NT2RP3003726//INSERTION ELEMENT IS136 HYPOTHETICAL 16.9 KD PROTEIN.//0.47:109:28//AGROBACTERIUM TUMEFACIENS.//P05680
 F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIXX 3' REGION (ORF1).//0.57:34:38//AZORHIZOBIUM CAULINODANS.//P26486

F-NT2RP3003795//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-10:40:90/
/HOMO SAPIENS (HUMAN).//P39195

F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PRECURSOR.//0.75:60:36//SC
HIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//P78744

F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112
) (P60-SRC).//4.2e-51:72:95//GALLUS GALLUS (CHICKEN).//P00523

F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DBP7-GCN3 INTERGENIC REG
ION.//0.00069:160:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36121

F-NT2RP3003809//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.028:135:35//
GALLUS GALLUS (CHICKEN).//P12105

F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT).//0.0026:90:33//HORDEUM VU
LGARE (BARLEY).//P06472

F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//5.6e-20:1
74:31//BOS TAURUS (BOVINE).//P02720

F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHAT
E-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//0.0017:111:38//CANIS FA
MILIARIS (DOG).//P30803

F-NT2RP3003831//ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G).//1.1e-3
7:187:42//MUS MUSCULUS (MOUSE).//008600

F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INTE-PIN INTERGENIC REGIO
N.//1.0:38:39//ESCHERICHIA COLI.//P75979

F-NT2RP3003842

F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPOR
TER RDGB).//0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P43125

F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.83:51:37//DROSOP
HILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2.//0.0017:151:27//SACCHARO
MYCES CEREVISIAE (BAKER'S YEAST).//P17065

F-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (

EC 2.4.1.-) (DUGT).//3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT FLY).
 //Q09332
 F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDIN
 G PROTEIN (VAP-33).//5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA
 HARE).//Q16943
 F-NT2RP3003932
 F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.96:46:32//THERMO
 TOGA MARITIMA.//P35874
 F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67).//0.
 0011:170:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P27476
 F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSR
 NA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//3.6e-21:134:45//RATTUS
 NORVEGICUS (RAT).//P51400
 F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGI
 ON.//0.00021:64:40//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (A
 CMNPV).//P41479
 F-NT2RP3004041//SPERM PROTAMINE P1.//0.0028:43:46//ORNITHORHYNCHUS ANATI
 NUS (DUCKBILL PLATYPUS).//P35307
 F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD CO
 LLAGENASE).//0.0079:194:24//CLOSTRIDIUM PERFRINGENS.//P43153
 F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.4e-11:51:72//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP3004078//DNA BINDING PROTEIN RFX2.//2.7e-114:243:87//MUS MUSCULUS
 (MOUSE).//P48379
 F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RHSE-NARV INTERGENIC REG
 ION (ORFB).//8.0e-13:111:41//ESCHERICHIA COLI.//P37757
 F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:72:65//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-10:51:72/

/HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP3004125//ZINC FINGER PROTEIN 75.//1.1e-28:118:47//HOMO SAPIENS (HUMAN).//P51815
 F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN.//0.012:45:33//AEROMONAS SOBRIA.//P09165
 F-NT2RP3004148//METALLOTHIONEIN-I (MT-1).//0.055:18:50//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786
 F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG.//1.7e-82:178:89//RATTUS NORVEGICUS (RAT).//Q63619
 F-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.7e-11:215:24//PODOSPORA ANSERINA.//Q00808
 F-NT2RP3004206//CROOKED NECK PROTEIN.//3.8e-101:241:73//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886
 F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR.//0.13:130:33//CAENORHABDITIS ELEGANS.//P20630
 F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//6.5e-16:207:29//HOMO SAPIENS (HUMAN).//Q13107
 F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT.//1.0:69:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35179
 F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.//1.1e-64:191:63//CAENORHABDITIS ELEGANS.//P34657
 F-NT2RP3004246//RING3 PROTEIN (KIAA9001).//0.060:101:28//HOMO SAPIENS (HUMAN).//P25440
 F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//1.1e-07:184:35//BOS TAURUS (BOVINE).//P02453
 F-NT2RP3004258//SUPPRESSOR PROTEIN SRP40.//4.9e-08:98:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.6e-63:210:61//HOMO SAPIENS (HUMAN).//P25685

F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G4.1 IN CHROMOSOME II (FRAGMENT).//1.6e-29:177:38//CAENORHABDITIS ELEGANS.//P54073

F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.030:118:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

F-NT2RP3004334

F-NT2RP3004341//ALPHA-INTERNEXIN (ALPHA-INK).//0.91:110:26//MUS MUSCULUS (MOUSE).//P46660

F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.60:198:24//CAENORHABDITIS ELEGANS.//P46012

F-NT2RP3004349//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-37:60:76//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN GNTR-GGT INTERGENIC REGION (O162).//0.0026:76:28//ESCHERICHIA COLI.//P46854

F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE PRIMARY RESPONSE PROTEIN).//4.4e-109:212:96//HOMO SAPIENS (HUMAN).//Q92674

F-NT2RP3004424//JTV-1 PROTEIN.//4.5e-18:60:70//HOMO SAPIENS (HUMAN).//Q13155

F-NT2RP3004428//METALLOTHIONEIN-A (MTA).//0.0010:36:47//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P04734

F-NT2RP3004451//MYOSIN IC HEAVY CHAIN.//0.00072:113:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-NT2RP3004454//VERPROLIN.//3.3e-07:156:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37370

F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215.//0.0013:125:32//HUMAN ADENOVIRUS TYPE 2.//P03291

F-NT2RP3004470//HYPOTHETICAL 15.4 KD PROTEIN C16C10.11 IN CHROMOSOME III
 .//1.0:33:51//CAENORHABDITIS ELEGANS.//Q09254
 F-NT2RP3004472//GERM CELL-LESS PROTEIN.//7.3e-33:170:40//DROSOPHILA MELA
 NOGASTER (FRUIT FLY).//Q01820
 F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//8.4
 e-54:214:46//HOMO SAPIENS (HUMAN).//P98171
 F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.9e
 -47:199:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110
 F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.
 0013:121:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REG
 ION PRECURSOR.//0.066:87:35//BACILLUS SUBTILIS.//P50840
 F-NT2RP3004503//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:102:69
 //HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40.//0.64:93:34//SACCHAROMYCES CER
 EVISIAE (BAKER'S YEAST).//P32583
 F-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//2.2e-16:90:42//SACCHAROMY
 CES CEREVISIAE (BAKER'S YEAST).//P40484
 F-NT2RP3004527
 F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6.//0.38:148:22//SACCHAROMYCES CERE
 VISIAE (BAKER'S YEAST).//P32943
 F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-BINDING PROTEIN 1).//0.38:89:38//RATTUS NORVEGICUS (RAT).//P21743
 F-NT2RP3004544//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY PROTEIN 2).//0.0024:200:24//MYCOPLASMA PNEUMONIAE.//P75471
 F-NT2RP3004566//GASTRULA ZINC FINGER PROTEIN XLCGF17.1 (FRAGMENT).//4.6e-25:126:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18713
 F-NT2RP3004569//ANKYRIN.//8.3e-07:150:28//MUS MUSCULUS (MOUSE).//Q02357

F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150).//1.6e-70:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325

F-NT2RP3004578//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//1.5e-10:210:26//HOMO SAPIENS (HUMAN).//Q02224

F-NT2RP3004594//P54 PROTEIN PRECURSOR.//0.0044:230:24//ENTEROCOCCUS FAECIUM (STREPTOCOCCUS FAECIUM).//P13692

F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.5e-14:113:34//MUS MUSCULUS (MOUSE).//P15533

F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//4.5e-08:149:30//CAENORHABDITIS ELEGANS.//P34681

F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.0e-24:75:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54352

F-NT2RP3004670//CUTICLE COLLAGEN 2.//0.00090:159:29//CAENORHABDITIS ELEGANS.//P17656

F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//4.0e-79:243:62//BOS TAURUS (BOVINE).//P35526

F-NT2RP4000023

F-NT2RP4000035//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-06:46:67//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP4000049//CALDESMON (CDM).//0.41:63:34//GALLUS GALLUS (CHICKEN).//P12957

F-NT2RP4000051//DUALIN.//2.3e-23:195:37//GALLUS GALLUS (CHICKEN).//Q90830

F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-24:182:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP4000102//XPAR7 PROTEIN.//1.0:54:33//BACILLUS LICHENIFORMIS.//Q99166

F-NT2RP4000109//SLIT PROTEIN PRECURSOR.//1.9e-60:230:46//DROSOPHILA MELA

NOGASTER (FRUIT FLY).//P24014

F-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
SUBUNIT (CPSF 100 KD SUBUNIT).//1.4e-91:157:100//BOS TAURUS (BOVINE).//Q
10568

F-NT2RP4000129//5E5 ANTIGEN.//0.00072:124:37//RATTUS NORVEGICUS (RAT).//
Q63003

F-NT2RP4000147//ZINC FINGER PROTEIN GCS1.//1.5e-26:119:43//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P35197

F-NT2RP4000150

F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III.//
4.2e-31:180:47//CAENORHABDITIS ELEGANS.//P32740

F-NT2RP4000159//SPORE COAT PROTEIN SP96.//0.84:107:28//DICTYOSTELIUM DIS
COIDEUM (SLIME MOLD).//P14328

F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC RE
GION.//2.4e-08:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEI
N).//5.4e-05:143:32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P2828

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F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.8e-40:258:35//SACCH
AROMYCES CEREVISIAE (BAKER'S YEAST).//P22579

F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//1.4e-20
:104:40//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//P15287

F-NT2RP4000214//FERREDOXIN.//1.0:19:42//MOORELLA THERMOACETICA (CLOSTRID
IUM THERMOACETICUM).//P00203

F-NT2RP4000218//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-15:48:60//
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP4000243//DUALIN.//5.8e-78:192:70//GALLUS GALLUS (CHICKEN).//Q9083

0

F-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//3.1e-83:20

7:76//MUS MUSCULUS (MOUSE).//Q03173
 F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5e-29:153:43/
 /HELIANTHUS ANNUUS (COMMON SUNFLOWER).//023968
 F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.98:42:40//BOS TAURUS
 S (BOVINE).//P20072
 F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.
 //3.5e-71:209:66//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115
 F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)
 .//8.9e-22:166:37//HOMO SAPIENS (HUMAN).//Q15404
 F-NT2RP4000321//VERPROLIN.//0.00018:260:28//SACCHAROMYCES CEREVISIAE (BA
 KER'S YEAST).//P37370
 F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B).//0.42:15:46//ANTHOPLEURA XA
 NTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531
 F-NT2RP4000355//HYPOTHETICAL 90.9 KD PROTEIN IN GCN20-CMK1 INTERGENIC RE
 GION.//0.75:125:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43596
 F-NT2RP4000360//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRA
 GMENT).//0.27:92:33//RATTUS NORVEGICUS (RAT).//P10164
 F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0
 .99:52:32//HUMAN ADENOVIRUS TYPE 41.//P23691
 F-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (M
 RF-1).//4.1e-40:163:52//HOMO SAPIENS (HUMAN).//075570
 F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-59:12
 5:80//RATTUS NORVEGICUS (RAT).//P54319
 F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PR
 OTEIN) (NF-H).//0.00058:194:30//MUS MUSCULUS (MOUSE).//P19246
 F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2e-45:153:39//HOM
 O SAPIENS (HUMAN).//Q99676
 F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC RE
 GION PRECURSOR.//0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST

).//P47179

F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//1.8e-25:196:40//MUS MUSCULUS (MOUSE).//P39098

F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.0e-15:72:61//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.0e-23:63:82//HOMO SAPIENS (HUMAN).//P39192

F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2).//1.3e-41:102:45//KLUYVEROMYCES LACTIS (YEAST).//P33294

F-NT2RP4000455//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.00014:92:30//GALLUS GALLUS (CHICKEN).//P19601

F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DE UBIQUITINATING ENZYME 7) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE).//1.0e-29:218:38//HOMO SAPIENS (HUMAN).//Q93009

F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.049:117:29//PSEUDOMONAS AERUGINOSA.//P15276

F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.3e-05:152:23//CAENORHABDITIS ELEGANS.//Q09475

F-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//2.3e-48:172:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484

F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.3e-23:165:35//CAENORHABDITIS ELEGANS.//P34535

F-NT2RP4000515//PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE PHOSPHODIESTERASE) (FRAGMENT).//1.0:48:37//BOS TAURUS (BOVINE).//P15396

F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//1.0:41:36//VICIA FABA (BROAD BEAN).//Q41657

F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.1e-11:93:36//SACCHAR

OMYCES CEREVISIAE (BAKER'S YEAST).//P45818
 F-NT2RP4000519//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.68:55:40//BO
 S TAURUS (BOVINE).//P25508
 F-NT2RP4000524//IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN).//0
 .37:187:24//STREPTOCOCCUS AGALACTIAE.//P27951
 F-NT2RP4000528//NPL4 PROTEIN.//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//P33755
 F-NT2RP4000541//HOMEBOX PROTEIN CHOX-1 (FRAGMENT).//0.23:28:50//GALLUS
 GALLUS (CHICKEN).//P13544
 F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME III./
 /4.3e-14:174:34//CAENORHABDITIS ELEGANS.//Q03574
 F-NT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III./
 /2.1e-19:155:36//CAENORHABDITIS ELEGANS.//P34679
 F-NT2RP4000588//HYPOTHETICAL PROTEIN E-115.//0.014:64:35//HUMAN ADENOVIR
 US TYPE 2.//P03290
 F-NT2RP4000614//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR
 SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//2.7e-27:188
 :44//GALLUS GALLUS (CHICKEN).//P30352
 F-NT2RP4000638//EARLY NODULIN 55-1 PRECURSOR (N-55-1) (FRAGMENT).//0.55:
 40:40//GLYCINE MAX (SOYBEAN).//Q05544
 F-NT2RP4000648//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-06:31:74//
 HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP4000657//HYPOTHETICAL PROTEIN MJ1065.//2.5e-40:237:40//METHANOCOC
 CUS JANNASCHII.//Q58465
 F-NT2RP4000704
 F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e
 -07:134:40//STREPTOMYCES FRADIAE.//P20186
 F-NT2RP4000724//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR
 ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.1e-62:109:88//HOMO SAPIENS

(HUMAN).//P10266
 F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.0033:190:2
 5//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.0e-05:114:34//H
 OMO SAPIENS (HUMAN).//P23246
 F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:20:50//
 ANAS PLATYRHYNCHOS (DOMESTIC DUCK).//P50655
 F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC RE
 GION.//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915
 F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3.//1.3e-13:79:39//HELIANTHUS
 ANNUUS (COMMON SUNFLOWER).//P29675
 F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40.//1.3e-05:255:21//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P32583
 F-NT2RP4000833
 F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.18:38:44//DROSOP
 HILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAF
 II-90).//0.026:38:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38129
 F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)
 (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//2.8e-64:2
 29:53//RATTUS NORVEGICUS (RAT).//009175
 F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.6e-84:174:54//
 HOMO SAPIENS (HUMAN).//P16415
 F-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//8.2e-88:227:74//MUS MUSCUL
 US (MOUSE).//035682
 F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.1e-55:
 268:43//HOMO SAPIENS (HUMAN).//P22314
 F-NT2RP4000907//BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.
 112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B).//5.4e-10:220:25//HOMO

SAPIENS (HUMAN).//Q16620
 F-NT2RP4000915//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.46:23:60/
 /ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407
 F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00010:148:3
 2//BACILLUS SUBTILIS.//P39217
 F-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROT
 EIN).//3.5e-27:220:36//HOMO SAPIENS (HUMAN).//Q06828
 F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN)
 (IER 2.9/ER2.6).//0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA)./
 /P29128
 F-NT2RP4000928//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DI
 GLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLY
 CEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG
 SYNTHASE).//3.1e-104:263:66//HOMO SAPIENS (HUMAN).//Q92903
 F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC
 REGION.//0.93:107:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288
 F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G8.6.//2.0e-05:102:37//CAEN
 ORHABDITIS ELEGANS.//P34391
 F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REG
 ION.//2.3e-17:78:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564
 F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P
 EPTIDE P-D] (FRAGMENT).//0.0041:142:33//HOMO SAPIENS (HUMAN).//P10162
 F-NT2RP4000979//HYPOTHETICAL 14.5 KD PROTEIN.//0.77:106:33//VACCINIA VIR
 US (STRAIN COPENHAGEN).//P20517
 F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E4.4 IN CHROMOSOME III.
 //0.90:94:25//CAENORHABDITIS ELEGANS.//P34343
 F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B).//0.76:41:41//ANTHOPLEURA XA
 NTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531
 F-NT2RP4000996//PROTEIN Q300.//0.00024:41:53//MUS MUSCULUS (MOUSE).//Q02

722

F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.7e-115:261:82//RATTUS NORVEGICUS (RAT).//054888

F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.50:61:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377

F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR.//0.010:152:29//BACILLUS SUBTILIS.//P50840

F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.9e-05:247:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.1e-14:175:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002

F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//1.5e-74:272:55//CAENORHABDITIS ELEGANS.//Q09996

F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//0.0064:76:38//CAENORHABDITIS ELEGANS.//P34664

F-NT2RP4001064//DUALIN.//2.5e-24:199:38//GALLUS GALLUS (CHICKEN).//Q90830

F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.11:139:38//HOMO SAPIENS (HUMAN).//000268

F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.5e-22:242:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P13586

F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I).//1.7e-82:178:69//SUS SCROFA (PIG).//Q29099

F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN.//0.00039:141:26//RATTUS NORVEGICUS (RAT).//P49911

F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//9.9e-07:79:43//HOMO SAPIENS (HUMAN).//P78563

F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.4e-16:207:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032

F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.1e-115:224:99//RATTUS NORVEGICUS (RAT).//P38378

F-NT2RP4001122//TIPD PROTEIN.//7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//015736

F-NT2RP4001126//TRICHOHYALIN.//1.4e-19:257:28//OVIS ARIES (SHEEP).//P22793

F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).//0.00010:204:25//METHANOCOCCUS JANNASCHII.//Q58896

F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-34:168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616

F-NT2RP4001148//SOF1 PROTEIN.//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33750

F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//1.3e-08:106:41//VOLVOX CARTERI.//P21997

F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.6e-24:194:32//GALLUS GALLUS (CHICKEN).//P35331

F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0056:17:25//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643

F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER).//P52178

F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0029:1

17:26//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
 F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1.//1.0e-07:144:28//SA
 CCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33307
 F-NT2RP4001210//DERMORPHIN 1 PRECURSOR [CONTAINS: DELTORPHIN (DERMENKEPH
 ALIN); DERMORPHIN].//0.019:130:30//PHYLLOMEDUSA SAUVAGEI (SAUVAGE'S LEAF
 FROG).//P05422
 F-NT2RP4001213//ZINC FINGER PROTEIN 177.//3.2e-28:176:39//HOMO SAPIENS (HUMAN).//Q13360
 F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1).//2.4e-1
 3:108:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12404
 F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-56:242:40//DRO
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP4001235//REGULATORY PROTEIN E2.//0.0080:100:38//HUMAN PAPILLOMAVI
 RUS TYPE 25.//P36787
 F-NT2RP4001256//CUTICLE COLLAGEN 1.//0.014:104:31//CAENORHABDITIS ELEGAN
 S.//P08124
 F-NT2RP4001260//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.00077:16:
 68//ESCHERICHIA COLI.//P05834
 F-NT2RP4001274//HISTONE H1.M6.1.//0.98:65:35//TRYPANOSOMA CRUZI.//P40273
 F-NT2RP4001276//ELAV PROTEIN.//0.00054:134:33//DROSOPHILA VIRILIS (FRUIT
 FLY).//P23241
 F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOP
 ROTEIN).//0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
 F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//2.3e-
 12:190:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54787
 F-NT2RP4001336//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.0037:108
 :31//PODOSPORA ANSERINA.//Q00808
 F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810.//1.2e-09:150:34//METHANOCOC
 CUS JANNASCHII.//Q58220

F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III./
/1.4e-18:244:27//CAENORHABDITIS ELEGANS.//Q10123

F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC
2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTE
ROL ACYLTRANSFERASE) (FRAGMENT).//4.0e-49:212:50//GALLUS GALLUS (CHICKEN
).//P53760

F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//5.7e-11:2
29:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)
./0.00088:84:28//HOMO SAPIENS (HUMAN).//Q15404

F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PRO
TEIN).//1.0e-22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180

F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL ANTIG
EN).//0.51:92:26//ONCHOCERCA VOLVULUS.//P36991

F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112
) (TYROSINE- PROTEIN KINASE 1).//3.5e-13:146:35//DICTYOSTELIUM DISCOIDEU
M (SLIME MOLD).//P18160

F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGENIC REG
ION.//1.2e-14:207:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38767

F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7
.6) (RPB1) (FRAGMENT).//0.073:112:33//CRICETULUS GRISEUS (CHINESE HAMSTE
R).//P11414

F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0019:233:24//
HOMO SAPIENS (HUMAN).//Q02224

F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//6.2e-89:195:81//HOMO SAPIE
NS (HUMAN).//Q14141

F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.5e-85:216
:56//HOMO SAPIENS (HUMAN).//P28160

F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7

.6) (VERSION 1).//0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)./
/P18616

F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12).//0.0046:69:33//A
RTEMIA SALINA (BRINE SHRIMP).//P02399

F-NT2RP4001474//CBP3 PROTEIN PRECURSOR.//0.0011:111:29//SACCHAROMYCES CE
REVISIAE (BAKER'S YEAST).//P21560

F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC
1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//6.2e-60:146:61//HOMO SAPI
ENS (HUMAN).//Q02218

F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//2
.3e-24:137:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RP4001502//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC
REGION.//6.0e-22:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40
206

F-NT2RP4001507//CUTICLE COLLAGEN 40.//0.00029:166:31//CAENORHABDITIS ELE
GANS.//P34804

F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN.//0.74:96:30//LACTOCOCCUS
LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS), AND LACTOCOCCUS LACTIS (
SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS).//Q00561

F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT
I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//2.8e-06:79:41//DROSO
PHILA MELANOGASTER (FRUIT FLY).//P13002

F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENI
C REGION.//5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25
656

F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68.//1.5e-18:243:30//SACCH
AROMYCES CEREVISIAE (BAKER'S YEAST).//P32558

F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//0.00030:158:24
//MYCOBACTERIUM TUBERCULOSIS.//P96902

F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT)./
/0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P52170

F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//8.0e-22:119:4
2//HOMO SAPIENS (HUMAN).//Q15057

F-NT2RP4001571//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-
50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//0.012:167:28//BOS T
AURUS (BOVINE).//P06836

F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).
//6.8e-115:208:98//BOS TAURUS (BOVINE).//P53620

F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR.//0.22:184:25//STREPTOCOCCUS
PYOGENES.//P16946

F-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA
LIGASE) (ILERS).//7.4e-45:229:39//SYNECHOCYSTIS SP. (STRAIN PCC 6803)./
/P73505

F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.41:74:28//
SUS SCROFA (PIG).//P27917

F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:29:37//HOMO
SAPIENS (HUMAN).//P02811

F-NT2RP4001634//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE (FRAGMENT)
./0.16:233:23//RATTUS NORVEGICUS (RAT).//P04462

F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//4.2e-21:2
49:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40469

F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//4.5e-1
8:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P25323

F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II./
/3.4e-13:175:32//CAENORHABDITIS ELEGANS.//Q09600

F-NT2RP4001677//HYPOTHETICAL 73.6' KD PROTEIN CY49.21.//0.065:66:43//MYCO
BACTERIUM TUBERCULOSIS.//Q10690

F-NT2RP4001679//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-36:103:72

//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//0.93:37:37//C
 HLORELLA VULGARIS.//P56338
 F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//4.3e-1
 1:128:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10282
 F-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//4.1e-22:201:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332
 F-NT2RP4001739//HOMEBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).//1.0:67:34//HOMO SAPIENS (HUMAN).//P31260
 F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGMENT).//1.2e-19:72:62//HOMO SAPIENS (HUMAN).//P21506
 F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN.//1.8e-13:179:28//HOMO SAPIENS (HUMAN).//P11274
 F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//7.9e-38:147:49//MUS MUSCULUS (MOUSE).//Q07231
 F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR.//0.40:48:39//CAENORHABDITIS ELEGANS.//P20630
 F-NT2RP4001822//NOVEL ANTIGEN 2 (NAG-2).//2.7e-27:173:36//HOMO SAPIENS (HUMAN).//O14817
 F-NT2RP4001823//PUTATIVE CUTICLE COLLAGEN F09G8.6.//3.3e-16:152:42//CAENORHABDITIS ELEGANS.//P34391
 F-NT2RP4001828//HOLIN.//0.99:33:36//BACTERIOPHAGE HP1.//P51727
 F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA1.//1.2e-07:95:31//HOMO SAPIENS (HUMAN).//Q13330
 F-NT2RP4001841//INTESTINAL MUCIN-LIKE PROTEIN (MLP) (FRAGMENT).//0.94:141:22//RATTUS NORVEGICUS (RAT).//P98089
 F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-52:276:45//MUS MUSCULUS (MOUSE).//P55194

F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN GALE-PEPT INTERGENIC REGION.//0.92:39:51//BACILLUS SUBTILIS.//P55185

F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN.//0.32:97:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.6e-07:124:29//MUS MUSCULUS (MOUSE).//Q05921

F-NT2RP4001896//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION.//3.9e-10:210:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42935

F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10).//2.4e-07:53:45//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038

F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//3.1e-19:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2.//1.3e-28:72:50//MUS MUSCULUS (MOUSE).//P24399

F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//4.8e-14:183:30//TRITICUM AESTIVUM (WHEAT).//Q43209

F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.7e-07:115:29//MUS MUSCULUS (MOUSE).//P11260

F-NT2RP4001953

F-NT2RP4001966//WALL-ASSOCIATED PROTEIN PRECURSOR.//0.13:151:27//BACILLUS SUBTILIS.//Q07833

F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAIN.//0.00031:190:31//RIETIA PACHYPTILA (TUBE WORM).//P30754

F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:185:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE GUF1).//4.0e-49:158:65/
/SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46943

F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I./
/0.0047:148:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844

F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELI
CASE F56D2.6.//0.057:66:30//CAENORHABDITIS ELEGANS.//Q20875

F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN CY251.09.//0.94:45:46/
/MYCOBACTERIUM TUBERCULOSIS.//Q10888

F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.44:
36:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P1880
4

F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7
).//2.6e-19:46:76//HOMO SAPIENS (HUMAN).//Q05481

F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACT
OR C) (EF-C).//2.8e-05:196:31//HOMO SAPIENS (HUMAN).//P22670

F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.0064:29
:55//OWENIA FUSIFORMIS.//P21260

F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.1e-37:159:53//SCHIZ
OSACCHAROMYCES POMBE (FISSION YEAST).//P38938

F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20.//1.0:73:26//HELICOBACTER PYLO
RI (CAMPYLOBACTER PYLORI).//P56027

F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352.//0.98:52:26//TREPONEMA PALL
IDUM.//O83371

F-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGME
NT).//5.9e-05:138:27//GLYCINE MAX (SOYBEAN).//P25012

F-NT2RP5003459//HOMEBOX PROTEIN HOX-A3 (HOX-1.5) (MO-10).//0.027:40:40/
/MUS MUSCULUS (MOUSE).//P02831

F-NT2RP5003461//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT
).//1.1e-12:142:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779

F-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.3e-13:21
5:28//PODOSPORA ANSERINA.//Q00808

F-NT2RP5003492//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.0055:144:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//9.0e-05:103:38//MUS MUSCULUS (MOUSE).//P05142

F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87F.//0.53:21:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYCB 3' REGION PRECURSOR (ORF2) (FRAGMENT).//0.92:49:32//PARACOCCLUS DENITRIFICANS.//P29969

F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.7e-18:165:39//PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).//P37116

F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//6.0e-08:125:41//RATTUS NORVEGICUS (RAT).//P02454

F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34).//0.88:37:45//HALOBACTERIUM VOLCANII (HALOFERAX VOLCANII).//Q48331

F-OVARC1000001//GAR22 PROTEIN.//1.9e-05:41:58//HOMO SAPIENS (HUMAN).//Q99501

F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN.//3.7e-08:186:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19658

F-OVARC1000006//HISTONE H2A.1.//4.7e-55:117:98//RATTUS NORVEGICUS (RAT).//P02262

F-OVARC1000013//WD-REPEAT PROTEIN POP1.//0.00022:126:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87060

F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.3e-05:220:30//GALLUS GALLUS (CHICKEN).//P02457

F-OVARC1000017//CUTICLE COLLAGEN DPY-13.//2.6e-05:97:30//CAENORHABDITIS ELEGANS.//P17657

F-OVARC1000035

F-OVARC1000058//RAS-RELATED PROTEIN RABC.//0.00015:110:24//DICTYOSTELIUM
DISCOIDEUM (SLIME MOLD).//P34143

F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (R
NASE LE).//6.8e-09:60:45//LYCOPERSICON ESCULENTUM (TOMATO).//P80022

F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN V-II-4).//1.0:27:44//NAJA MOSSA
MBICA (MOZAMBIQUE COBRA).//P01452

F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROTEIN 15
) (PP15).//5.2e-06:115:29//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (
RAT).//P13662

F-OVARC1000085

F-OVARC1000087//HISTONE MACRO-H2A.1.//1.2e-13:174:26//RATTUS NORVEGICUS
(RAT).//Q02874

F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.0013:137:32//MUS MUSCU
LUS (MOUSE).//Q06666

F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7.//0.97:46:39//ACANTHA
MOEBA CASTELLANII (AMOEBA).//P46756

F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC R
EGION.//0.0012:165:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53935

F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (F
RAGMENT).//0.18:35:34//DAUCUS CAROTA (CARROT).//P06600

F-OVARC1000113//HYPOTHETICAL PROTEIN C18.//1.0:26:26//SWINEPOX VIRUS (ST
RAIN KASZA) (SPV).//P32217

F-OVARC1000114//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-28:57:63/
/HOMO SAPIENS (HUMAN).//P39194

F-OVARC1000133

F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (U
BIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DE
UBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//1.9e-09:

200:29//HOMO SAPIENS (HUMAN).//Q13107
 F-OVARC1000145//HOMEBOX PROTEIN DLX-3.//1.0:65:30//BRACHYDANIO RERIO (Z
 EBRAFISH) (ZEBRA DANIO).//Q01702
 F-OVARC1000148//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.12
 :175:29//CANDIDA ALBICANS (YEAST).//P46593
 F-OVARC1000151//HYPOTHETICAL PROTEIN KIAA0161.//5.6e-20:197:30//HOMO SAP
 IENS (HUMAN).//P50876
 F-OVARC1000168//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0030:77:38//H
 OMO SAPIENS (HUMAN).//P39188
 F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN WCAH.//0.95:56:35//ESC
 HERICHIA COLI.//P32056
 F-OVARC1000198//HISTONE H1.C2.//0.96:70:25//TRYPANOSOMA CRUZI.//P40268
 F-OVARC1000209//HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGENIC REG
 ION.//2.5e-33:178:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03677
 F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.7e-05:66:46//MUS
 MUSCULUS (MOUSE).//P05142
 F-OVARC1000240//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-10:41:78/
 /HOMO SAPIENS (HUMAN).//P39193
 F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1 (EPAS-1) (HIF-1 ALPHA-L
 IKE FACTOR) (MHLF) (HIF-RELATED FACTOR) (HRF).//7.4e-54:177:54//MUS MUSC
 ULUS (MOUSE).//P97481
 F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REG
 ION.//2.9e-20:115:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821
 F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (TRANSCO
 RTIN).//1.0:79:25//MUS MUSCULUS (MOUSE).//Q06770
 F-OVARC1000304//PROTEIN MOV-10.//1.6e-79:181:83//MUS MUSCULUS (MOUSE).//
 P23249
 F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//6.9e-36:156:42//ASHBY
 A GOSSYPPII (EREMOTHECIUM GOSSYPPII).//Q00063

F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I.//5
 .2e-45:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014179
 F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE IB-1.//0.036:67:35//HOMO SAPI
 ENS (HUMAN).//P04281
 F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REG
 ION.//1.2e-16:200:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004
 F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.69:41:43//CYANOPHO
 RA PARADOXA.//P48273
 F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.98:49:34//PSEUDOPLEUR
 ONECTA AMERICANUS (WINTER FLOUNDER).//P02734
 F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).//8.1e-05:1
 15:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q05049
 F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYP
 EPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00076:100:29//RATTUS NORVEGI
 CUS (RAT).//P28023.
 F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLTR-SPOIIC INTERGENIC R
 EGION.//1.0:46:34//BACILLUS SUBTILIS.//P54431
 F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRA
 GMENT).//0.0028:97:37//HOMO SAPIENS (HUMAN).//P25067
 F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PRFA-SPOIIR INTERGENIC R
 EGION.//0.70:21:47//BACILLUS SUBTILIS.//P39150
 F-OVARC1000431
 F-OVARC1000437//TENSIN.//9.2e-42:195:52//GALLUS GALLUS (CHICKEN).//Q0420
 5
 F-OVARC1000440//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTE
 IN).//3.4e-31:37:97//HOMO SAPIENS (HUMAN).//P48059
 F-OVARC1000442
 F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0056:163:34//HAEMONCH
 US CONTORTUS.//P16252

F-OVARC1000461//FIXU PROTEIN.//0.36:36:44//RHIZOBIUM LEGUMINOSARUM (BIOV
AR TRIFOLII).//P42710

F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//2.4e-14:222:26//SACCHAR
OMYCES CEREVISIAE (BAKER'S YEAST).//P11075

F-OVARC1000466//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.3e-08:29:93/
/HOMO SAPIENS (HUMAN).//P39192

F-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC
3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE MKP-X) (FRAGMENT).//2.8
e-06:96:36//RATTUS NORVEGICUS (RAT).//Q63340

F-OVARC1000479//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//0.99:4
8:37//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//P31567

F-OVARC1000486

F-OVARC1000496//HYPOTHETICAL PROTEIN MJ1213.//1.0:62:32//METHANOCOCCUS J
ANNASCHII.//Q58610

F-OVARC1000520//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).//0.0011:66:4
0//EIMERIA ACERVULINA.//P09125

F-OVARC1000526//PROTEIN Q300.//1.2e-05:51:43//MUS MUSCULUS (MOUSE).//Q02
722

F-OVARC1000533//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.74:43:41//HOMO S
APIENS (HUMAN).//Q16612

F-OVARC1000543//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.
41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTI
DE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.3e-23:192:35//HO
MO SAPIENS (HUMAN).//Q10472

F-OVARC1000556

F-OVARC1000557//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-08:80:47//
HOMO SAPIENS (HUMAN).//P39188

F-OVARC1000564//VPX PROTEIN (X ORF PROTEIN) (VIRAL ACCESSORY PROTEIN).//
0.45:32:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194) (HIV-2)./

/P17760

F-OVARC1000573

F-OVARC1000576//BETA-DEFENSIN 1 (BNDB-1).//0.47:29:41//BOS TAURUS (BOVINE).//P46159

F-OVARC1000578//COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).//0.023:96:36//BOS TAURUS (BOVINE).//P02459

F-OVARC1000588//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3.//0.75:57:29//HOMO SAPIENS (HUMAN).//P09001

F-OVARC1000605//AUTOLYSIN PRECURSOR (EC 3.4.24.38) (GAMETE LYTIC ENZYME) (GLE).//0.91:134:28//CHLAMYDOMONAS REINHARDTII.//P31178

F-OVARC1000622//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.6e-36:100:80//HOMO SAPIENS (HUMAN).//P39189

F-OVARC1000640//HYPOTHETICAL 8.5 KD PROTEIN YCF40 (ORF73).//0.96:34:38//ODONTELLA SINENSIS.//P49535

F-OVARC1000649//ANTHER-SPECIFIC PROTEIN SF18 PRECURSOR (FRAGMENT).//0.0036:64:37//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//P22357

F-OVARC1000661//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//0.21:53:47//RATTUS NORVEGICUS (RAT).//P02466

F-OVARC1000678//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//1.0:17:58//ESCHERICHIA COLI.//P05834

F-OVARC1000679//DNA-DIRECTED RNA POLYMERASE OMEGA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT).//0.096:67:29//ESCHERICHIA COLI.//P08374

F-OVARC1000681//PROTEIN Q300.//0.72:16:43//MUS MUSCULUS (MOUSE).//Q02722

F-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//7.6e-70:102:99//MUS MUSCULUS (MOUSE).//P39098

F-OVARC1000689//CADMIUM-METALLOTHIONEIN (CD-MT).//0.032:30:40//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187

F-OVARC1000700//BRAIN NEURON CYTOPLASMIC PROTEIN 2.//0.17:60:40//RATTUS

NORVEGICUS (RAT).//P02684

F-OVARC1000703//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.57:42:42//HOMO
SAPIENS (HUMAN).//P02811

F-OVARC1000722//N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUC
OSAMINE (BETA 1->4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHAS
E A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).//1.1e-20:44:70/
/BOS TAURUS (BOVINE).//P08037

F-OVARC1000730//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//
/5.2e-29:224:36//CAENORHABDITIS ELEGANS.//Q18262

F-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//6.2e-12:78:48//DROSOPH
ILA MELANOGASTER (FRUIT FLY).//P25159

F-OVARC1000769

F-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1e-46:121:79//HOMO SAPIENS
(HUMAN), AND CANIS FAMILIARIS (DOG).//P08886

F-OVARC1000781//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC
HOMEBOX PROTEIN 2).//0.81:36:52//HOMO SAPIENS (HUMAN).//P52951

F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMENT).//0.96:37:48//SUS S
CROFA (PIG).//Q29303

F-OVARC1000800//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.5e-31:47:82/
/HOMO SAPIENS (HUMAN).//P39189

F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.2 IN CHROMOSOME X.//0.
16:55:40//CAENORHABDITIS ELEGANS.//Q10926

F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (
P68-PAK) (P21- ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).//0.8
7:140:31//RATTUS NORVEGICUS (RAT).//P35465

F-OVARC1000846//NUCLEOLIN (PROTEIN C23).//7.0e-07:109:30//MESOCRICETUS A
URATUS (GOLDEN HAMSTER).//P08199

F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ERG8-UBP8 INTERGENIC REG
ION.//6.9e-09:180:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04991

F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//0.0020:74:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52490

F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//9.8e-39:154:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484

F-OVARC1000883//METALLOTHIONEIN-I.//0.87:38:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15113

F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//2.8e-18:170:34//ESCHERICHIA COLI.//P37440

F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.00033:60:45//BOS TAURUS (BOVINE).//P02465

F-OVARC1000890//PROBABLE E5 PROTEIN.//0.92:7:71//HUMAN PAPILLOMAVIRUS TYPE 70.//P50774

F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF5).//1.0:36:36//PARAMECIUM TETRAURELIA.//P15606

F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87).//1.0:34:44//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010337

F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4.//4.0e-07:98:35//CAENORHABDITIS ELEGANS.//Q09455

F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-47:115:76//HOMO SAPIENS (HUMAN).//P56524

F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.99:54:24//BOA CONSTRICTOR (BOA).//P92848

F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC REGION.//1.0:48:33//ESCHERICHIA COLI.//P45505

F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:135:31//HOMO SAPIENS (HUMAN).//P02452

F-OVARC1000945//EARLY E1A 11 KD PROTEIN.//0.087:81:24//MOUSE ADENOVIRUS TYPE 1 (MAV-1).//P12533

F-OVARC1000948

F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//0.99:67:28//METHANOCOCCUS
JANNASCHII.//Q58343

F-OVARC1000960//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-32:56:75/
/HOMO SAPIENS (HUMAN).//P39193

F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-IIA ANTAGONIST) (PLATELET AGGRE
GATION INHIBITOR) (DENDROASPIN).//1.0:30:36//DENDROASPIS JAMESONI KAIMOS
AE (EASTERN JAMESON'S MAMBA).//P28375

F-OVARC1000971

F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC
REGION PRECURSOR.//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
.//P53832

F-OVARC1000996//MO25 PROTEIN.//1.9e-39:80:95//MUS MUSCULUS (MOUSE).//Q06
138

F-OVARC1000999//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 1 (BRN-1 PROT
EIN).//0.00020:50:40//HOMO SAPIENS (HUMAN).//P20264

F-OVARC1001000//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-16:43:90/
/HOMO SAPIENS (HUMAN).//P39195

F-OVARC1001004//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.95:33:42//DROSOP
HILA MELANOGASTER (FRUIT FLY).//Q01642

F-OVARC1001010//HYPOTHETICAL PROTEIN MJ0926.//0.50:71:23//METHANOCOCCUS
JANNASCHII.//Q58336

F-OVARC1001011//CORTISTATIN PRECURSOR.//0.81:45:37//RATTUS NORVEGICUS (R
AT).//Q62949

F-OVARC1001032//FERREDOXIN LIKE PROTEIN.//1.0:26:46//RHIZOBIUM LEGUMINOS
ARUM (BIOVAR PHASEOLI).//Q05561

F-OVARC1001034//METALLOTHIONEIN-IG (MT-1G).//0.14:9:77//HOMO SAPIENS (HU
MAN).//P13640

F-OVARC1001038//NUCLEOLIN (PROTEIN C23).//3.2e-07:36:80//HOMO SAPIENS (H

UMAN).//P19338

F-OVARC1001040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-18:45:60/
/HOMO SAPIENS (HUMAN).//P39194

F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6
.1.41) (DIADENOSINE TETRAPHOSPHATASE).//0.88:43:39//ESCHERICHIA COLI.//P
05637

F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLE
ID PROTEIN).//0.34:117:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319

F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.6e-33:43:97//H
OMO SAPIENS (HUMAN).//P43490

F-OVARC1001062

F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRN
A LIGASE) (METRS).//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIRO
CHETE).//Q44951

F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT).//5.3e-15:100
:44//BRADYRHIZOBIUM JAPONICUM.//069162

F-OVARC1001072//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0076:41:56//H
OMO SAPIENS (HUMAN).//P39188

F-OVARC1001074//60S RIBOSOMAL PROTEIN L38.//1.0:32:40//LYCOPERSICON ESCU
LENTUM (TOMATO).//P46291

F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME I./
/0.73:135:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10197

F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PET54-DIE2 INTERGENIC RE
GION.//5.6e-05:30:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50079

F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1.//1.8e-08:52:51//SCHIZOSAC
CHAROMYCES POMBE (FISSION YEAST).//P78963

F-OVARC1001113//DIAPHANOUS PROTEIN.//1.9e-33:218:35//DROSOPHILA MELANO
GASTER (FRUIT FLY).//P48608

F-OVARC1001117//GENE 7 PROTEIN.//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4).

//P11339

F-OVARC1001118

F-OVARC1001129//30S RIBOSOMAL PROTEIN S17.//0.15:57:22//AQUIFEX AEOLICUS
./066439

F-OVARC1001154//GRANULINS PRECURSOR (ACROGRANIN).//2.3e-95:99:77//MUS MU
SCULUS (MOUSE).//P28798

F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//0.17:8
7:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P49177

F-OVARC1001162

F-OVARC1001167//TRBD PROTEIN.//0.92:24:45//ESCHERICHIA COLI.//P41070

F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,
6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT).//0.82:35:40//MUS
MUSCULUS (MOUSE).//P97323

F-OVARC1001170//PROLINE-RICH PEPTIDE P-B.//0.17:27:37//HOMO SAPIENS (HUM
AN).//P02814

F-OVARC1001171//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00023:28:75//
HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001173

F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN.//2.7e-05:158:31//EPSTEIN-BAR
R VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.4e-12:208:25//SACCHAROMY
CES CEREVISIAE (BAKER'S YEAST).//P48510

F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC R
EGION.//3.3e-31:129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5321

5

F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REG
ION.//0.018:148:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236.//2.5e-27:141:39//METHANOCOC
CUS JANNASCHII.//Q58633

F-OVARC1001240
 F-OVARC1001243
 F-OVARC1001244//RING3 PROTEIN (KIAA9001).//1.7e-13:37:91//HOMO SAPIENS (HUMAN).//P25440
 F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.3e-07:109:35//MUS MUSCULUS (MOUSE).//Q06666
 F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4).//0.71:43:41//PSEUDOMONAS AERUGINOSA.//P24563
 F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVSW-UVSY INTERGENIC REGION.//1.0:44:29//BACTERIOPHAGE T4.//P32281
 F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR.//0.00015:188:23//CAENORHABDITIS ELEGANS.//P46504
 F-OVARC1001282
 F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//0.022:101:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
 F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.023:134:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013695
 F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.3e-14:150:28//ZEA MAYS (MAIZE).//P49133
 F-OVARC1001330
 F-OVARC1001339//RIBONUCLEOPROTEIN RB97D.//0.0013:55:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02926
 F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.9e-17:110:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
 F-OVARC1001342
 F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:39:23//STAPHYLOCOCCUS CARNOSUS.//P36253
 F-OVARC1001357//METALLOTHIONEIN.//0.99:28:42//XENOPUS LAEVIS (AFRICAN CL

AWED FROG).//Q05890

F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).//0.86:109:31//HOMO SAPIENS (HUMAN).//P48634

F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//6.7e-05:124:36//BOS TAURUS (BOVINE).//P02465

F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGENIC REGION PRECURSOR.//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMONAS SP. (STRAIN B13).//Q47100

F-OVARC1001376//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.8e-24:96:61//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.1.34) (SUL-ATPASE EPSILON).//0.96:46:39//SULFOLOBUS ACIDOCALDARIUS.//P23039

F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00024:189:29//HOMO SAPIENS (HUMAN).//P10162

F-OVARC1001399//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.062:18:77//HOMO SAPIENS (HUMAN).//P39195

F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSOME III.//0.010:185:23//CAENORHABDITIS ELEGANS.//Q03570

F-OVARC1001419//A-TYPE INCLUSION PROTEIN (ATI).//0.50:135:28//CAMELPOX VIRUS (STRAIN CP-1).//Q05482

F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.//0.43:85:40//HOMO SAPIENS (HUMAN).//Q03692

F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN).//0.031:100:30//TOMATO YELLOW LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV).//P36283

F-OVARC1001442//HOMEBOX PROTEIN HTR-A2 (FRAGMENT).//1.0:32:34//HELOBDELLA TRISERIALIS (LEECH).//P17138

F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.74:19:47//MUS MUSCULUS (MOUSE).//P28184

F-OVARC1001476//GTP-BINDING PROTEIN GTR2.//3.0e-12:114:34//SACCHAROMYCES

CEREVISIAE (BAKER'S YEAST).//P53290
 F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.00019:134:32//M
 US MUSCULUS (MOUSE).//Q02788
 F-OVARC1001489//HYPOTHETICAL PROTEIN HI1270.//0.98:30:43//HAEMOPHILUS IN
 FLUENZAE.//P44149
 F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2.//4.0e-65:132:100//HOMO SAP
 IENS (HUMAN).//P56545
 F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDN
 EY DISEASE PROTEIN 1).//3.2e-70:159:94//HOMO SAPIENS (HUMAN).//P98161
 F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14).//
 1.0:36:33//MUS MUSCULUS (MOUSE).//Q61077
 F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.69:57:33//HOM
 O SAPIENS (HUMAN).//P35325
 F-OVARC1001547
 F-OVARC1001555//NGG1-INTERACTING FACTOR 3.//7.6e-16:148:34//SACCHAROMYCE
 S CEREVISIAE (BAKER'S YEAST).//P53081
 F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR
 SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//8.8e-38:94:
 81//GALLUS GALLUS (CHICKEN).//P30352
 F-OVARC1001600//GENE 7 PROTEIN.//0.80:38:39//SPIROPLASMA VIRUS SPV1-R8A2
 B.//P15898
 F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (S
 N-1,2- DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT).//1.6e-22:122:3
 9//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17898
 F-OVARC1001611
 F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0
 .30:43:34//CAENORHABDITIS ELEGANS.//Q11116
 F-OVARC1001668//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.0e-19:45:82/
 /HOMO SAPIENS (HUMAN).//P39192

F-OVARC1001702//SOX-20 PROTEIN.//2.4e-28:71:83//HOMO SAPIENS (HUMAN).//0
60248

F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE
NUCLEOTIDE- BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE PROTEIN MAG-1
).//0.00018:88:36//MUS MUSCULUS (MOUSE).//Q01514

F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1
B).//2.7e-05:98:32//MUS MUSCULUS (MOUSE).//Q62267

F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATE
D DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.5e-20:46:67//BOS TAURUS (BOVI
NE).//P07106

F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMY
LASE INHIBITOR OF MICROBES I).//0.59:23:56//STREPTOMYCES OLIVACEOVIRIDIS
(STREPTOMYCES CORCHORUSII).//P09921

F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//2.1e-75:176:8
7//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q01173

F-OVARC1001745//GENE 11 PROTEIN.//0.31:36:52//SPIROPLASMA VIRUS SPV1-R8A
2 B.//P15902

F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERM
INAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//2.8e-23:197:35//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P12945

F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS
ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE
ISOMERASE) (FKBP-70).//2.2e-06:99:40//SACCHAROMYCES CEREVISIAE (BAKER'S
YEAST).//P38911

F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//
0.99:113:27//ESCHERICHIA COLI.//P23839

F-OVARC1001768

F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MPT5-SAE2 INTERGENIC REG
ION.//0.090:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46945

F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION.//0.81:21:38//BACTERIOPHAGE T4.//P07878

F-OVARC1001802//PLECTOXIN VIII (PLT-VIII) (PLTVIII).//0.41:19:36//PLECTR EURYS TRISTIS (SPIDER).//P36984

F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.67:24:58//SACCHARO MYCES CEREVISIAE (BAKER'S YEAST).//P14796

F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.23:111:31//RAT TUS NORVEGICUS (RAT).//P02454

F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:28:42//HALICHOERUS GRYPUS (GRAY SEAL).//P38592

F-OVARC1001813//HYPOTHETICAL 9.9 KD PROTEIN.//0.41:36:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20562

F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137.//0.80:58:29//MUS MUSCULUS (MOUSE).//P11260

F-OVARC1001828

F-OVARC1001846

F-OVARC1001861//METALLOTHIONEIN (MT).//0.18:11:54//PLEURONECTES PLATESSA (PLAICE).//P07216

F-OVARC1001873

F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//2.3e-05:73:31//CAENORHABDITIS ELEGANS.//Q09296

F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//2.4e-11:203:32//HOMO SAPIENS (HUMAN).//P02812

F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-16:86:59//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F22B7.5 IN CHROMOSOME III.//0.0053:48:47//CAENORHABDITIS ELEGANS.//P34408

F-OVARC1001901

F-OVARC1001911//40S RIBOSOMAL PROTEIN S28.//1.0:33:36//ARABIDOPSIS THALI
ANA (MOUSE-EAR CRESS).//P34789

F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO
/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//0.00082:114:27//HOMO SAPIEN
S (HUMAN).//P98174

F-OVARC1001928//FERREDOXIN III (FDIII).//1.0:64:29//ANABAENA VARIABILIS.
//P46050

F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERM
INAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//3.0e-07:93:37//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P12945

F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III./
/1.7e-23:147:43//CAENORHABDITIS ELEGANS.//P34664

F-OVARC1001949//ZINC FINGER PROTEIN 177.//2.0e-23:56:66//HOMO SAPIENS (H
UMAN).//Q13360

F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.011:57:47//HO
MO SAPIENS (HUMAN).//P39188

F-OVARC1001987//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.39:14:6
4//MUS MUSCULUS (MOUSE).//P02319

F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-13:55:72//
HOMO SAPIENS (HUMAN).//P39188

F-OVARC1002044

F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP).//3
.6e-12:221:25//HOMO SAPIENS (HUMAN).//P46939

F-OVARC1002066

F-OVARC1002082

F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.99:149:
24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-OVARC1002112//HISTONE MACRO-H2A.1.//2.8e-64:133:98//RATTUS NORVEGICUS
(RAT).//Q02874

F-OVARC1002127//60S RIBOSOMAL PROTEIN L22.//0.0023:95:35//DROSOPHILA MEL
ANOGASTER (FRUIT FLY).//P50887

F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG
6).//6.4e-51:198:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40328

F-OVARC1002143

F-OVARC1002156//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC RE
GION.//0.00010:64:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915

F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGI
ON.//8.2e-07:119:35//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.00023:90:
45//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204

F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN
D2013.2 IN CHROMOSOME II.//1.3e-34:165:35//CAENORHABDITIS ELEGANS.//Q189
64

F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A2.05C IN CHROMOSOME I.
//8.8e-05:148:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09725

F-PLACE1000005//PROTEIN Q300.//0.30:10:100//MUS MUSCULUS (MOUSE).//Q0272
2

F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3
(EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING P
ROTEASE) (DEUBIQUITINATING ENZYME).//2.3e-39:134:62//CAENORHABDITIS ELEG
ANS.//P34547

F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)
) (RO(SS-A)).//0.00036:63:39//HOMO SAPIENS (HUMAN).//P19474

F-PLACE1000031

F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-12:97:41/
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT).//0.98:31:38//BACIL

LUS SP. (STRAIN C-125).//P38373
 F-PLACE1000050//COLLAGEN ALPHA 1(III) CHAIN.//0.00062:190:33//BOS TAURUS
 (BOVINE).//P04258
 F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A.//6.4e-19:51:86//GALLUS GALLU
 S (CHICKEN).//P32046
 F-PLACE1000066//SSU72 PROTEIN.//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//P53538
 F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6).//1.7e-06:21:95/
 /HOMO SAPIENS (HUMAN).//Q92934
 F-PLACE1000081//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.0053:146:33
 //MUS MUSCULUS (MOUSE).//P06798
 F-PLACE1000094
 F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTIO
 N FACTOR 3).//1.8e-62:158:81//HOMO SAPIENS (HUMAN).//P20290
 F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.1
 7) (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1).//9.
 8e-12:104:34//HOMO SAPIENS (HUMAN).//P30084
 F-PLACE1000184//AC PROTEIN.//0.44:31:29//BACTERIOPHAGE T4.//P18924
 F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10C PREC
 URSOR.//0.11:48:33//MYCOBACTERIUM TUBERCULOSIS.//Q10637
 F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-AL
 PHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.4e-05:194:26//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
 F-PLACE1000214
 F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.027:63:34//GA
 LLUS GALLUS (CHICKEN).//P02457
 F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN).//0.78:100:26//EQUINE
 HERPESVIRUS TYPE 4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUB
 TYPE 2).//Q00039

F-PLACE1000292

F-PLACE1000308//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.049:28:4

2//MEDICAGO SATIVA (ALFALFA).//P11728

F-PLACE1000332

F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420.//0.15:24:54//TREPONEMA PALL

IDUM.//083435

F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE C)

.//1.0:63:25//ORYCTOLAGUS CUNICULUS (RABBIT).//P16973

F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (

PROTEIN KINASE A INTERFERENCE PROTEIN).//0.018:169:28//SACCHAROMYCES CER

EVISIAE (BAKER'S YEAST).//P36027

F-PLACE1000383//MYOTUBULARIN.//1.2e-65:215:57//HOMO SAPIENS (HUMAN).//Q1

3496

F-PLACE1000401//ELASTIN PRECURSOR (TROPOLASTIN).//0.00023:145:30//MUS M

USCULUS (MOUSE).//P54320

F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)).//3.4e-27:9

0:63//HOMO SAPIENS (HUMAN).//Q15233

F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-

OXO-DGTPASE).//4.7e-07:134:29//MUS MUSCULUS (MOUSE).//P53368

F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C11D3.01C IN CHROMOSOME I.//

0.48:72:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10080

F-PLACE1000424

F-PLACE1000435

F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.0e-31:129:63

//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1000453//PROTEIN Q300.//0.013:16:68//MUS MUSCULUS (MOUSE).//Q0272

2

F-PLACE1000481//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.14:63:36//HOMO

SAPIENS (HUMAN).//P08547

F-PLACE1000492//BASPI PROTEIN.//0.17:114:28//HOMO SAPIENS (HUMAN).//P807

23

F-PLACE1000540

F-PLACE1000547//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP
-MANNOSE-1- PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE
).//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562.//1.0:35:34//METHANOCOCCUS J
ANNASCHII.//Q57982

F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2).//0.13:66:37/
/HOMO SAPIENS (HUMAN).//P15803

F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e
-45:192:47//HOMO SAPIENS (HUMAN).//P51522

F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE
NUCLEOTIDE- BINDING PROTEIN 1).//5.3e-63:122:88//HOMO SAPIENS (HUMAN).//
P32455

F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN).//2.6e-12:120:38//DRO
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR.//0.83:53:32//HUMAN
ADENOVIRUS TYPE 12.//P36707

F-PLACE1000610

F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MCK1-RPS19B INTERGENIC R
EGION.//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48558

F-PLACE1000636//MALE STERILITY PROTEIN 2.//3.7e-09:83:43//ARABIDOPSIS TH
ALIANA (MOUSE-EAR CRESS).//Q08891

F-PLACE1000653//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (A
CETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE)./
/1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687

F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOP
ROTEIN).//0.0029:75:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPR
 ESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.1e-38:180:42//HOMO SAPIENS
 (HUMAN).//Q13263

F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.//0.
 93:49:34//MYCOBACTERIUM TUBERCULOSIS.//P71934

F-PLACE1000716

F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SPAT 3' REGION (ORF-11)./
 /0.90:53:37//SHIGELLA FLEXNERI.//P55794

F-PLACE1000749//HYPOTHETICAL PROTEIN MG148.//0.0014:142:27//MYCOPLASMA G
 ENITALIUM.//P47394

F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//1.1e-1
 5:98:48//CAENORHABDITIS ELEGANS.//P34529

F-PLACE1000769//VIGILIN.//0.51:60:33//GALLUS GALLUS (CHICKEN).//P81021

F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C10.04.//1.0:22:45//MYCO
 BACTERIUM TUBERCULOSIS.//006360

F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.
 //2.6e-38:159:51//CAENORHABDITIS ELEGANS.//P34657

F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0097:12
 8:30//HOMO SAPIENS (HUMAN).//P50552

F-PLACE1000798//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.4e-07:47:61//
 HOMO SAPIENS (HUMAN).//P39188

F-PLACE1000841

F-PLACE1000849//ELAV PROTEIN.//3.5e-05:140:35//DROSOPHILA VIRILIS (FRUIT
 FLY).//P23241

F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008.//0.95:100:23//METHANOCOCCUS
 JANNASCHII.//Q60319

F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2
 .3e-46:172:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32899

F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./

/0.00022:105:35//HOMO SAPIENS (HUMAN).//P16157
 F-PLACE1000931//KILLER TOXIN HM-1.//0.95:24:33//WILLIOPSIS MRKII (YEAST
) (HANSENULA MRKII).//P10410
 F-PLACE1000948//SL CYTOKINE PRECURSOR (FLT3 LIGAND).//0.97:52:40//HOMO S
 APIENS (HUMAN).//P49771
 F-PLACE1000972//MYOSIN ID HEAVY CHAIN.//1.9e-06:79:43//DICTYOSTELIUM DIS
 COIDEUM (SLIME MOLD).//P34109
 F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III./
 /2.5e-23:105:41//CAENORHABDITIS ELEGANS.//P46941
 F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC F
 INGER PROTEIN HF.16).//0.91:83:30//HOMO SAPIENS (HUMAN).//P17097
 F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G7.02 IN CHROMOSOME I./
 /0.10:128:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09796
 F-PLACE1001000
 F-PLACE1001007//ZYXIN.//2.2e-05:135:30//GALLUS GALLUS (CHICKEN).//Q04584
 F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR COMPONENT PRECURSOR (
 BUNGAROTOXIN, B1 CHAIN).//1.0:30:40//BUNGARUS MULTICINCTUS (MANY-BANDED
 KRAIT).//P00987
 F-PLACE1001015
 F-PLACE1001024
 F-PLACE1001036
 F-PLACE1001054//HOLOTRICIN 3 PRECURSOR.//0.0044:56:39//HOLOTRICHIA DIOMP
 HALIA.//Q25055
 F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+, L-GLUTAMATE FORMING]
 (EC 1.5.1.10).//0.0013:38:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./
 /P38999
 F-PLACE1001076
 F-PLACE1001088//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.95:32:50
 //MEDICAGO SATIVA (ALFALFA).//P11728

F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.0026:81:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X.//0.00063:125:32//CAENORHABDITIS ELEGANS.//Q11102

F-PLACE1001118//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//2.6e-77:209:63//MUS MUSCULUS (MOUSE).//Q03309

F-PLACE1001136//ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (EC 3.2.1.49) (ALPHA- GALACTOSIDASE B).//0.99:107:30//HOMO SAPIENS (HUMAN).//P17050

F-PLACE1001168

F-PLACE1001171//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00012:37:59//HOMO SAPIENS (HUMAN).//P12895

F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//3.6e-12:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867

F-PLACE1001238

F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMENT).//0.13:30:53//COLINUS VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE).//P27087

F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.1e-24:125:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSGA 3' REGION (ORF L5) (FRAGMENT).//1.0:24:45//MYCOPLASMA CAPRICOLUM.//P43040

F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-II-3).//0.98:31:41//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01470

F-PLACE1001280//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0051:156:32//MUS MUSCULUS (MOUSE).//P28481

F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//3.7e-56:109:93//MUS MUSCULUS (MOUSE).//P50636

F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35).//3.2e-30:75:57//MUS MUSCULUS (MOUSE).//P15620

F-PLACE1001311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.7e-31:66:66/

/HOMO SAPIENS (HUMAN).//P39189

F-PLACE1001323

F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEIN) (ART/RS).//0.11:66:27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE) (SIV-AGM).//P27971

F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-12).//0.070:18:33//NAJA HAJE ANNULIFERA (BANDED EGYPTIAN COBRA).//P01422

F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION INHIBITOR).//4.9e-06:50:46//TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE).//P17495

F-PLACE1001383//M PROTEIN, SEROTYPE 49 PRECURSOR.//0.080:136:24//STREPTOCOCCUS PYOGENES.//P16947

F-PLACE1001384

F-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8./1.9e-22:142:39//HOMO SAPIENS (HUMAN).//Q12929

F-PLACE1001395//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.98:67:34//BACTERIOPHAGE T4.//P22917

F-PLACE1001399//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.1e-32:47:74//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1001412//GLYCOPHORIN C (PAS-2') (GLYCOPROTEIN BETA) (GLPC) (GLYCOCONNECTIN) (SIALOGLYCOPROTEIN D) (GLYCOPHORIN D) (GPD).//0.00021:125:36//HOMO SAPIENS (HUMAN).//P04921

F-PLACE1001414//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//0.99:37:35//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852

F-PLACE1001440//PROLINE-RICH PEPTIDE P-B.//0.35:16:50//HOMO SAPIENS (HUMAN).//P02814

F-PLACE1001456//RELAXIN.//0.48:38:36//BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).//P11184

F-PLACE1001468//HYPOTHETICAL PROTEIN MJ0602.//0.10:86:32//METHANOCOCCUS

JANNASCHII.//Q58019

F-PLACE1001484//HYPOTHETICAL 7.5 KD PROTEIN IN DNAC-RPLI INTERGENIC REGION.//1.0:47:34//BACILLUS SUBTILIS.//P37480

F-PLACE1001502//COLLAGEN 1(X) CHAIN PRECURSOR.//0.00029:118:34//BOS TAURUS (BOVINE).//P23206

F-PLACE1001503//HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME III./2.2e-07:107:30//CAENORHABDITIS ELEGANS.//P34561

F-PLACE1001517//SMALL PROTEIN INHIBITOR OF INSECT ALPHA-AMYLASES 2 (SI ALPHA-2).//0.56:22:45//SORGHUM BICOLOR MILO (SORGHUM).//P21924

F-PLACE1001534//PUTATIVE GENE PROTEIN 54.//0.43:44:40//BACTERIOPHAGE SPO1.//048408

F-PLACE1001545//HYPOTHETICAL 7.9 KD PROTEIN IN CELF-KATE INTERGENIC REGION.//0.99:70:32//ESCHERICHIA COLI.//P37795

F-PLACE1001551//CHLOROPLAST 50S RIBOSOMAL PROTEIN L32.//1.0:66:28//MARCHANTIA POLYMORPHA (LIVERWORT).//P12196

F-PLACE1001570//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//0.024:120:27//HOMO SAPIENS (HUMAN).//Q15431

F-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.1e-30:90:78//MUS MUSCULUS (MOUSE).//Q60809

F-PLACE1001603//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.054:77:33//RATTUS NORVEGICUS (RAT).//P10164

F-PLACE1001608

F-PLACE1001610//PROBABLE E4 PROTEIN.//0.90:58:29//HUMAN PAPILLOMAVIRUS TYPE 28.//P51896

F-PLACE1001611//METALLOTHIONEIN-IG (MT-1G).//0.35:30:40//HOMO SAPIENS (HUMAN).//P13640

F-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.6e-28:144:43//HOMO SAPIENS (HUMAN).//P51523

F-PLACE1001634//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//1.0:36:41//CY

ANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//019926
 F-PLACE1001640//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.24:
 47:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P1880
 4
 F-PLACE1001672//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0:27:66//HOMO
 SAPIENS (HUMAN).//P39188
 F-PLACE1001691//HYPOTHETICAL 15.5 KD PROTEIN IN PIK1-POL2 INTERGENIC REG
 ION.//0.40:81:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53842
 F-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (E
 C 3.1.2.14) (THIOESTERASE II).//8.3e-41:103:55//RATTUS NORVEGICUS (RAT).
 //P08635
 F-PLACE1001705
 F-PLACE1001716//HYPOTHETICAL 138.5 KD PROTEIN C17H9.01 IN CHROMOSOME I./
 /6.1e-07:157:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013798
 F-PLACE1001720
 F-PLACE1001729//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//6.5e-05:196:32//M
 US MUSCULUS (MOUSE).//P05143
 F-PLACE1001739//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PR
 OTEIN) (NF-M).//0.00050:213:23//RATTUS NORVEGICUS (RAT).//P12839
 F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-17:90:56//
 HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125.//0.96:38:36//HOMO SAPIENS
 (HUMAN).//Q14138
 F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN.//0.98:23:43//LUPINUS ANGU
 STIFOLIUS (NARROW-LEAVED BLUE LUPINE).//P09930
 F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//2.9e-28:167:38
 //SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//042908
 F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.2e-43:126:77
 //HOMO SAPIENS (HUMAN).//P39189

F-PLACE1001761//50S RIBOSOMAL PROTEIN L35.//0.26:42:38//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56057

F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN.//4.8e-35:223:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48994

F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION.//9.5e-41:194:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03262

F-PLACE1001799

F-PLACE1001810

F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.8e-40:115:61//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587

F-PLACE1001821

F-PLACE1001844//IG KAPPA CHAIN V-I REGION (HAU).//0.59:89:35//HOMO SAPIENS (HUMAN).//P01600

F-PLACE1001845

F-PLACE1001869//MPA43 PROTEIN.//3.5e-14:153:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53583

F-PLACE1001897//LIGATOXIN A.//1.0:43:27//PHORADENDRON LIGA (ARGENTINE MISTLETOE).//P01540

F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C).//0.57:44:45//ASTROTIA STOKESI (STOKES'S SEA SNAKE) (DSTEIRA STOKESI).//P01381

F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEIN GP4) (GPF).//0.89:75:29//BACTERIOPHAGE NF.//P09877

F-PLACE1001928

F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180.//0.0049:51:45//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//8.9e-08:125:36//MORAXELLA CATARRHALIS.//Q49091

F-PLACE1002004

F-PLACE1002046//LIGATIN (FRAGMENT).//1.6e-84:191:84//MUS MUSCULUS (MOUSE).//Q61211

F-PLACE1002052

F-PLACE1002066

F-PLACE1002072//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.16:77:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602

F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.//4.0e-11:174:28//CAENORHABDITIS ELEGANS.//Q09564

F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//2.8e-57:112:99//HOMO SAPIENS (HUMAN).//076094

F-PLACE1002115//P8 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE A) (MTCP-1 TYPE A) (P8MTCP1).//1.0:49:30//MUS MUSCULUS (MOUSE).//Q61908

F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED) (CHX1) (IMMEDIATE EARLY RESPONSE 2 PROTEIN).//2.7e-11:118:36//MUS MUSCULUS (MOUSE).//P17950

F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MOBL 3' REGION (ORF 4).//0.0086:39:46//THIOBACILLUS FERROOXIDANS.//P20088

F-PLACE1002150

F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.4e-34:56:82//HOMO SAPIENS (HUMAN).//P39189

F-PLACE1002163//NEUROTOXIN 1.//1.0:17:52//CENTRUROIDES SCULPTURATUS (BAR K SCORPION).//P01492

F-PLACE1002170

F-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX C COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32591

F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.77:21:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

F-PLACE1002213//HISTONE H4 (FRAGMENT).//0.62:31:32//BLEPHARISMA JAPONICU

M.//P80738

F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5' REGION.//0.41:49:36//RHIZOBIUM LEGUMINOSARUM.//P14310

F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2).//0.61:95:29//CAENORHABDITIS ELEGANS.//P24890

F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SPS1-QCR7 INTERGENIC REGION.//0.99:22:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P56508

F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//0.91:18:72//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867

F-PLACE1002342//HYPOTHETICAL PROTEIN C16.//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32219

F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//6.4e-05:127:37//PLASMODIUM VIVAX.//P08677

F-PLACE1002399

F-PLACE1002433//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00094:182:25//RATTUS NORVEGICUS (RAT).//P28023

F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.5e-19:62:77//MUS MUSCULUS (MOUSE).//P41233

F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC REGION.//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04545

F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//3.9e-28:159:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749

F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-).//0.0014:148:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13765

F-PLACE1002474//FIBRILLIN 2 PRECURSOR.//2.1e-24:203:33//MUS MUSCULUS (MOUSE).//Q61555

F-PLACE1002477//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.15:65:41//HO

MO SAPIENS (HUMAN).//P39193
 F-PLACE1002493//SEMENOGELIN II PRECURSOR (SGII).//1.0:72:31//MACACA MULA
 TTA (RHESUS MACAQUE).//Q95196
 F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//2
 .9e-11:67:35//CAENORHABDITIS ELEGANS.//Q11096
 F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFL
 UX SYSTEM PROTEIN CZCD).//8.4e-11:143:32//ALCALIGENES EUTROPHUS.//P13512
 F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGI
 ON (071).//1.0:15:60//ESCHERICHIA COLI.//P46878
 F-PLACE1002529
 F-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.1e-76:183:81//MUS MUSCULUS (M
 OUSE).//P70396
 F-PLACE1002537//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-18:51:86/
 /HOMO SAPIENS (HUMAN).//P39195
 F-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//6.0e-56:140:47//DROSOPHILA MELA
 NOGASTER (FRUIT FLY).//P45890
 F-PLACE1002578
 F-PLACE1002583
 F-PLACE1002591//CORONIN-LIKE PROTEIN P57.//5.5e-26:78:69//BOS TAURUS (BO
 VINE).//Q92176
 F-PLACE1002598
 F-PLACE1002604
 F-PLACE1002625//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC RE
 GION.//6.4e-08:193:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781
 F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN).//7.1e-100:210:89//MUS
 MUSCULUS (MOUSE).//Q60604
 F-PLACE1002665//MOBILIZATION PROTEIN MOBS.//0.35:60:30//THIOBACILLUS FER
 ROOXIDANS.//P20086
 F-PLACE1002685//ACTIN BINDING PROTEIN.//0.052:115:29//SACCHAROMYCES EXIG

UUS (YEAST).//P38479

F-PLACE1002714//CIS-GOLGI MATRIX PROTEIN GM130.//1.8e-06:214:30//RATTUS NORVEGICUS (RAT).//Q62839

F-PLACE1002722//THROMBIN RECEPTOR PRECURSOR.//2.0e-19:134:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P47749

F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) (FRAGMENT).//0.43:40:35//MUS MUSCULUS (MOUSE).//P35378

F-PLACE1002772

F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5).//4.8e-07:96:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14007

F-PLACE1002782//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//1.1e-07:114:35//ALCALIGENES EUTROPHUS.//P13512

F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR.//0.0068:98:39//CAENORHABDITIS ELEGANS.//P20630

F-PLACE1002811//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//1.1e-09:137:34//MUS MUSCULUS (MOUSE).//Q60772

F-PLACE1002815//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.46:35:42//HORDEUM VULGARE (BARLEY).//P17991

F-PLACE1002816//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.0e-86:201:74//HOMO SAPIENS (HUMAN).//P56524

F-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.6e-30:54:96//HOMO SAPIENS (HUMAN).//P51522

F-PLACE1002839//METALLOTHIONEIN-I (MT-I).//1.0:43:37//MUS MUSCULUS (MOUSE).//P02802

F-PLACE1002851//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI).//0.77:35:37//VICIA ANGUSTIFOLIA (COMMON VETCH).//P01065

F-PLACE1002853//HYPOTHETICAL 7.9 KD PROTEIN IN PE 5' REGION (ORF1).//1.0:
18:55//LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMNPV).
//P36866

F-PLACE1002881//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.1e-27:91:70//
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1002908//HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III.
//2.0e-31:148:46//CAENORHABDITIS ELEGANS.//P34548

F-PLACE1002941//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-11:40:85/
/HOMO SAPIENS (HUMAN).//P39195

F-PLACE1002962//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//0.90:38:36//C
ANIS FAMILIARIS (DOG).//P13206

F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT).//0.97:26:
38//TITYUS SERRULATUS (BRAZILIAN SCORPION).//P01496

F-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//3.3e-20:120:41//METHANOC
OCCUS JANNASCHII.//Q58560

F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REG
ION (F158).//0.00045:93:23//ESCHERICHIA COLI.//P52121

F-PLACE1002996//PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATED CLON
E 22 HOMOLOG).//0.17:91:29//GALLUS GALLUS (CHICKEN).//Q91012

F-PLACE1003025//SUPPRESSOR PROTEIN SRP40.//0.0079:214:24//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32583

F-PLACE1003027//HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME II
I.//1.3e-49:167:63//CAENORHABDITIS ELEGANS.//P34609

F-PLACE1003044//SPORE COAT PROTEIN D.//0.97:24:45//BACILLUS SUBTILIS.//P
07791

F-PLACE1003045

F-PLACE1003092

F-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//3.9e-51:188:57//HOMO SAPIENS
(HUMAN).//Q13268

F-PLACE1003108

F-PLACE1003136

F-PLACE1003145//BUTYROPHILIN PRECURSOR (BT).//0.00024:170:24//BOS TAURUS
(BOVINE).//P18892

F-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT).//1.0:32:37//LOCUSTA MIGRAT
ORIA (MIGRATORY LOCUST).//Q01777

F-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBI
QUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//6.3e-05:54:
38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743

F-PLACE1003176//HYPOTHETICAL 62.3 KD PROTEIN IN PCS60-ABD1 INTERGENIC RE
GION.//0.24:74:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38319

F-PLACE1003190//SQF1 PROTEIN.//1.0e-52:158:41//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P33750

F-PLACE1003200

F-PLACE1003205//SPERM PROTAMINE P1.//0.074:20:45//CAENOLESTES FULIGINOSU
S.//P42131

F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//0.013:20:
55//HOMO SAPIENS (HUMAN).//Q15391

F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125.//0.98:48:37//HOMO SAPIENS
(HUMAN).//Q14138

F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SHAKER P
EPTIDE).//0.84:53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE).//P01522

F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//4.1e-18:70:47//CAEN
ORHABDITIS ELEGANS.//P21541

F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE.//0.063:160:24//HOMO SA
PIENS (HUMAN).//P11277

F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//9.4e
-69:84:94//HOMO SAPIENS (HUMAN).//P51522

F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDI

NG PROTEIN).//0.029:125:24//RATTUS NORVEGICUS (RAT).//Q63083
 F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.97:44:40//DROSOP
 HILA MELANOGASTER (FRUIT FLY).//Q01643
 F-PLACE1003343//GENE 11 PROTEIN.//1.0:37:37//SPIROPLASMA VIRUS SPV1-R8A2
 B.//P15902
 F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2).//6.4e
 -05:69:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87378
 F-PLACE1003361//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.6e-23:66:75/
 /HOMO SAPIENS (HUMAN).//P39192
 F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1.//0.62:19:57//HOMO SAPIEN
 S (HUMAN).//P35326
 F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.3e-06:102:
 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE).//Q0272
 2
 F-PLACE1003375//OLFACTORY RECEPTOR 11 (M49) (FRAGMENT).//0.99:46:34//MUS
 MUSCULUS (MOUSE).//Q60890
 F-PLACE1003383
 F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTUS NORV
 EGICUS (RAT).//P35287
 F-PLACE1003401
 F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//8.1e-17:138:37/
 /SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556
 F-PLACE1003454
 F-PLACE1003478
 F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:123:32//
 HOMO SAPIENS (HUMAN).//Q13201
 F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68:76//HO
 MO SAPIENS (HUMAN).//P08547

F-PLACE1003519//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.2e-17:77:50//
HOMO SAPIENS (HUMAN).//P39188
F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWLPOX VIR
US (ISOLATE HP-438 [MUNICH]).//P14366
F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:32:40/
/XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931
F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q01436
F-PLACE1003553
F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWLPOX VIR
US (ISOLATE HP-438 [MUNICH]).//P14366
F-PLACE1003575
F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAVIRUS T
YPE 35.//P27226
F-PLACE1003584
F-PLACE1003592//EXCISIONASE.//0.26:19:52//BACTERIOPHAGE PHI-80.//P05998
F-PLACE1003593//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:30//
OVIS ARIES (SHEEP).//078751
F-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//6.3e-8
7:238:67//CAENORHABDITIS ELEGANS.//P46975
F-PLACE1003602//HYPOTHETICAL 11.0 KD PROTEIN IN FAA3-MAS3 INTERGENIC REG
ION.//8.4e-17:98:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40554
F-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//2.0e-09:82:35//SACCHARO
MYCES CEREVISIAE (BAKER'S YEAST).//Q02516
F-PLACE1003611//PANCREATIC SECRETORY TRYPSIN INHIBITOR.//0.99:32:43//CAN
IS FAMILIARIS (DOG).//P04542
F-PLACE1003618//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:229:58//H
OMO SAPIENS (HUMAN).//P08547
F-PLACE1003625//30S RIBOSOMAL PROTEIN S20 (FRAGMENT).//1.0:56:26//PROTEU
S MIRABILIS.//P42275

F-PLACE1003638//PROTEIN Q300.//0.079:41:39//MUS MUSCULUS (MOUSE).//Q0272

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F-PLACE1003669//TRICHOHYALIN.//2.9e-07:180:30//OVIS ARIES (SHEEP).//P227

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F-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//3.3e-16:98:40//HOMO SAPIENS (HUMAN).//Q08170

F-PLACE1003709//HYPOTHETICAL 59.5 KD PROTEIN IN CCT3-CCT8 INTERGENIC REGION.//2.8e-07:128:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47074

F-PLACE1003711//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-IV).//5.0e-05:88:30//TRITICUM AESTIVUM (WHEAT).//P04724

F-PLACE1003723//TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70).//6.0e-06:98:36//MUS MUSCULUS (MOUSE).//Q62270

F-PLACE1003738//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//2.5e-45:147:46//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749

F-PLACE1003760//CYTOCHROME B (EC 1.10.2.2).//0.91:49:34//TRYPANOSOMA BRUCEI BRUCEI.//P00164

F-PLACE1003762//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.98:28:32//MALUS DOMESTICA (APPLE) (MALUS SYLVESTRIS).//O24058

F-PLACE1003768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.5e-19:123:37//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1003771

F-PLACE1003783//SRY-RELATED PROTEIN ADW2 (FRAGMENT).//1.0:29:37//ALLIGATOR MISSISSIPPIENSIS (AMERICAN ALLIGATOR).//P40634

F-PLACE1003784//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//1.2e-13:199:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-PLACE1003795//EC PROTEIN I/II (ZINC-METALLOTHIONEIN CLASS II).//0.67:53:30//TRITICUM AESTIVUM (WHEAT).//P30569

F-PLACE1003833//METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9).//0.99:158:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P43523

F-PLACE1003850

F-PLACE1003858//HUNCHBACK PROTEIN (FRAGMENT).//0.37:28:42//LITHOBIUS FOR
FICATUS.//Q02030

F-PLACE1003864//OUTER MEMBRANE LIPOPROTEIN LOLB PRECURSOR.//0.0046:116:3
1//ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS ACTINOMYCETEMCOMITA
NS).//052727

F-PLACE1003870

F-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A
DENYLYLTRANSFERASE) (FRAGMENT).//1.6e-92:166:75//HOMO SAPIENS (HUMAN).//
P51003

F-PLACE1003886//IMMEDIATE-EARLY PROTEIN IE180.//0.54:96:34//PSEUDORABIES
VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS
E DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III
) (FRAGMENT).//8.8e-54:260:46//BOS TAURUS (BOVINE).//P10895

F-PLACE1003892//PROBABLE E5 PROTEIN.//1.0:13:61//HUMAN PAPILLOMAVIRUS TY
PE 18.//P06792

F-PLACE1003900//BETA-FRUCTOFURANOSIDASE, SOLUBLE ISOENZYME I (EC 3.2.1.2
6) (SUCROSE-6- PHOSPHATE HYDROLASE) (INVERTASE) (FRAGMENTS).//0.58:49:36
//DAUCUS CAROTA (CARROT).//P80065

F-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYN
THETASE).//3.8e-52:92:85//HOMO SAPIENS (HUMAN).//P17812

F-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.
19) (ARGININE- -TRNA LIGASE) (ARGRS).//2.6e-26:202:36//SACCHAROMYCES CER
EVISIAE (BAKER'S YEAST).//Q05506

F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA
LIGASE) (HISRS).//0.94:65:29//STREPTOCOCCUS EQUISIMILIS.//P30053

F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC RE
GION.//0.098:79:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53074

F-PLACE1003936

F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//4.7e-68:164:78//RATTUS NORVEGICUS (RAT).//P80385

F-PLACE1004103//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.9e-14:60:73//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5.//0.020:202:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P89102

F-PLACE1004114//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-15:69:60//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1004118//REGULATORY PROTEIN E2.//0.73:58:36//CANINE ORAL PAPILLOMAVIRUS (COPV).//Q89420

F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//7.7e-62:108:100//MUS MUSCULUS (MOUSE).//P29387

F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN.//0.0011:73:42//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33485

F-PLACE1004156//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.00061:39:48//OWENIA FUSIFORMIS.//P21260

F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT).//0.033:108:27//STREPTOCOCCUS PYOGENES.//P49054

F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC REGION.//4.0e-07:146:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38817

F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//5.9e-11:208:27//MUS MUSCULUS (MOUSE).//Q62556

F-PLACE1004203//PROTEIN A39.//8.5e-18:139:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062

F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//1.0:28:42//PISUM SATIVUM (GARDEN PEA).//P13555

F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D).//0.73:134:25//CAENORHABDITIS ELEGANS.//P02567

F-PLACE1004257//HYPOTHETICAL PROTEIN HI0490.//0.13:75:29//HAEMOPHILUS IN
FLUENZAE.//P44006

F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRA
GMENT).//0.027:128:35//HOMO SAPIENS (HUMAN).//P25067

F-PLACE1004270//LARGE TEGUMENT PROTEIN.//1.8e-10:100:44//EPSTEIN-BARR VI
RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03186

F-PLACE1004274//HYPOTHETICAL PROTEIN E-95.//0.44:61:42//HUMAN ADENOVIRUS
TYPE 2.//P03286

F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:55:38//
BOS TAURUS (BOVINE).//P25508

F-PLACE1004284//7 KD PROTEIN (ORF 4).//1.0:63:23//CHRYSANTHEMUM VIRUS B
(CVB).//P37990

F-PLACE1004289//SPERM PROTAMINE P3.//0.00057:22:77//MUS MUSCULUS (MOUSE)
.//Q62100

F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-).//0.00
65:148:29//STREPTOMYCES COELICOLOR.//P54741

F-PLACE1004316//AUTOPHAGY PROTEIN APG5.//8.8e-06:117:29//SACCHAROMYCES C
EREVISIAE (BAKER'S YEAST).//Q12380

F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0027:83:36//HOM
O SAPIENS (HUMAN).//P53420

F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.9e-05:200:33/
/GALLUS GALLUS (CHICKEN).//P02457

F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN MST101(2).//2.4e-05:179:29//D
ROSOPHILA HYDEI (FRUIT FLY).//Q08696

F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.6e-28:46:76/
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REG
ION.//5.7e-34:202:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722

F-PLACE1004405//NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMI